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(71) Applicant *(for all designated States except US)*: PHAGETECH, INC. [CA/CA]; Place du Parc, Case Postale 387, Montreal H2W 2N9 (CA).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: PELLETIER, Jerry [CA/CA]; 8 Lakeview, Baie D'Urfe, Quebec H9X 3B1 (CA). GROS, Phillippe [CA/CA]; 107 Montrose, St. Lambert, Quebec J4R 1X4 (CA). DUBOW, Michael [CA/CA]; 4901 Coolbrook Avenue, Montreal, Quebec H3X 2K8 (CA).

(74) Agents: MORROW, Joy, D. et al.; Smart & Biggar, 900 – 55 Metcalfe Street, P.O. Box 2999, Station D, Ottawa, Ontario K1P 5Y6 (CA).

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(54) Title: DEVELOPMENT OF NOVEL ANTI-MICROBIAL AGENTS BASED ON BACTERIOPHAGE GENOMICS

(57) Abstract

A method for identifying suitable targets for antibacterial agents based on identifying targets of bacteriophage-encoded proteins is described. Also described are compositions useful in the identification methods and in inhibiting bacterial growth, and methods for preparing and using such compositions.

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DESCRIPTION

Development of Novel Anti-Microbial Agents Based on Bacteriophage Genomics

BACKGROUND OF THE INVENTION

The present invention relates to the field of antibacterial agents and the treatment of infections of animals or other complex organisms by bacteria.

The frequency and spectrum of antibiotic-resistant infections have, in recent years, increased in both the hospital and community. Certain infections have become essentially untreatable and are growing to epidemic proportions in the developing world as well as in institutional settings in the developed world. The staggering spread of antibiotic resistance in pathogenic bacteria has been attributed to microbial genetic characteristics, widespread use of antibiotic drugs, and changes in society that enhance the transmission of drug-resistant organisms. This spread of drug resistant microbes is leading to ever increasing morbidity, mortality and health-care costs.

Ironically, it is the very success of antibiotics, resulting in their widespread use, that has contributed the most to rising numbers of drug resistant bacterial strains. The longer a bacterial strain is exposed to a drug, the more likely it is to acquire resistance. Today, a total of 160 antibiotics, all based on a few basic chemical structures and targeting a small number of metabolic pathways, have found their way to market. Over-prescription of these drugs, as well as the failure of patients to comply with the complete antibiotic regimen, has lead to the rapid emergence of antibiotic resistant strains. Such misuse of prescriptions, careless use of antibiotics in virtually all commercial production of beef and fowl, and changing societal conditions, such as the growth of day-care centers, increased long-term care in hospitals, and increased mobility of the population, has provided an environment where drug-resistant microbes can emerge and spread. Thus, virtually all common infectious bacteria are becoming, or have already become, resistant to one or more groups of antibiotics. Such resistance now reaches all classes of antibiotics currently in use, including: β-lactams, fluoroquinolones, aminoglycosides, macrolide peptides, chloramphenicol, tetracyclines, rifampicin, folate inhibitors, glycopeptides, and mupirocin.

Over the last 45 years bacteria have adapted genetically to avoid the destruction/alteration of the essential pathways that these chemotherapeutic agents

target. Antibiotic resistant bacterial strains are now emerging at a higher rate than the rate at which new antibiotics are being developed. The consequence of this dilemma has been a dramatic increase in the cost of treating infections what would otherwise easily succumb to routine antibiotic therapy. Furthermore, and perhaps most importantly, the emergence of multiple drug resistant pathogenic bacteria has led to a significant increase in morbidity and mortality, particularly in institutional settings.

Most major pharmaceutical companies have on-going drug discovery programs for novel anti-microbials. These are based on screens for small molecule inhibitors (natural products, bacterial culture media, libraries of small molecules, combinatorial chemistry) of crucial metabolic pathways of the micro-organism of interest (*e.g.*, bacteria, fungi, parasites, worms). The screening process is largely for cytotoxic compounds and in most cases is not based on a known mechanism of action of the compounds. Pharmaceutical companies have large programs in this area. Classical drug screening programs are being exhausted and many of these pharmaceutical companies are looking towards rational drug design programs.

Several small to mid-size biotechnology companies as well as large pharmaceutical companies have developed systematic high-throughput sequencing programs to decipher the genetic code of specific micro-organisms of interest. The goal is to identify, through sequencing, unique biochemical pathways or intermediates that are unique to the microorganism. Knowledge of this may, in turn, form the rationale for a drug discovery program based on the mechanism of action of the identified enzymes/proteins. Genome Therapeutics Corp., The Institute for Genome Research, Human Genome Sciences Inc., and other companies have such sequencing programs in place. However, one of the most critical steps in this approach is the ascertainment that the identified proteins and biochemical pathways are 1) non-redundant and essential for bacterial survival, and 2) constitute suitable and accessible targets for drug discovery.

SUMMARY OF THE INVENTION

While animals such as humans are, on occasion, infected by pathogenic bacteria, bacteria also have natural enemies. A number of host-specific viruses, known as bacteriophages or phages, infect and kill bacteria in the natural environment. Such bacteriophages generally have small compact genomes and bacteria are their exclusive hosts. Many known bacteria are host to a large number of bacteriophages that have been described in the literature. During the 1940's - 1960's, phage biology was an area of active research. As a testimony to this, the study of phages which infect and inhibit the enteric bacterium *Escherichia coli* (*E. coli*) contributed much to the early understanding of molecular biology and virology.

As is generally understood, bacteriophage (or phages) are viruses that infect and kill bacteria. They are natural enemies of bacteria and, over the course of evolution, have developed proteins (products of DNA sequences) which enable them to infect a host bacteria, replicate their genetic material, usurp host metabolism, and ultimately kill their host. The scientific literature well documents the fact that many known bacteria have a large number of such bacteriophages (Ackermann and DuBow, 1987) that can infect and kill them (for example, see the ATCC bacteriophage collection at http://www.atcc.org).

This invention utilizes the observation that bacteriophages successfully infect and inhibit or kill host bacteria, targeting a variety of normal host metabolic and physiological traits, some of which are shared by all bacteria, pathogenic and nonpathogenic alike. The term "pathogenic" as used herein denotes a contribution to or implication in disease or a morbid state of an infected organism. The invention thus involves identifying and elucidating the molecular mechanisms by which phages interfere with host bacterial metabolism, an objective being to provide novel targets for drug design. Whether the phage blocks bacterial RNA transcription or translation, or attacks other important metabolic pathways, such as cell wall assembly or membrane integrity, the basic blueprint for a phage's bacteria-inhibiting ability is encoded in its genome and can be unlocked using bioinformatics, functional genomics, and proteomics. By these means, the invention utilizes sequence information from the genomics of bacteriophage to identify novel antimicrobials that can be further used to actively and/or prophylactically treat bacterial infection.

Two important components of the invention thus are: i) the identification of bacteria-inhibiting phage open reading frames ("ORF"s) and corresponding products that can be used to develop antibiotics based on amino acid sequence and secondary structural characteristics of the ORF products, and ii) the use of bacteriophages to map

out essential bacterial target genes and homologs, which can in turn lead to the development of suitable anti-microbial agents. These two avenues represent new and general methods for developing novel antimicrobials.

The invention thus concerns the identification of bacteriophage ORFs that supply bacteria-inhibiting functions. In this regard, use of the terms "inhibit", "inhibition", "inhibitory", and "inhibitor" all refer to a function of reducing a biological activity or function. Such reduction in activity or function can, for example, be in connection with a cellular component, *e.g.*, an enzyme, or in connection with a cellular process, *e.g.*, synthesis of a particular protein, or in connection with an overall process of a cell, *e.g.*, cell growth. In reference to bacterial cell growth, for example, an inhibitory effect (i.e., a bacteria-inhibiting effect) may be bacteriocidal (killing of bacterial cells) or bacteriostatic (i.e., stopping or at least slowing bacterial cell growth). The latter slows or prevents cell growth such that fewer cells of the strain are produced relative to uninhibited cells over a given period of time. From a molecular standpoint, such inhibition may equate with a reduction in the level of, or elimination of, the transcription and/or translation of a specific bacterial target(s), or reduction or elimination of activity of a particular target biomolecule.

It is particularly advantageous to evaluate a plurality of different phage ORFs for inhibitory activity that may be from one, but is preferably from a plurality of different phage. For example, evaluating ORFs from a number of different phage of the same bacterial host provides at least two advantages. One is that the multiple phages will provide identification of a variety of different targets. Second, it is likely that multiple phage will utilize the same cellular target

As used herein, the terms "bacteriophage" and "phage" are used interchangeably to refer to a virus which can infect a bacterial strain or a number of different bacterial strains.

In the context of this invention, the term "bacteriophage ORF" or ""phage ORF" or similar term refers to a nucleotide sequence in or from a bacteriophage. In connection with a particular ORF, the terms refer an open reading frame which has at least 95% sequence identity, preferably at least 97% sequence identity, more preferably at least 98% sequence identity with an ORF from the particular phage identified herein (e.g., with an ORF as identified herein) or to a nucleic acid sequence which has the specified sequence identify percentage with such an ORF sequence.

A first aspect of the invention thus provides a method for identifying a bacteriophage nucleic acid coding region encoding a product active on an essential bacterial target by identifying a nucleic acid sequence encoding a gene product which

provides a bacteria-inhibiting function when the bacteriophage infects a host bacterium, preferably one that is an animal or plant pathogen, more preferably a bird or mammalian pathogen, and most preferably a human pathogen. The bacteriophage is an uncharacterized bacteriophage. Thus, the method excludes, for example, phage λ, ϕx174, m13 and other *E.coli*-specific bacteriophage that have been studied with respect to gene number and/or function. It also excludes, for example, the nucleic acid coding regions described in Tables 12-14, and in preferred embodiments, excludes the phage in which those regions are naturally located.

In connection with bacteriophage, the term "uncharacterized" means that a certain bacteriophage's genome has not yet been fully identified such that the genes having function involved in inhibiting host cells have not been identified. In particular, phage for which the description of genomic or protein sequence was first provided herein are uncharacterized. Phage sequences for which host bacteria-inhibiting functions have been identified prior to the filing of the present application (or alternatively prior to the present invention) are specifically excluded from the aspects involving utilization of sequences from uncharacterized bacteriophage, except that aspects may involve a plurality of phage where one or more of those phage are uncharacterized and one or more others have been characterized to some extent. A number of different bacteria-inhibiting phage ORFs are indicated in Tables 11-14. The phage ORFs or sequences identified therein are not within the term "uncharacterized; alternatively, in preferred embodiments the phage containing those ORFs are excluded from this term. Further, any additional phage ORFs (or alternatively the phage which contain those ORFs) which have previously been described in the art as bacteria-inhibiting ORFs are expressly excluded; those ORFs or phage are known to those skilled in the art and the exclusion can be made express by specifically naming such ORFs or phage as needed (likewise for uncharacterized targets as described below). For the sake of brevity, such a listing is not expressly presented, as such information is readily available to those skilled in the art.

Stating that an agent or compound is "active on" a particular cellular target, such as the product of a particular gene, means that the target is an important part of a cellular pathway which includes that target and that the agent acts on that pathway. Thus, in some cases the agent may act on a component upstream or downstream of the stated target, including on a regulator of that pathway or a component of that pathway.

By "essential", in connection with a gene or gene product, is meant that the host cannot survive without, or is significantly growth compromised, in the absence depletion, or alteration of functional product. An "essential gene" is thus one that encodes a product that is beneficial, or preferably necessary, for cellular growth *in*

vitro in a medium appropriate for growth of a strain having a wild-type allele corresponding to the particular gene in question. Therefore, if an essential gene is inactivated or inhibited, that cell will grow significantly more slowly, preferably less than 20%, more preferably less than 10%, most preferably less than 5% of the growth rate of the uninhibited wild-type, or not at all, in the growth medium. Preferably, in the absence of activity provided by a product of the gene, the cell will not grow at all or will be non-viable, at least under culture conditions similar to the *in vivo* conditions normally encountered by the bacterial cell during an infection. For example, absence of the biological activity of certain enzymes involved in bacterial cell wall synthesis can result in the lysis of cells under normal osmotic conditions, even though protoplasts can be maintained under controlled osmotic conditions. In the context of the invention, essential genes are generally the preferred targets of antimicrobial agents. Essential genes can encode target molecules directly or can encode a product involved in the production, modification, or maintenance of a target molecule.

A "target" refers to a biomolecule that can be acted on by an exogenous agent, thereby modulating, preferably inhibiting, growth or viability of a cell. In most cases such a target will be a nucleic acid sequence or molecule, or a polypeptide or protein. However, other types of biomolecules can also be targets, *e.g.*, membrane lipids and cell wall structural components.

The term "bacterium" refers to a single bacterial strain, and includes a single cell, and a plurality or population of cells of that strain unless clearly indicated to the contrary. In reference to bacteria or bacteriophage, the term "strain" refers to bacteria or phage having a particular genetic content. The genetic content includes genomic content as well as recombinant vectors. Thus, for example, two otherwise identical bacterial cells would represent different strains if each contained a vector, *e.g.*, a plasmid, with different phage ORF inserts.

In preferred embodiments, the phage is *Staphylococcus aureus* phage 77, 3A, 96, or 44 AHJD, *Enterococcus* sp. phage 182, or *Streptococcus pneumoniae* phage Dp-1.

In preferred embodiments, the phage is selected from. Preferred embodiments involve expressing at least one recombinant phage ORF(s) in a bacterial host followed by inhibition analysis of that host. Inhibition following expression of the phage ORF is indicative that the product of the ORF is active on an essential bacterial target. Such evaluation can be carried out in a variety of different formats, such as on a support matrix such as a solidified medium in a petri dish, or in liquid culture.

Preferably a plurality of phage ORFs are expressed in at least one bacterium. The plurality of phage ORFs can be from one or a plurality of phage. With respect to a single phage or at least one phage in a plurality of phages, the plurality of expressed ORFs preferably represents at least 10%, more preferably at least 20%, 40%, or 60%, still more preferably at least 80% or 90%, and most preferably at least 95% of the ORFs in the phage genome. Preferably, for a plurality of phage, the plurality of expressed ORFs preferably represents at least 10%, more preferably at least 20%, 40%, or 60%, still more preferably at least 80% or 90%, and most preferably at least 95% of the ORFs in the phage genome of each phage. The plurality of phage ORFs can be expressed in a single bacterium, or in a plurality of bacteria where one ORF is expressed in each bacterium, or in a plurality of bacteria where a plurality of ORFs are expressed in at least one or in all of the plurality of bacteria, or combinations of these.

In embodiments of the above aspect (as well as in other aspects herein) in which a plurality of phage are utilized, a plurality of phage have the same bacterial host species; have different bacterial host species; or both. The plurality of phage includes at least two different phage, preferably at least 3,4,5,6,8,10,15,20, or more different phage. Indeed, more preferably, the plurality of phage will include 50, 75, 100, or more phage. As described herein, the larger number of phage is useful to provide additional target and target evaluation information useful in developing antibacterial agents, for example, by providing identification of a larger range of bacterial targets, and/or providing further indication of the suitability of a particular target (for example, utilization of a target by a number of different unrelated phage can suggest that the target is particularly stable and accessible and effective) and/or can indicate alternate sites on a target which interact with different inhibitors.

Further embodiments involve confirmation of the inhibitor function of the phage ORF, such as by utilizing or incorporating a control(s) designed to confirm the inhibitory nature of the ORF(s) being evaluated. The control can, for example, be provided by expression of an inactive or partially inactive form of the ORF or ORF product, and/or by the absence of expression of the ORF or ORF product in the same or a closely comparable bacterial strain as that used for expression of the test ORF. The reduced level of activity or the absence of active ORF product in the control will thus not provide the inhibition provided by a corresponding inhibitory ORF, or will provide a distinguishably lower level of inhibition. An inactivated or partially inactivated control has a mutation(s), *e.g.*, in the coding region or in flanking regulatory elements, that reduce(s) or eliminate(s) the normal function of the ORF. Thus, the inhibition of a bacterium following expression of a phage ORF is determined by comparison with the effects of expression of an inactivated ORF or the

response of the bacteria in the absence of expression in the same or similar type bacterium. Such determination of inhibition of the bacterium following expression of the ORF is indicative of a bacteria-inhibiting function. These manipulations are routinely understood and accomplished by those of skill in the art using standard techniques. In embodiments utilizing absence of expression of the ORF, the bacteria can, for example, contain an empty vector or a vector which allows expression of an unrelated sequence which is preferably non-inhibitory. Alternatively, the bacteria may have no vector at all. Combinations of such controls or other controls may also be utilized as recognized by those skilled in the art.

In embodiments involving expression of a phage ORF in a bacterial strain, in preferred embodiments that expression is inducible.

By "inducible" is meant that expression is absent or occurs at a low level until the occurrence of an appropriate environmental stimulus provides otherwise. For the present invention such induction is preferably controlled by an artificial environmental change, such as by contacting a bacterial strain population with an inducing compound (*i.e.*, an inducer). However, induction could also occur, for example, in response to build-up of a compound produced by the bacteria in the bacterial culture, *e.g.*, in the medium. As uncontrolled or constitutive expression of inhibitory ORFs can severely compromise bacteria to the point of eradication, such expression is therefore undesirable in many cases because it would prevent effective evaluation of the strain and inhibitor being studied. For example, such uncontrolled expression could prevent any growth of the strain following insertion of a recombinant ORF, thus preventing determination of effective transfection or transformation. A controlled or inducible expression is therefore advantageous and is generally provided through the provision of suitable regulatory elements, *e.g.*, promoter/operator sequences that can be conveniently transcriptionally linked to a coding sequence to be evaluated. In most cases, the vector will also contain sequences suitable for efficient replication of the vector in the same or different host cells and/or sequences allowing selection of cells containing the vector, *i.e.*, "selectable markers." Further, preferred vectors include convenient primer sequences flanking the cloning region from which PCR and/or sequencing may be performed.

As knowledge of the nucleotide sequence of phage ORFs is useful, *e.g.*, for assisting in the identification of phage proteins active against essential bacterial host targets, preferred embodiments involve the sequencing of at least a portion of the phage genome in combination with the above methods. This can be done either before or after or independent of expression and inhibition of the ORF in the bacteria, and provides information on the nature and characteristics of the ORF. Such a portion is

preferably at least 10%, 20%, 40%, 80%, 90%, or 100% of the phage genome. For embodiments in which a plurality of phage are utilized, preferably each phage is sequenced to an extent as just specified.

Such sequencing is preferably accompanied by computer sequence analysis to define and evaluate ORF(s), ORF products, structural motifs or functional properties of ORF products, and/or their genetic control elements. Thus, certain embodiments incorporate computer sequence analyses or nucleic acid and/or amino acid sequences. Further, existing data banks can provide phage sequence and product information which can be utilized for analysis and identification of ORFs in the sequence. Computer analysis may further employ known homologous sequences from other species that suggest or indicate conserved underlying biochemical function(s) for the inhibitory or potentially inhibitory ORF sequence(s) being evaluated. This can include the sequences of signature motifs of identified classes of inhibitors.

In the context of the phage nucleic acid sequences, e.g., gene sequences, of this invention, the terms "homolog" and "homologous" denote nucleotide sequences from different bacteria or phage strains or species or from other types of organisms that have significantly related nucleotide sequences, and consequently significantly related encoded gene products, preferably having related function. Homologous gene sequences or coding sequences have at least 70% sequence identity (as defined by the maximal base match in a computer-generated alignment of two or more nucleic acid sequences) over at least one sequence window of 48 nucleotides, more preferably at least 80 or 85%, still more preferably at least 90%, and most preferably at least 95%. The polypeptide products of homologous genes have at least 35% amino acid sequence identity over at least one sequence window of 18 amino acid residues, more preferably at least 40%, still more preferably at least 50% or 60%, and most preferably at least 70%, 80%, or 90%. Preferably, the homologous gene product is also a functional homolog, meaning that the homolog will functionally complement one or more biological activities of the product being compared. For nucleotide or amino acid sequence comparisons where a homology is defined by a % sequence identity, the percentage is determined using BLAST programs (with default parameters (Altschul et al., 1997, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs, Nucleic Acid Res. 25:3389-3402). Any of a variety of algorithms known in the art which provide comparable results can also be used, preferably using default parameters. Performance characteristics for three different algorithms in homology searching is described in Salamov et al., 1999, "Combining sensitive database searches with multiple intermediates to detect distant

homologues." *Protein Eng.* 12:95-100. Another exemplary program package is the GCG™ package from the University of Wisconsin.

Homologs may also or in addition be characterized by the ability of two complementary nucleic acid strands to hybridize to each other under appropriately stringent conditions. Hybridizations are typically and preferably conducted with probe-length nucleic acid molecules, preferably 20-100 nucleotides in length. Those skilled in the art understand how to estimate and adjust the stringency of hybridization conditions such that sequences having at least a desired level of complementarity will stably hybridize, while those having lower complementarity will not. For examples of hybridization conditions and parameters, see, *e.g.*,. Maniatis, T. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor University Press, Cold Spring, N.Y.; Ausubel, F.M. et al. (1994) Current Protocols in Molecular Biology. John Wiley & Sons, Secaucus, N.J. Homologs and homologous gene sequences may thus be identified using any nucleic acid sequence of interest, including the phage ORFs and bacterial target genes of the present invention.

A typical hybridization, for example, utilizes, besides the labeled probe of interest, a salt solution such as 6xSSC (NaCl and Sodium Citrate base) to stabilize nucleic acid strand interaction, a mild detergent such as 0.5% SDS, together with other typical additives such as Denhardt's solution and salmon sperm DNA. The solution is added to the immobilized sequence to be probed and incubated at suitable temperatures to preferably permit specific binding while minimizing nonspecific binding. The temperature of the incubations and ensuing washes is critical to the success and clarity of the hybridization. Stringent conditions employ relatively higher temperatures, lower salt concentrations, and/or more detergent than do non-stringent conditions. Hybridization temperatures also depend on the length, complementarity level, and nature (ie, "GC content") of the sequences to be tested. Typical stringent hybridizations and washes are conducted at temperatures of at least 40°C, while lower stringency hybridizations and washes are typically conducted at 37°C down to room temperature (~25°C). One of skill in the art is aware that these conditions may vary according to the parameters indicated above, and that certain additives such as formamide and dextran sulphate may also be added to affect the conditions.

By "stringent hybridization conditions" is meant hybridization conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4, pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart's solution at 42°C overnight; washing with 2X SSC, 0.1% SDS at 45°C; and washing with 0.2X SSC, 0.1% SDS at 45°C.

In sequence comparison analyses, an ORF, or motif, or set of motifs in a bacteriophage sequence can be compared to known inhibitor sequences, *e.g.*, homologous sequences encoding homologous inhibitors of bacterial function. Likewise, the analysis can include comparison with the structure of essential bacterial gene products, as structural similarities can be indicative of similar or replacement biological function. Such analysis can include the identification of a signature, or characteristic motif(s) of an inhibitor or inhibitor class.

Also, the identification of structural motifs in an encoded product, based on nucleotide or amino acid sequence analysis, can be used to infer a biochemical function for the product. A database containing identified structural motifs in a large number of sequences is available for identification of motifs in phage sequences. The database is PROSITE, which is available at www.expasy.ch/cgi~bin/scanprosite. The identification of motifs can, for example, include the identification of signature motifs for a class or classes of inhibitory proteins. Other such databases may also be used.

In aspects and preferred embodiments described herein, in which a bacterium or host bacterium is specified, the bacterium or host bacterium is preferably selected from a pathogenic bacterial species, for example, one selected from Table 1. Preferably, an animal or plant pathogen is used. For animals, preferably the bacterium is a bird or mammalian pathogen, still more preferably a human pathogen.

In aspects and preferred embodiments involving a bacteriophage or sequences from a bacteriophage, one or more bacteriophage are preferably selected from those listed in Table 1. Those exemplary bacteriophge are readily obtained from the indicated sources.

In some cases, it is advantageous to utilize phage with non-pathogenic host bacteria. The genome, structural motif, ORF, homolog, and other analyses described herein can be performed on such phage and bacteria. Such analysis provides useful information and compositions. The results of such analyses can also be utilized in aspects of the present invention to identify homologous ORFs, especially inhibitor ORFs in phage with pathogenic bacterial hosts. Similarly, identification of a target in a non-pathogenic host can be used to identify homologous sequences and targets in pathogenic bacteria, especially in genetically closely related bacteria. Those skilled in the art are familiar with bacterial genetic relationships and with how to determine relatedness based on levels of genomic identity or other measures of nucleotide sequence and/or amino acid sequence similarity, and/or other physical and culture characteristics such as morphology, nutritional requirements, or minimal media to support growth.

Also in preferred embodiments, an embodiments of this aspect is combined with an embodiment of the following aspect.

A related aspect of the invention provides methods for identifying a target for antibacterial agents by identifying the bacterial target(s) of at least one uncharacterized or untargeted inhibitor protein or RNA from a bacteriophage. Such identification allows the development of antibacterial agents active on such targets. Preferred embodiments for identifying such targets involve the identification of binding of target and phage ORF products to one another. The phage ORF products may be subportions of a larger ORF product that also binds the host target. In preferred embodiments, the phage protein or RNA is from an uncharacterized bacteriophage in Table 1. This aspect preferably includes the identification of a plurality of such targets in one or a plurality of different bacteria, preferably in one or a plurality of bacteria listed in Table 1.

In preferred embodiments of this aspect and other aspects of this invention involving particular phage ORFs or phage sequences, the ORF is *Staphylococcus aureus* phage 77 ORF 17, 19, 43, 102, 104, or 182 as identified in U.S. application 09/407,804, *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

As indicated for the above aspect, preferably the method involves the use of a plurality of different phage, and thus a plurality of different phage inhibitors and/or inhibitor ORFs.

In addition to uncharacteized phage ORF products, it is also useful to identify the targets of phage ORF products which are known to be inhibitors of host bacteria, but where the target has not been identified. Thus, such inhibitors can likewise be utilized as "untargeted" inhibitor phage ORFs and ORF products, *e.g.*, proteins or RNAs.

In the context of inhibitor proteins or RNAs from a phage, the term "uncharacterized" means that a bacteria-inhibiting function for the protein has not previously been identified. Preferably, but not necessarily, the sequence of the protein or the corresponding coding region or ORF was not described in the art before the filing of the present application for patent (or alternatively prior to the present invention). Thus, this term specifically excludes any bacteria-inhibiting phage protein and its associated bacterial target which has been identified as inhibitory before the present invention or alternatively before the filing of the present application, for example those identified in Tables 12-14 or otherwise identified herein. For example, from *E. coli*, phage T7 genes 0.7 and 2.0 target the host RNA polymerase, phage T4

gp55/gp33 alter the specificity of host RNA polymerase. The T4 *regB* gene product also targets the host translation apparatus. As with the uncharacterized bacteriophage ORFs or bacteriophage above, for such identified proteins, the sequences encoding those proteins are excluded from the uncharacterized inhibitor proteins.

The term "fragment" refers to a portion of a larger molecule or assembly. For proteins, the term "fragment" refers to a molecule which includes at least 5 contiguous amino acids from the reference polypeptide or protein, preferably at least 8, 10, 12, 15, 20, 30, 50 or more contiguous amino acids. In connection with oligo- or polynucleotides, the term "fragment" refers to a molecule which includes at least 15 contiguous nucleotides from a reference polynucleotide, preferably at least 24, 30, 36, 45, 60, 90, 150, or more contiguous nucleotides.

Preferred embodiments involve identification of binding that include methods for distinguishing bound molecules, for example, affinity chromatography, immunoprecipitation, crosslinking, and/or genetic screen methods that permit protein:protein interactions to be monitored. One of skill in the art is familiar with these techniques and common materials utilized (see, *e.g.*, Coligan, J. et al. (eds.) (1995) Current Protocols in Protein Science, John Wiley & Sons, Secaucus, N.J.).

Genetic screening for the identification of protein:protein interactions typically involves the co-introduction of both a chimeric bait nucleic acid sequence (here, the phage ORF to be tested) and a chimeric target nucleic acid sequence that, when co-expressed and having affinity for one another in a host cell, stimulate reporter gene expression to indicate the relationship. A "positive" can thus suggest a potential inhibitory effect in bacteria. This is discussed in further detail in the Detailed Description section below. In this way, new bacterial targets can be identified that are inhibited by specific phage ORF products or derivatives, fragments, mimetics, or other molecules.

Other embodiments involve the identification and/or utilization of mutant targets by virtue of their host's relatively unresponsive nature in the presence of expression of ORFs previously identified as inhibitory to the non-mutant or wild-type strain. Such mutants have the effect of protecting the host from an inhibition that would otherwise occur and indirectly allow identification of the precise responsible target for follow-up studies and anti-microbial development. In certain embodiments, rescue from inhibition occurs under conditions in which a bacterial target or mutant target is highly expressed. This is performed, for example, through coupling of the sequence with regulatory element promoters, *e.g.*, as known in the art, which regulate expression at levels higher than wild-type, *e.g.*, at a level sufficiently higher that the

inhibitor can be competitively bound to the highly expressed target such that the bacterium is detectably less inhibited.

Identification of the bacterial target can involve identification of a phage-specific site of action. This can involve a newly identified target, or a target where the phage site of action differs from the site of action of a previously known antibacterial agent or inhibitor. For example, phage T7 genes 0.7 and 2.0 target the host RNA polymerase, which is also the cellular target for the antibacterial agent, rifampin. To the extent that a phage product is found to act at a different site than previously described inhibitors, aspects of the present invention can utilize those new, phage-specific sites for identification and use of new agents. The site of action can be identified by techniques well-known to those skilled in the art, for example, by mutational analysis, binding competition analysis, and/or other appropriate techniques.

Once a bacterial host target protein or nucleic acid or mutant target sequence has been identified and/or isolated, it too can be conveniently sequenced, sequence analyzed (*e.g.*, by computer), and the underlying gene(s), and corresponding translated product(s) further characterized. Preferred embodiments include such analysis and identification. Preferably such a target has not previously been identified as an appropriate target for antibacterial action.

Certain embodiments include the identification of at least one inhibitory phage ORF or ORF product, *e.g.*, as described for the above aspect, and thus are a combination of the two aspects.

Additionally, the invention provides methods for identifying targets for antibacterial agents by identifying homologs of a bacterial target *e.g.*, *S. aureus*, *Enterococcus faecalis* or other *Enterococci*, and *Streptococcus pneumoniae* of a bacteriophage inhibitory ORF product. Such homologs may be utilized in the various aspects and embodiments described herein as describded for the host *Enterococcus* sp. for bacteriophage 182.

Other aspects of the invention provide isolated, purified, or enriched specific phage nucleic acid and amino acid sequences, subsequences, and homologs thereof for phage selected from uncharacterized phage listed in Table 1, preferably from bacteriophage 77, 3A, 96, 44AHJD (*Staphylococcus aureus* host bacterium), Dp-1 (*Streptococcus pneumoniae* host), or 182 (*Enterococcus* host) or other phage listed in Table 1 for those bacteria. For example, such sequences do not include sequences identified in any of Tables 11-14. Nucleotide sequences of this aspect are at least 15 nucleotides in length, preferably at least 18, 21, 24, or 27 nucleotides in length, more preferably at least 30, 50, or 90 nucleotides in length. In certain embodiments, longer

nucleic acids are preferred, for example those of at least 120, 150, 200, 300, 600, 900 or more nucleotides. Such sequences can, for example, be amplification oligonucleotides (*e.g.*, PCR primers), oligonucleotide probes, sequences encoding a portion or all of a phage-encoded protein, or a fragment or all of a phage-encoded protein. In preferred embodiments, the nucleic acid sequence contains a sequence which is within a length range with a lower length as specified above, and an upper length limit which is no more than 50, 60, 70, 80, or 90% of the length of the corresponding full-length ORF. The upper length limit can also be expressed in terms of the number of base pairs of the ORF (coding region). In preferred embodiments, the nucleic acid sequence is from *Staphylococcus aureus* phage 77 ORF 17, 19, 43, 102, 104, or 182 as identified in U.S. application 09/407,804, *S.* aureus phage 44 AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

As it is recognized that alternate codons will encode the same amino acid for most amino acids due to the degeneracy of the genetic code, the sequences of this aspect includes nucleic acid sequences utilizing such alternate codon usage for one or more codons of a coding sequence. For example, all four nucleic acid sequences GCT, GCC, GCA, and GCG encode the amino acid, alanine. Therefore, if for an amino acid there exists an average of three codons, a polypeptide of 100 amino acids in length will, on average, be encoded by 3^{100}, or 5×10^{47}, nucleic acid sequences. Thus, a nucleic acid sequence can be modified (*e.g.*, a nucleic acid sequence from a phage as specified above) to form a second nucleic acid sequence encoding the same polypeptide as encoded by the first nucleic acid sequence using routine procedures and without undue experimentation. Thus, all possible nucleic acid sequences that encode the specified amino acid sequences are also fully described herein, as if all were written out in full, taking into account the codon usage, especially that preferred in the host bacterium. The alternate codon descriptions are available in common texbooks, for example, Stryer, BIOCHEMISTRY 3rd ed., and Lehninger, BIOCHEMISTRY 3rd ed., along wth many others. Codon preference tables for various types of organisms are available in the literature. Sequences with alternate codons at one or more sites can also be utilized in the computer-related aspects and embodiments herein. Because of the number of sequence variations involving alternate codon usage, for the sake of brevity, individual sequences are not separately listed herein. Instead the alternate sequences are described by reference to the natural sequence with replacement of one or more (up to all *e.g.*, up to 3, 5, 10, 15, 20, 30, 40, 50, or more) of the degenerate codons with alternate codons from the alternate codon

table (Table 6), or a modified table applicable to a particular organism that has differing codon usage, preferably with selection according to preferred codon usage for the normal host organism or a host organism in which a sequence is intended to be expressed. Those skilled in the art also understand how to alter the alternate codons to be used for expression in organisms where certain codons code differently than shown in the "universal" codon table.

For amino acid sequences or polypeptides, sequences contain at least 5 peptide-linked amino acid residues, and preferably at least 6, 7, 10, 15, 20, 30, or 40, amino acids having identical amino acid sequence as the same number of contiguous amino acid residues in a particular phage ORF product. In some cases longer sequences may be preferred, for example, those of at least 50, 60, 70, 80, or 100 amino acids in length. In preferred embodiments, the amino acid sequence contains a sequence which is within a length range with a lower length as specified above, and an upper length limit which is no more than 50, 60, 70, 80, or 90% of the length of the corresponding full-length ORF product. The upper length limit can also be expressed in terms of the number of amino acid residues of the ORF product. In preferred embodiments, the amino acid sequence or polypeptide has bacteria-inhibiting function when expressed or otherwise present in a bacterial cell which is a host for the bacteriophage from which the sequence was derived.

By "isolated" in reference to a nucleic acid is meant that a naturally occurring sequence has been removed from its normal cellular (*e.g.*, chromosomal) environment or is synthesized in a non-natural environment (*e.g.*, artificially synthesized). Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only nucleotide chain present, but that it is essentially free (about 90-95% pure at least) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

The term "enriched" means that the specific DNA or RNA sequence constitutes a significantly higher fraction (2-5 fold) of the total DNA or RNA present in the cells or solution of interest than in normal or diseased cells or in cells from which the sequence was originally taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased.

The term "significant" is used to indicate that the level of increase is useful to the person making such an increase and an increase relative to other nucleic acids of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level, this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6-fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

The terms "isolated", "enriched", and "purified" as respect nucleic acids, above, may similarly be used to denote the relative purity and abundance of polypeptides (multimers of amino acids joined one to another by α-carboxyl:α-amino group (peptide) bonds). These, too, may be stored in, grown in, screened in, and selected from libraries using biochemical techniques familiar in the art. Such polypeptides may be natural, synthetic or chimeric and may be extracted using any of a variety of methods, such as antibody immunoprecipitation, other "tagging" techniques, conventional chromatography and/or electrophoretic methods. Some of the above utilize the corresponding nucleic acid sequence.

As indicated above, aspects and embodiments of the invention are not limited to entire genes and proteins. The invention also provides and utilizes fragments and portions thereof, preferably those which are "active" in the inhibitory sense described above. Such peptides or oligopeptides and oligo or polynucleotides have preferred lengths as specified above for nucleic acid and amino acid sequences from phage; corresponding recombinant constructs can be made to express the encoded same. Also included are homologous sequences and fragments thereof.

Nucleic acid sequences of the present invention can be isolated using a method similar to those described herein or other methods known to those skilled in the art. In addition, such nucleic acid sequences can be chemically synthesized by well-known methods. Also, by having particular phage ORFs, e.g., the phage ORFs identified herein (*e.g.*, anti-bacterial ORFs of the present invention, portions thereof, or oligonucleotides derived therefrom as described), other antimicrobial sequences from other bacteriophage sources can be identified and isolated using methods described here or other methods, including methods utilizing nucleic acid hybridization and/or computer-based sequence alignment methods.

The invention also provides bacteriophage antimicrobial DNA segments from other phages based on nucleic acids and sequences hybridizing to the presently identified inhibitory ORF under high stringency conditions or sequences that are highly homologous. The bacteriophage segment from a specific phage, e.g., an antimicrobial DNA segment, can be used to identify a related segment from another unrelated phage based on stringent conditions of hybridization or on being a homolog based on nucleic acid and/or amino acid sequence comparisons. As with identified inhibitory sequences, such homologous coding sequences and products can be used as antimicrobials, to construct active portions or derivatives, to construct peptidomimetics, and to identify bacterial targets.

The nucleotide and amino acid sequences identified herein are believed to be correct, however, certain sequences may contain a small percentage of errors, *e.g.*, 1-5%. In the event that any of the sequences have errors, the corrected sequences can be readily provided by one skilled in the art using routine methods. For example, the nucleotide sequences can be confirmed or corrected by obtaining and culturing the relevant phage, and purifying phage genomic nucleic acids. A region or regions of interest can be amplified, *e.g.*, by PCR from the appropriate genomic template, using primers based on the described sequence. The amplified regions can then be sequenced using any of the available methods (*e.g.*, a dideoxy termination method).

This can be done redundantly to provide the corrected sequence or to confirm that the described sequence is correct. Alternatively, a particular sequence or sequences can be identified and isolated as an insert or inserts in a phage genomic library and isolated, amplified, and sequenced by standard methods. Confirmation or correction of a nucleotide sequence for a phage gene provides an amino acid sequence of the encoded product by merely reading off the amino acid sequence according to the normal codon relationships and/or expressed in a standard expression system and the polypeptide product sequenced by standard techniques. The sequences described herein thus provide unique identification of the corresponding genes, coding sequences, and other sequences, allowing those sequences to be used in the various aspects of the present invention.

In other aspects, the invention provides recombinant vectors and cells harboring at least one of the phage ORFs or portion thereof, or bacterial target sequences described herein. As understood by those skilled in the art, vectors may be provided in different forms, including, for example, plasmids, cosmids, and virus-based vectors. See, *e.g.*, Maniatis, T. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor University Press, Cold Spring, N.Y.; See also, Ausubel, F.M. et al. (eds.) (1994) Current Protocols in Molecular Biology. John Wiley & Sons, Secaucus, N.J.

In preferred embodiments, the vectors will be expression vectors, preferably shuttle vectors that permit cloning, replication, and expression within bacteria. An "expression vector" is one having regulatory nucleotide sequences containing transcriptional and translational regulatory information that controls expression of the nucleotide sequence in a host cell. Preferably the vector is constructed to allow amplification from vector sequences flanking an insert locus. In certain embodiments, the expression vectors may additionally or alternativley support expression, and/or replication in animal, plant and/or yeast cells due to the presence of suitable regulatory sequences, *e.g.*, promoters, enhancers, 3' stabilizing sequences, primer sequences, etc. In preferred embodiments, the promoters are inducible and specific for the system in which expression is desired, *e.g.*, bacteria, animal, plant, or yeast. The vectors may optionally encode a "tag" sequence or sequences to facilitate protein purification. Convenient restriction enzyme cloning sites and suitable selective marker(s) are also optionally included. Such selective markers can be, for example, antibiotic resistance markers or markers which supply an essential nutritive growth factor to an otherwise deficient mutant host, *e.g.*, tryptophan, histidine, or leucine in the Yeast Two-Hybrid systems described below.

The term "recombinant vector" relates to a single- or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with appropriate restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a desired product can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together. Preferably the vector is an expression vector, *e.g.*, a shuttle expression vector as described above.

By " recombinant cell" is meant a cell possessing introduced or engineered nucleic acid sequences, *e.g.*, as described above. The sequence may be in the form of or part of a vector or may be integrated into the host cell genome. Preferably the cell is a bacterial cell.

In another aspect, the invention also provides methods for identifying and/or screening compounds "active on" at least one bacterial target of a bacteriophage inhibitor protein or RNA. Preferred embodiments involve contacting such a bacterial target or targets (e.g., bacterial target proteins) with a test compound, and determining whether the compound binds to or reduces the level of activity of the bacterial target (*e.g.*, a bacterial target protein). Preferably this is done either *in vivo* (*i.e.*, in a cell-based assay) or *in vitro*, e.g., in a cell-free system under approximately physiological conditions.

The compounds that can be used may be large or small, synthetic or natural, organic or inorganic, proteinaceous or non-proteinaceous. In preferred embodiments, the compound is a peptidomimetic, as described herein, a bacteriophage inhibitor protein or fragment or derivative thereof, preferably an "active portion", or a small molecule.

In preferred embodiments, the bacterial target is a target of a phage ORF identified herein, *e.g., S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

In particular embodiments, the methods include the identification of bacterial targets or the site of action of an inhibitor on a bacterial target as described above or otherwise described herein.

In embodiments involving binding assays, preferably binding is to a fragment or portion of a bacterial target protein, where the fragment includes less than 90%, 80%, 70%, 60%, 50%, 40%, or 30% of an intact bacterial target protein. Preferably,

the at least one bacterial target includes a plurality of different targets of bacteriophage inhibitor proteins, preferably a plurality of different targets. The plurality of targets can be in or from a plurality of different bacteria, but preferably is from a single bacterial species.

A "method of screening" refers to a method for evaluating a relevant activity or property of a large plurality of compounds (e.g., a bacteria-inhibiting activity), rather than just one or a few compounds. For example, a method of screening can be used to conveniently test at least 100, more preferably at least 1000, still more preferably at least 10,000, and most preferably at least 100,000 different compounds, or even more.

In the context of this invention, the term "small molecule" refers to compounds having molecular mass of less than 2000 Daltons, preferably less than 1500, still more preferably less than 1000, and most preferably less than 600 Daltons. Preferably but not necessarily, a small molecule is not an oligopeptide.

In a related aspect or in preferred embodiments, the invention provides a method of screening for potential antibacterial agents by determining whether any of a plurality of compounds, preferably a plurality of small molecules, is active on at least one target of a bacteriophage inhibitor protein or RNA. Preferred embodiments include those described for the above aspect, including embodiments which involve determining whether one or more test compounds bind to or reduce the level of activity of a bacterial target, and embodiments which utilize a plurality of different targets as described above.

The identification of bacteria-inhibiting phage ORFs and their encoded products also provides a method for identifying an active portion of such an encoded product. This also provides a method for identifying a potential antibacterial agent by identifying such an active portion of a phage ORF or ORF product. In preferred embodiments, the identification of an active portion involves one or more of mutational analysis, deletion analysis, or analysis of fragments of such products. The method can also include determination of a 3-dimensional structure of an active portion, such as by analysis of crystal diffraction patterns. In further embodiments, the method involves constructing or synthesizing a peptidomimetic compound, where the structure of the peptidomimetic compound corresponds to the structure of the active portion. In this context, "corresponds" means that the peptidomimetic compound structure has sufficient similarities to the structure of the active portion that the peptidomimetic will interact with the same molecule as the phage protein and preferably will elicit at least one cellular response in common which relates to the inhibition of the cell by the phage protein.

In preferred embodiments, the ORF or ORF product is or is derived or obtained from *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014 or product thereof.

The methods for identifying or screening for compounds or agents active on a bacterial target of a phage-encoded inhibitor can also involve identification of a phage-specific site of action on the target.

Preferably in the methods for identifying or screening for compounds active on such a bacterial target, the target is uncharacterized; the target is from an uncharacterized bacterium from Table 1; the site of action is a phage-specfic site of action.

Further embodiments include the identification of inhibitor phage ORFs and bacterial targets as in aspects above.

An "active portion" as used herein denotes an epitope, a catalytic or regulatory domain, or a fragment of a bacteriophage inhibitor protein that is responsible for, or a significant factor in, bacterial target inhibition. The active portion preferably may be removed from its contiguous sequences and, in isolation, still effect inhibition.

By "mimetic" is meant a compound structurally and functionally related to a reference compound that can be natural, synthetic, or chimeric. In terms of the present invention, a "peptidomimetic," for example, is a compound that mimics the activity-related aspects of the 3-dimensional structure of a peptide or polyeptide in a non-peptide compound, for example mimics the structure of a peptide or active portion of a phage- or bacterial ORF-encoded polypeptide.

A related aspect provides a method for inhibiting a bacterial cell by contacting the bacterial cell with a compound active on a bacterial target of a bacteriophage inhibitor protein or RNA, where the target was uncharacterized. In preferred embodiments, the compound is such a protein, or a fragment or derivative thereof; a structural mimetic, *e.g.*, a peptidomimetic, of such a protein or fragment; a small molecule; the contacting is performed *in vitro*, the contacting is performed *in vivo* in an infected or at risk organism, *e.g.*, an animal such as a mammal or bird, for example, a human, or other mammal described herein; the bacterium is selected from a genus and/or species listed in Table 1; the bacteriophage inhibitor protein is uncharacterized; the bacteriophage inhibitor protein is from an uncharacterized phage listed in Table 1; the phage inhibitor protein is from one of *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

In the context of targets in this invention, the term "uncharacterized" means that the target was not recognized as an appropriate target for an antibacterial agent prior to the filing of the present application or alternatively prior to the present invention. Such lack of recognition can include, for example, situations where the target and/or a nucleotide sequence encoding the target were unknown, situations where the target was known, but where it had not been identified as an appropriate target or as an essential cellular component, and situations where the target was known as essential but had not been recognized as an appropriate target due to a belief that the target would be inaccessible or otherwise that contacting the cell with a compound active on the target *in vitro* would be ineffective in cellular inhibition, or ineffective in treatment of an infection. Methods described herein utilizing bacterial targets, *e.g.*, for inhibiting bacteria or treating bacterial infections, can also utilize "uncharacterized target sites", meaning that the target has been previously recognized as an appropriate target for an antibacterial agent, but where an agent or inhibitor of the invention is used which acts at a different site than that at which the previously utilized antibacterial agent, *i.e.*, a phage-specific site. Preferably the phage-specific site has different functional characteristics from the previously utilized site. In the context of targets or target sites, the term "phage-specific" indicates that the target or site is utilized by at least one bacteriophage as an inhibitory target and is different from previously identified targets or target sites.

In the context of this invention, the term "bacteriophage inhibitor protein" refers to a protein encoded by a bacteriophage nucleic acid sequence which inhibits bacterial function in a host bacterium. Thus, it is a bacteria-inhibiting phage product.

In the context of this invention, the phrase "contacting the bacterial cell with a compound active on a bacterial target of a bacteriophage inhibitor protein" or equivalent phrases refer to contacting with an isolated, purified, or enriched compound or a composition including such a compound, but specifically does not rely on contacting the bacterial cell with an intact phage which encodes the compound. Preferably no intact phage are involved in the contacting.

Related aspects provide methods for prophylactic or therapeutic treatment of a bacterial infection by administering to an infected, challenged or at risk organism a therapeutically or prophylactically effective amount of a compound active on a target of a bacteriophage inhibitor protein or RNA, or as described for the previous aspect. Preferably the bacterium involved in the infection or risk of infection produces the identified target of the bacteriophage inhibitor protein or alternatively produces a homologous target compound. In preferred embodiments, the host organism is a plant or animal, preferably a mammal or bird, and more preferably, a human or other

mammal described herein. Preferred embodiments include, without limitation, those as described for the preceding aspect.

Compounds useful for the methods of inhibiting, methods of treating, and pharmaceutical compositions can include novel compounds, but can also include compounds which had previously been identified for a purpose other than inhibition of bacteria. Such compounds can be utilized as described and can be included in pharmaceutical compositions.

In preferred embodiments of this and other aspects of the invention utilizing bacterial target sequences of a bacteriiophage inhibitory ORF product, the target sequence is encoded by a *Staphylococcus* nucleic acid coding sequence, preferably *S. aureus*, a *Streptococcus* nucleic acid coding sequence, preferably *Streptococcus pneumoniae*, or *Enterococcus* nucleic acid coding sequence. Possible target sequences are described herein by reference to sequence source sites.

The amino acid sequence of a polypeptide target is readily provided by translating the corresponding coding region. For the sake of brevity, the sequences are not reproduced herein. For the sake of brevity, the sequences are described by reference to the GenBank entries instead of being written out in full herein. In cases where the TIGR or GenBank entry for a coding region is not complete, the complete sequence can be readily obtained by routine methods, e.g., by isolating a clone in a phage host genomic library, and sequencing the clone insert to provide the relevant coding region. The boundaries of the coding region can be identified by conventional sequence analysis and/or by expression in a bacterium in which the endogenous copy of the coding region has been inactivated and using subcloning to identify the functional start and stop codons for the coding region.

In the context of nucleic acid or amino acid sequences of this invention, the term "corresponding" indicates that the sequence is at least 95% identical, preferably at least 97% identical, and more preferably at least 99% identical to a sequence from the specified phage genome, a ribonucleotide equivalent, a degenerate equivalent (utilizing one or more degenerate codons), or a homologous sequence, where the homolog provides functionally equivalent biological function.

By "treatment" or "treating" is meant administering a compound or pharmaceutical composition for prophylactic and/or therapeutic purposes. The term "prophylactic treatment" refers to treating a patient or animal that is not yet infected but is susceptible to or otherwise at risk of a bacterial infection. The term "therapeutic treatment" refers to administering treatment to a patient already suffering from infection.

The term "bacterial infection" refers to the invasion of the host organism, animal or plant, by pathogenic bacteria. This includes the excessive growth of bacteria which are normally present in or on the body of the organism, but more generally, a bacterial infection can be any situation in which the presence of a bacterial population(s) is damaging to a host organism. Thus, for example, an organism suffers from a bacterial population when excessive numbers of a bacterial population are present in or on the organism's body, or when the effects of the presence of a bacterial population(s) is damaging to the cells, tissue, or organs of the organism.

The terms "administer", "administering", and "administration" refer to a method of giving a dosage of a compound or composition, *e.g.*, an antibacterial pharmaceutical composition, to an organism. Where the organism is a mammal, the method is, *e.g.*, topical, oral, intravenous, transdermal, intraperitoneal, intramuscular, or intrathecal. The preferred method of administration can vary depending on various factors, *e.g.*, the components of the pharmaceutical composition, the site of the potential or actual bacterial infection, the bacterium involved, and the infection severity.

The term "mammal" has its usual biological meaning referring to any organism of the Class Mammalia of higher vertebrates that nourish their young with milk secreted by mammary glands, *e.g.*, mouse, rat, and, in particular, human, bovine, sheep, swine, dog, and cat.

In the context of treating a bacterial infection a "therapeutically effective amount" or "pharmaceutically effective amount" indicates an amount of an antibacterial agent, *e.g.*, as disclosed for this invention, which has a therapeutic effect. This generally refers to the inhibition, to some extent, of the normal cellular functioning of bacterial cells that renders or contributes to bacterial infection.

The dose of antibacterial agent that is useful as a treatment is a "therapeutically effective amount." Thus, as used herein, a therapeutically effective amount means an amount of an antibacterial agent that produces the desired therapeutic effect as judged by clinical trial results and/or animal models. This amount can be routinely determined by one skilled in the art and will vary depending on several factors, such as the particular bacterial strain involved and the particular antibacterial agent used.

In connection with claims to methods of inhibiting bacteria and therapeutic or prophylactic treatments, "a compound active on a target of a bacteriophage inhibitor protein" or terms of equivalent meaning differ from administration of or contact with an intact phage naturally encoding the full-length inhibitor compound. While an intact phage may conceivably be incorporated in the present methods, the method at

least includes the use of an active compound as specified different from a full length inhibitor protein naturally encoded by a bacteriophage and/or a delivery or contacting method different from administration of or contact with an intact phage encoding the full-length protein. Similarly, pharmaceutical compositions described herein at least include an active compound different from a full-length inhibitor protein naturally encoded by a bacteriophage or such a full-length protein is provided in the composition in a form different from being encoded by an intact phage. Preferably the methods and compositions do not include an intact phage.

In accord with the above aspects, the invention also provides antibacterial agents and compounds active on bacterial targets of bacteriophage inhibitor proteins or RNAs, where the target was uncharacterized as indicated above. As previously indicated, such active compounds include both novel compounds and compounds which had previously been identified for a purpose other than inhibition of bacteria. Such previously identified biologically active compounds can be used in embodiments of the above methods of inhibiting and treating. In preferred embodiments, the targets, bacteriophage, and active compound are as described herein for methods of inhibiting and methods of treating. Preferably the agent or compound is formulated in a pharmaceutical composition which includes a pharmaceutically acceptable carrier, excipient, or diluent. In addition, the invention provides agents, compounds, and pharmaceutical compositions where an active compound is active on an uncharacterized phage-specific site.

In preferred embodiments, the target is as described for embodiments of aspects above.

Likewise, the invention provides a method of making an antibacterial agent. The method involves identifying a target of a bacteriophage inhibitor polypeptide or protein or RNA, screening a plurality of compounds to identify a compound active on the target, and synthesizing the compound in an amount sufficient to provide a therapeutic effect when administered to an organism infected by a bacterium naturally producing the target. In preferred embodiments, the identification of the target and identification of active compounds include steps or methods and/or components as described above (or otherwise herein) for such identification. Likewise, the active compound can be as described above, including fragments and derivatives of phage inhibitor proteins, peptidomimetics, and small molecules. As recognized by those skilled in the art, peptides can be synthesized by expression systems and purified, or can be synthesized artificially. In preferred embodiments the inhibitory phage ORF products is from *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus*

pneumoniae phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

As indicated above, sequence analysis of nucleotide and/or amino acid sequences can beneficially utilize computer analysis. Thus, in additional aspects the invention provides computer-related hardware and media and methods utilizing and incorporating sequence data from uncharacterized phage, *e.g.*, uncharacterized phage listed in Table 1, preferably at least one of *Staphylococcus aureus* phage *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014, or 44 AHJD, *Enterococcus* sp. phage 182, or *Streptococcus pneumoniae* phage Dp-1. In general, such aspects can facilitate the above-described aspects. Various embodiments involve the analysis of genetic sequence and encoded products, as applied to the evaluating bacteriophage inhibitor ORFs and compounds and fragments related thereto. The various sequence analyses, as well as function analyses, can be used separately or in combination, as well as in preceding aspects and embodiments. Use in combination is often advantageous as the additional information allows more efficient prioritizing of phage ORFs for identification of those ORFs that provide bacteria-inhibiting function.

In one aspect, the invention provides a computer-readable device which includes at least one recorded amino acid or nucleotide sequence corresponding to one of the specified phage and a sequence analysis program for analyzing a nucleotide and/or amino acid sequence. The device is arranged such that the sequence information can be retrieved and analyzed using the analysis program. The analysis can identify, for example, homologous sequences or the indicated %s of the phage genome and structural motifs. Preferably the sequence includes at least 1 phage ORF or encoded product, more preferably at least 10%, 20%, 30%, 40%, 50%, 70%, 90%, or 100% of the genomic phage ORFs and/or equivalent cDNA, RNA, or amino acid sequences. Preferably the sequence or sequences in the device are recorded in a medium such as a floppy disk, a computer hard drive, an optical disk, computer random access memory (RAM), or magnetic tape. The program may also be recorded in such medium. The sequences can also include sequences from a plurality of different phage.

In this context, the term "corresponding" indicates that the sequence is at least 95% identical, preferably at least 97% identical, and more preferably at least 99% identical to a sequence from the specified phage genome, a ribonucleotide equivalent, a degenerate equivalent (utilizing one or more degenerate codons), or a homologous sequence, where the homolog provides functionally equivalent biological function.

Similarly, the invention provides a computer analysis system for identifying biologically important portions of a bacteriophage genome. The system includes a data storage medium, *e.g.*, as identified above, which has recorded thereon a nucleotide sequence corresponding to at least a portion of at least one uncharacterized bacteriophage genome, a set of program instructions to allow searching of the sequence or sequences to analyze the sequence, and an output device where the portion includes at least the sequence length as specified in the preceding aspect. The output device is preferably a printer, a video display, or a recording medium. More one than one output device may be included. For each of the present computer-related asepcts, the bacteriophage are preferably selected from the uncharacterized phage listed in Table 1, more preferably from bacteriophage 77, 3A, 96, 44 AHJD (*S. aureus*), Dp-1 (*Streptococcus pneumoniae*), or 182 (*Enterococcus*).

In keeping with the computer device aspects, the invention also provides a method for identifying or characterizing a bacteriophage ORF by providing a computer-based system for analyzing nucleotide or amino acid sequences, *e.g.*, as describe above. The system includes a data storage medium which has recorded a sequences or sequences as described for the above devices, a set of instructions as in the preceding aspect, and an output device as in the preceding aspect. The method further involves analyzing at least one sequence, and outputting the analysis results to at least one output device.

In preferred embodiments, the analysis identifies a sequence similarity or homology with a sequence or sequences selected from bacterial ORFs encoding products with related biological function; ORFs encoding known inhibitors; and essential bacterial ORFs. Preferably the analysis identifies a probable biological function based on identification of structural elements or characteristic or signature motifs of an encoded product or on sequence similarity or homology. Preferably the uncharacterized bacteriophage is from Table 1, more preferably at least one of bacteriophage 77, 3A, 96, 44 AHJD (*S. aureus*), Dp-1 (*Streptococcus pneumoniae*), or 182 (*Enterococcus*). In preferred embodiments, the method also involves determining at least a portion of the nucleotide sequence of at least one uncharacterized bacteriophage as indicated, and recording that sequence on data storage medium of the computer-based system. In preferred embodiments, the analysis identifies a sequence similarity of homology with a *S. aureus* phage 44AHJD ORF 1, 9, or 12, *Streptococcus pneumoniae* phage Dp-1 ORF 001, 002, 004, 008, 010, 013, 016, 021, 029, 030, 038, or 041, or *Enterococcus* sp. phage 182 ORF 002, 008, or 014.

As used in the claims to describe the various inventive aspects and embodiments, "comprising" means including, but not limited to, whatever follows the word "comprising". Thus, use of the term "comprising" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present. By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of". Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present. By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

Further embodiments will be apparent from the following Detailed Description and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1A and 1B are flow schematics showing the manipulations used to convert pT0021, an arsenite inducible vector containing the luciferase gene, into pTHA or pTM, two *ars* inducible vectors. Vector pTHA contains BamH I, Sal I, and Hind III cloning sites and a downstream HA epitope tag. Vector pTM contains Bam HI and Hind III cloning sites and no HA epitope tag.

FIGURE 2 is a schematic representation of the cloning steps involved to place the DNA segments of any of ORFs 17/ 19/ 43/ 102/104/182 or other sequences into pTHA to assess inhibitory potential. For subcloning into pTM or pT0021, Individual ORFs were amplified by the PCR using oligonucleotides targeting the ATG and stop codons of the ORFs. Using this strategy, Bam HI and Hind III sites were positioned immediately upstream or downstream, respectively of the start and stop codons of each ORF. Following digestion with Bam HI and Hind III, the PCR fragments were subcloned into the same sites of pT0021 or pTM. Clones were verified by PCR and direct sequencing.

FIGURE 3 shows a schematic representation of the functional assays used to characterize the bactericidal and bacteriostatic potential of all predicted ORFs (>33 amino acids) encoded by bacteriophage 77. Fig. 3A) Functional assay on semi-solid support media. Fig. 3B) Functional assay in liquid culture.

FIGURE 4A, B, and C is a bar graph showing the results of a screen in liquid media to assess bacteriostatic or bactericidal activity of 93 predicted ORFs (>33 amino acids) encoded by bacteriophage 77. Growth inhibition assays were performed as detailed in the Detailed Description. The relative growth of Staphylococcus aureus transformants harboring a given bacteriophage 77 ORF (identified on the bottom of the graph), in the absence or presence of arsenite, is plotted relative to growth of a Staphylococcus aureus transformant containing ORF 5, a non-toxic bacteriophage 77 ORF (which is set at 100%). Each bar represents the average obtained from three Staph A transformants grown in duplicate. Bacteriophage 77 ORFs showing significant growth inhibition consist of ORFs 17, 19, 102, 104, and 182.

FIGURE 5 shows a block diagram of major components of a general purpose computer.

FIGURE 6 shows an ORF map for *Streptococcus pneumoniae* bacteriophage Dp-1 showing the ORF identifiers, genomic locations, and orientations of the 85 identified ORFs that were found to have ribosomal binding sites and thus are expected to be expressed.

FIGURE 7 shows a schematic representation of the arsenite-inducible expression system present in a shuttle vector designed to express individual *Streptococcus* bacteriophage Dp-1 ORFs in *Streptococcus*. Various modifications can be readily made to such a vector, or other vectors can be readily constructed to provide inducible expression of ORFs in a particular host bacterium using well-known techniques.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The invention may be more clearly understood from the following description.

The tables will first be briefly described.

Table 1 is a listing of a large number of available bacteriophage that can be readily obtained and used in the present invention.

Table 2 shows the complete nucleotide sequence of the genome of *Staphylococcus aureus* bacteriophage 77.

Table 3 shows a list of all the ORFs from Bacteriophage 77 that were screened in the functional assay to identify those with anti-microbial activity.

Table 4 shows the predicted nucleotide sequence, predicted amino acid sequence, and physiochemical parameters of ORF 17/ 19/ 43/ 102/ 104/ 182]. These include the primary amino acid sequence of the predicted protein, the average molecular weight, amino acid composition, theoretical pI, hydrophobicity map, and predicted secondary structure map.

Table 5 shows homology search results. BLAST analysis was performed with ORFs 17/ 19/ 43/ 102/ 104/ 182 against NCBI non-redundant nucleotide and Swissprot databases. The results of this search indicate that: I) ORF 17 has no significant homology to any gene in the NCBI non-NCBI non-redundant nucleotide database, II) ORF 19 has significant homology to one gene in the NCBI non-redundant nucleotide database - the gene encoding ORF 59 of bacteriophage phi PVL, III) ORF 43 has significant homology to one gene in the NCBI non-redundant nucleotide database - the gene encoding ORF 39 of phi PVL, IV) ORF 102 has significant homology to one gene in the NCBI non-redundant nucleotide database - the gene encoding ORF 38 of phi PVL, V) ORF 104 has no significant homology to any gene in the NCBI non-redundant nucleotide database, VI) ORF 182 has significant homology to one gene in the NCBI non-redundant nucleotide database - the gene encoding ORF 39 of phi PVL.

Table 6 is a table from Alberts et al., MOLECULAR BIOLOGY OF THE CELL 3rd ed., showing the redundancy of the "universal" genetic code.

Table 7 shows the complete nucleotide sequence of *Staphylococcus aureus* bacteriophage 3A.

Table 8 is a listing of the ORFs identified in *Staphylococcus aureus* bacteriophage 3A.

Table 9 shows the complete nucleotide sequence of *Staphylococcus aureus* bacteriophage 96.

Table 10 is a listing of the ORFs identified in *Staphylococcus aureus* bacteriophage 96.

Table 11 is a listing of sequences deposited in the NCBI public database (GeneBank) for bacteriophage listed in Table 1.

Table 12 is a listing of phage which encode a known lysis function , including the identified lysis gene.

Table 13 is a listing of bacteriophage which encode holin genes, where holin genes encode proteins which form pores and eventually enable other enzymes to kill the host bacterium.

Table 14 is a listing of bacteriophage which encode kil genes.

Table 15 is a list of *Staphylococcus aureus* sequences identified by accession number which may include sequences from genes coding for target sequences for the phage 77-encoded antimicrobial proteins or peptides. The sequences were obtained by searching GenBank for listings.

Table 16 shows the nucleotide sequence of the genome of *Staphylococcus aureus* phage 44 AHJD.

Table 17 lists and shows the sequence position of the 73 ORFs predicted to be encoded by *Staphylococcus aureus* bacteriophage 44 AHJD that are greater than 33 amino acids.

Table 18 shows the ORF sequences and putative amino acid sequences for the *Staphylococcus aureus* bacteriophage 44AHJD ORFs greater than 33 amino acids.

Table 19 shows the similarities in sequence identified between predicted *Staphylococcus aureus* bacteriophage 44 AHJD ORFs and sequences present in public databases.

Table 20 shows the homology alignments between predicted *Staphylococcus aureus* bacteriophage 44AHJD ORFs and the corresponding protein sequences present in public sequence databases.

Table 21 shows the complete nucleotide sequence of the genome of *Enterococcus* bacteriophage 182.

Table 22 lists and shows the sequence position of the 80 ORFs identified in bacteriophage 182 and that are greater than 33 amino acids.

Table 23 shows the nucleotide and predicted amino acid sequence of all 80 ORFs identified in bacteriophage 182.

Table 24 shows the similarities identified to date in sequence between *Enterococcus* phage 182 ORFs greater than 33 amino acids and sequences present in public sequence databases.

Table 25 shows the predicted amino acid sequence as well as the predicted secondary structures map for two *Enterococcus* bacteriophage 182 ORFs.

Table 26 shows the homology alignments between predicted *Enterococcus* bacteriophage 182 ORFs and the corresponding protein sequences present in public sequence databases.

Table 27 list *Enterococcus* sequences listed in GenBank providing possible Enterococcal target sequences for inhibitory *Enterococcus* bacteriophage 182 ORFs and other compounds with antibacterial activity.

Table 28 shows the complete nucleotide sequence of the genome of *Streptococcus* bacteriophage Dp-1.

Table 29 lists and shows sequence position of the 273 ORFs identified in Pneumococcal bacteriophage Dp-1 that are greater than 33 amino acids, 85 of which are predicted to be expressed in Dp-1 as having a ribosomal binding site. That set of 85 ORFs is shown in the attached drawings.

Table 30 shows the nucleotide and predicted amino acid sequence of all 273 ORFs identified in bacteriophage Dp-1 that are identified as being expressed.

Table 31 shows the similarities identified in sequence between *Streptococcus* phage Dp-1 ORFs greater than 33 amino acids and sequences present in public sequence databases.

Table 32 shows the 4731 bp sequence of Dp-1 published by Sheehan et al., 1997).

Table 33 lists *Streptococcus pneumoniae* sequences listed in GenBank providing possible target sequences for inhibitory *Streptococcus pneumoniae* bacteriophage Dp-1 ORFs and other compounds with antibacterial activity

Background:

As indicated above, the present invention is concerned, in part, with the use of bacteriophage coding sequences and the encoded polypeptides or RNA transcripts to identify bacterial targets for potential new antibacterial agents. Thus, the invention concerns the selection of relevant bacteria. Particularly relevant bacteria are those which are pathogens of a complex organism such as an animal, *e.g.*, mammals,

reptiles, and birds, and plants. Examples include *Stapylococcus aureus*, *Enterococcus* species, and *Streptococcus pneumoniae*. However, the invention can be applied to any bacterium (whether pathogenic or not) for which bacteriophage are available or which are found to have cellular components closely homologous to components targeted by phage of another bacterium.

Thus, the invention also concerns the bacteriophage which can infect a selected bacterium. Identification of ORFs or products from the phage which inhibit the host bacterium both provides an inhibitor compound and allows identification of the bacterial target affected by the phage-encoded inhibitor. Such targets are thus identified as potential targets for development of other antibacterial agents or inhibitors and the use of those targets to inhibit those bacteria. As indicated above, even if such a target is not initially identified in a particular bacterium, such a target can still be identified if a homologous target is identified in another bacterium. Usually, but not necessarily, such another bacterium would be a genetically closely related bacterium. Indeed, in some cases, a phage-encoded inhibitor can also inhibit such a homologous bacterial cellular component.

The demonstration that bacteriophage have adapted to inhibiting a host bacterium by acting on a particular cellular component or target provides a strong indication that that component is an appropriate target for developing and using antibacterial agents, *e.g.*, in therapeutic treatments. Thus, the present invention provides additional guidance over mere identification of bacterial essential genes, as the present invention also provides an indication of accessability of the target to an inhibitor, and an indication that the target is sufficiently stable over time (*e.g.*, not subject to high rates of mutation) as phage acting on that target were able to develop and persist. Thus, the present invention identifies a subset of essential cellular components which are particularly likely to be appropriate targets for development of antibacterial agents.

The invention also, therefore, concerns the development or identification of inhibitors of bacteria, in addition to the phage-encoded inhibitory proteins (or RNA transcripts), which are active on the targets of bacteriophage-encoded inhibitors. As described herein, such inhibitors can be of a variety of different types, but are preferably small molecules.

The following description provides preferred methods for use in the various aspects of the invention. However, as those skilled in the art will readily recognize, other approaches can be used to obtain and process relevant information. Thus the invention is not limited to the specifically described methods. In addition, the following description provides a set of steps in a particular order. That series of steps

describes the overall development involved in the present invention. However, it is clear that individual steps or portions of steps may be usefully practiced separately, and, further, that certain steps may be performed in a different order or even bypassed if appropriate information is already available or is provided by other sources or methods.

Selecting and Growing Phage, and Isolating DNA

Conceptually, the first step involves selecting bacterial hosts of interest. Preferably, but not necessarily, such hosts will be pathogens of clinical importance. Alternatively, because bacteria all share certain fundamental metabolic and structural features, these features can be targeted for study in one strain, for example a nonpathogenic one, and extrapolated to similarly succeed in pathogenic ones. Nonpathogenic strains may also exhibit initial advantages in being not only less dangerous, but also, for example, in having better growth and culturing characteristics and/or better developed molecular biology techniques and reagents. Consequently, advantageously the invention provides the ability target virtually any bacteria, but preferably pathogenic bacteria, with antimicrobial compounds designed and/or developed using bacteriophage inhibitory proteins and peptides from phage with non-pathogenic and/or pathogenic hosts.

We have selected *Staphylococcus aureus*, *Streptococcus pneumoniae*, various *Enterococci*, and *Pseudomonas aeruginosa* as initial exemplary pathogens. These bacteria are a major cause of morbidity and mortality in hospital-based infections, and the appearance of antibiotics resistance in all three organisms makes it increasingly difficult to treat benign infections involving these organisms. Such infections can include, for example, otitis media, sinusitis, and skin, and airway infections (Neu, H.C. (1992). *Science* 257, 1064-1073). However, the approach described below is clearly applicable to any human bacterial pathogens including but not restricted to *Mycobacterium tuberculosis*, *Nesseria gonorrhoeae*, *Haemophilus influenza*, *Acinobacter*, *Escherichia coli*, *Shigella dysenteria*, *Streptococcus pyogenes*, *Helicobacter pylori*, and *Mycoplasma* species. This invention can also be applied to the discovery of anti-bacterial compounds directed against pathogens of animals other than humans, for example, sheep, cattle, swine, dogs, cats, birds, and reptiles. Similarly, the invention is not limited to animals, but also applies to plants and plant pathogens.

In general, the bacteria are grown according to standard methodologies employed in the art, including solid, semi-solid or liquid culturing, which procedures can be found in or extrapolated from standard sources such as Maloy, S.R., Stewart,

V.J., and Taylor, R.K. Genetic Analysis of Pathogenic Bacteria (1996) Cold Spring Harbor Laboratory Press, or Maniatis, T. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor University Press, Cold Spring, N.Y.; or Ausubel, F.M. et al. (1994) Current Protocols in Molecular Biology. John Wiley & Sons, Secaucus, N.J. Culture conditions are selected which are adapted to the particular bacterium generally using culture conditions known in the art as appropriate, or adaptations of those conditions.

Nucleic acids within these bacteria can be routinely extracted through common procedures such as described in the above-referenced manuals and as generally known to those skilled in the art. Those nucleic acid stocks can then be used to practice the other inventive aspects described below.

Selection and Growth of Bacteriophage, and Isolation of DNA

The second step involves assembling a group of bacteriophages (phage collection) for one or more of the targeted bacterial hosts. While the invention can be utilized with a single bacteriophage for a pathogen or other bacterium, it is preferable to utilize a plurality of phage for each bacterium, as comparisons between a plurality of such phage provides useful additional information. Non-limiting examples of phage and sources for some of the above-mentioned pathogenic bacteria are found in Table 1. The criteria used to select such phages is that they are infectious for the microbe targeted, and replicate in, lyse, or otherwise inhibit growth of the bacterium in a measurable fashion. These phages can be very different from one another (representing different families), as judged by criteria such as morphology (head, tail, plate, etc.), and similarity of genome nucleotide sequence (cross-hybridization). Since such diverse bacteriophages are expected to block bacterial host metabolism and ultimately inhibit by a variety of mechanisms, their combined study will lead to the identification of different mechanisms by which the phages independently inhibit bacterial targets. Examples include degradation of host DNA (Parson K.A., and Snustad, D.P. (1975). *J. Virol.* 15, 221-444) and inhibition of host RNA transcription (Severinova, E., Severinov, K. and Darst, S.A. (1998). *J.Mol. Biol.* 279, 9-18). This, in turn, yields novel information on phage proteins that can inhibit the targeted microbe. As explained below, this 1) forms the basis of novel drug discovery efforts based on knowledge of the primary amino acid sequence of the phage inhibitor protein (*e.g.*, peptide fragments or peptidomimetics) and/or 2) leads to the identification of bacterial biochemical pathways, the proteins of which are essential or significant for survival of the targeted microbe, and which enzymatic steps or

chemical reactions can be targeted by classical drug discovery methods using molecular inhibitors, for example, small molecule inhibitors.

Bacteriophage are generally either of two types, lytic or filamentous, meaning they either outright destroy their host and seek out new hosts after replication, or else continuously propogate and extrude progeny phage from the same host without destroying it. Regardless of the phage life cycle and type, preferred embodiments incorporate phage which impede cell growth in measurable fashion and preferably stop cell growth. To this end, lytic phage are preferred, although certain nonlytic species may also suffice, *e.g.*, if sufficiently bacteriostatic.

Various procedures that are commonly understood by those of skill in the art can be routinely employed to grow, isolate, and purify phage. Such procedures are exemplified by those found in such common laboratory aids such as Maloy, S.R., Stewart, V.J., and Taylor, R.K. Genetic Analysis of Pathogenic Bacteria (1996) Cold Spring Harbor Laboratory Press; Maniatis, T. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor University Press, Cold Spring, N.Y.; and Ausubel, F.M. et al. (eds.) (1994) Current Protocols in Molecular Biology. John Wiley & Sons, Secaucus, N.J. The techniques generally involve the culturing of infected bacterial cells that are lysed naturally and/or chemically assisted, for example, by the use of an organic solvent such as chloroform that destroys the host cells thereby liberating the phage within. Following this, the cellular debris is centrifuged away from the supernatant containing the phage particles, and the phage then subsequently and selectively precipitated out of the supernatant using various methods usually employing the use of alcohols and/or other chemical compounds such as polyethylene glycol (PEG). The resulting phage can be further purified using various density gradient/centrifugation methodologies. The resulting phage are then chemically lysed, thereby releasing their nucleic acids that can be conveniently precipitated out of the supernatant to yield a viral nucleic acid supply of the phage of interest.

Exemplary bacteriophage are indicated in Table 1, along with sources where those phage may be obtained.

Exemplary bacteria include the reference bacteria for the identified bacteriophage, available from the same sources.

Characterizing Bacteriophage Genomes for ORFs

The third step involves systematically characterizing the genetic information contained in the phage genome. Within this genetic information is the sequence of all RNAs and proteins encoded by the phage, including those that are essential or

instrumental in inhibiting their host. This characterization is preferably done in a systematic fashion. For example, this can be done by first isolating high molecular weight genomic DNA from the phage using standard bacterial lysis methods, followed by phage purification using density gradient ultracentrifugation, and extraction of nucleic acid from the purified phage preparation. The high molecular weight DNA is then analyzed to determine its size and to evaluate a proper strategy for its sequencing. The DNA is broken down into smaller size fragments by sonication or partial digestion with frequently cutting restriction enzymes such as Sau3A to yield predominantly 1 to 2 kilobase length DNA, which DNA can then be resolved by gel electrophoresis followed by extraction from the gel.

The ends of the fragments are enzymatically treated to render them suitable for cloning and the pools of fragments are cloned in a bacterial plasmid to generate a library of the phage genome. Several hundred of these random DNA fragments contained in the plasmid vector are isolated as clones after introduction into an appropriate bacterium, usually *Escherichia coli*. They are then individually expanded in culture and the DNA from each individual clone is purified. The nucleotide sequences of the inserts of these clones are determined by standard automated or manual methods, using oligonucleotide primers located on either side of the cloning site to direct polymerase mediated sequencing (*e.g.*, the Sanger sequencing method or a modification of that method). Other sequencing methods can also be used.

The sequence of individual clones is then deposited in a computer, and specific software programs (for example, Sequencher™, Gene Codes Corp.) are used to look for overlap between the various sequences, resulting in ordering of contig sequences and ultimately providing the complete sequence of the entire bacteriophage genome (one such example is given in Table 2 for *Staphylococcus aureus* bacteriophage 77; others are also provided herein). This complete nucleotide sequence is preferably determined with a redundancy of at least 3- to 5-fold (number of independent sequencing events covering the same region) in order to minimize sequencing errors.

Preferably, the bacterial strain used as a phage host should not possess any other innate plasmids, transposons, or other phage or incompatible sequences that would complicate or otherwise make the various manipulations and analyses more difficult.

Commercially available computer software programs are used to translate the nucleotide sequence of the phage to identify all protein sequences encoded by the phage (hereafter called open reading frames or ORFs). (Customized software can clearly also be used.) As phages are known to transcribe their genome into RNA from

both strands, in both directions, and sometimes in more than one frame for the same sequence, this exercise is done for both strands and in all six possible reading frames. As evolutionary constraints have forced the phage to conserve all of its vital protein sequences in as small a genome as possible, it is straightforward to identify all the proteins encoded by the phage by simple examination of the 6 translation frames of the genome. Once these ORFs are identified, they are cataloged into a phage proteome database (Table 3 lists ORFs identified from phage 77; ORF lists are also provided for other exemplary phage). This analysis is preferably performed for each phage under study. The process of ORF identification can be varied depending on the desired results. For example, the minimum length for the putative encoded polypeptide can be varied, and/or putative coding regions that have an associated Shine-Dalgarno sequence can be selected. In the case of phage 77 ORFs, such parameter adjustment was performed and resulted in the identification of ORFs as listed herein. Different parameters had resulted in the identification of the ORFs listed in the preceding U.S. Provisional Application 60/110,992, filed December 3, 1998, which is hereby incorporated by reference in its entirety.

Exemplary phage 77 ORFs identified in that provisional application and as identified herein are shown in the following table:

ORF ID from 60/110,992	Genomic position	a.a. size	Start codon	ORF ID from 241/190	Genomic position	a.a. size	Start codon
77ORF016	2369-24024	251	TTG	77ORF017	23269-23982	237	ATG
77ORF019	39845-40501	218	ATA	77ORF019	39851-40501	216	ATG
77ORF050	29268-29564	98	ATG	77ORF182	29268-29564	98	ATG
77ORF050	29268-29564	98	ATG	77ORF043	29304-29564	86	ATG
77ORF067	34312-34551	79	CTG	77ORF104	34393-34551	52	ATG
77ORF146	29051-29212	53	ATG	77ORF102	29051-29212	53	ATG

<u>Identifying and Characterizing Inhibitory Phage ORFs</u>

The fourth step entails identifying the phage protein or proteins or RNA transcripts that have the ability to inhibit their bacterial hosts. This can be accomplished, for example, by either or both of two non-mutually exclusive methods. The first method makes use of bioinformatics. Over the past few years, a large amount of nucleotide sequence information and corresponding translated products have become available through large genome sequencing projects for a variety of organisms including mammals, insects, plants, unicellular eukaryotes (yeast and fungi), as well as several bacterial genomes such as *E. coli, Mycobacterium tuberculosis, Bacillus subtilis, Staphylococcus aureus* and many others. Such sequences have been deposited in public databases (for example, non-redundant

sequence database at GenBank and SwissProt protein sequence database) (http://www.ncbi.nlm.nih.gov)) and can be freely accessed to compare any specific query sequence to those present in such databases. For example, GenBank contains over 1.6 billion nucleotides corresponding to 2.3 million sequence records. Several computer programs and servers (*e.g.*, TBLASTN) have been created to allow the rapid identification of homology between any given sequence from one organism to that of another present in such databases, and such programs are public and available free of charge.

In addition, it has been well established that basic biochemical pathways can be conserved in very distant organisms (for example bacteria and man), and that the proteins performing the various enzymatic steps in these pathways are themselves conserved at the amino acid sequence level. Thus, proteins performing similar functions (*e.g.* DNA repair, RNA transcription, RNA translation) have frequently preserved key structural signatures, identifiable by similarities across regions of proteins (domains and motifs). The antimicrobials of the present invention will preferably target features and targets that are highly characteristic or conserved in microbes, and not higher organisms.

Most genomes encode individual proteins or groups of proteins that can be assembled into protein families that have been evolutionarily conserved. Therefore, similarity between a new query sequence and that of a member of a protein family (reference sequences from public databases) can immediately suggest a biochemical function for the novel query sequence, which in our case is a phage ORF.

The sequence homology between individual members of evolutionarily distant members of a protein family is usually not randomly distributed along the entire length of the sequence but is often clustered into "motifs" and "domains". These correspond to key three-dimensional folds that form key catalytic and/or regulatory structures that perform key biochemical function(s) for the group of proteins. Commercially available computer software programs can identify such motifs in a new query sequence, again providing functional information for the query sequence. Such structural and functional motifs have also been derived from the combined analysis of primary sequence databases (protein sequences) and protein structure databases (X-ray crystallography, nuclear magnetic resonance) using so-called "threading" methods (Rost B,l and Sander C. (1996)*Ann. Rev. Biophy. Biomol. Struct.* 25, 113-136).

Such motifs and folds are themselves deposited in public databases which can be directly accessed (for example, SwissProt database; 3D-ALI at EMBL, Heidelberg; PROSITE). This basic exercise leads to a structural homology map in which each of

the phage ORFs has been probed for such similarities, and where initial structural and functional hits are identified (selected examples of sequence homologies detected between individual ORFs from the genome of *Staphylococcus aureus* bacteriophage 77 and sequences deposited in public databases are shown in Table 5 for ORFs 17/19/43/102/104/182).

This analysis can point out phage proteins with similarity to proteins from other phages (such as those for *E. coli*) playing an important role in the basic biochemical pathways of the phage (such as DNA replication, RNA transcription, tRNAs, coat protein and assembly). Selected examples of such proteins include integrase and capsid protein. Therefore, this analysis enables identification and elimination of non-essential ORFs as candidates for an inhibitor function, as well as the identification of (potentially) useful ones.

In addition, this analysis can point out specific ORFs as possible inhibitor ORFs. For example these ORFs may encode proteins or enzymes that alter bacterial cell structure, metabolism or physiology, and ultimately viability. Examples of such proteins present in the genome of *Staphylococcus aureus* bacteriophage 77 include orf14 (deoxyuridine triphosphatase from bacteriophage T5), and orf15 (sialidase). (These ORF identifications are as listed in provisional application 60/110,992.) Other examples include ORFs 9 and 12 of *S. aureus* phage 44 AHJD, which encode the putative lysis functions found in many bacteriophages – a "holin" and an "amidase".

In addition, it is well known that bacterial and eukaryotic viruses can usurp pathways from their host in order to use them to their advantage in blocking host cellular pathways upon infection. The phage can achieve this by 1) directly producing an inhibitor of a key host pathway (e.g. T7 gene 0.5 and 2), 2) directly producing a novel activity (e.g. T4 DNA polymerase), and 3) altering concentrations of cell components by producing similar functions (e.g. T4 transfer RNAs). The identification of sequence similarity between phage ORFs and bacterial host genome sequences will be highly indicative of such a mechanism. (Selected examples of such homologies are listed in Figure 4 of the provisional application 60/110,992 and include orf4 (homologous to autolysin), orf20 (hypothetical protein from *Staphyloccus aureus*) and orf29 (hypothetical protein from *Staphyloccus aureus*.)) These ORFs can be analyzed by a standard biochemical approach to directly test their inhibitor functions (*e.g.*, as described below).

Alternatively, a homology search may reveal that a given phage ORF is related to a protein present in the databases having an activity known to be inhibitory, (*e.g.* inhibitor of host RNA polymerase by *E. coli* bacteriophage T7. Such a finding would implicate the phage ORF product in a related activity. This will also suggest that a

new antimicrobial could be derived by a mimetic approach (*e.g.*, peptidomimetic) imitating this function or by a small molecule inhibitor to the bacterial target of the phage ORF, or any steps in the relevant host metabolic pathway, *e.g.*, high throughput screening of small molecule libraries. Selected examples of such similarity between ORFs of *Staphyloccus aureus* bacteriophage 77 and proteins with inhibitor functions for bacterial hosts are listed in Figure 4 of the provisional application 60/110,992. These include orf9 (similar to bacteriophage P1 *kilA* function), and orf4 (autolysin of *Staphylococcus aureus*, amidase enzymatic activity).

A reason for the biochemical study of individual ORFs for inhibitor function is that their expression or overexpression will block cellular pathways of the host, ultimately leading to arrest and/or inhibition of host metabolism. In addition, such ORFs can alter host metabolism in different ways, including modification of pathogenicity. Therefore, individual ORFs identified above are expressed, preferably overexpressed, in the host and the effect of this expression or overexpression on host metabolism and viability is measured. This approach can be systematically applied to every ORF of the phage, if necessary, and does not rely on the absolute identification of candidate ORFs by bioinformatics. Individual ORFs are resynthesized from the phage genomic DNA, *e.g.*, by the polymerase chain reaction (PCR), preferably using oligonucleotide primers flanking the ORF on either side. These single ORFs are preferably engineered so that they contain appropriate cloning sites at their extremities to allow their introduction into a new bacterial expression plasmid, allowing propagation in a standard bacterial host such as *E. coli,* but containing the necessary information for plasmid replication in the target microbe such as *S. aureus* (hereafter referred to as shuttle vector). Shuttle vectors and their use are well known in the art.

Such shuttle vectors preferably also contain regulatory sequences that allow inducible expression of the introduced ORF. As the candidate ORF may encode an inhibitor function that will eliminate the host, it is beneficial that it not be expressed prior to testing for activity. Thus, screening for such sequences when expressed in a constitutive fashion is less likely to be successful when the inhibitor is lethal. In the exemplary inducible system presented in Figure 1A, 1B, 2, and 7, regulatory sequences from the *ars* operon of *S. aureus* are used to direct individual ORF expression in *S. aureus* (or other bacteria in which the *ars* system is functional). The *ars* operon encodes a series of proteins which normally mediate the extrusion of arsenite and other trivalent oxyanions from the cells when they are exposed to such toxic substances in their environment. The operon encoding this detoxifying mechanism is normally silent and only induced when arsenite-related compounds are

present. (Tauriainen, S. et al. (1997) *App. Env. Microb.*, Vol. 63, No. 11, p. 4456-4461.)

Therefore, individual phage ORFs can be expressed in *S. aureus* in an inducible fashion by adding to the culture medium non-toxic arsenite concentrations during the growth of individual *S. aureus* clones expressing such individual phage ORFs. Toxicity of the phage inhibitor ORF for the host is monitored by reduction or arrest of growth under induction conditions, as measured by optical density in liquid culture or after plating the induced cultures on solid medium. Subsequently, interference of the phage ORF with the host biochemical pathways ultimately leading to reduced or arrested host metabolism can be measured by pulse-chase experiments using radiolabeled precursors of either DNA replication, RNA transcription, or protein synthesis. Similar constructs can be made and used for other bacteria using well-known techniques.

Those skilled in the art are familiar with a variety of other inducible systems which can also be used for the controlled expression of phage ORFs, including, for example, lactose (see *e.g.*, Stratagene's LacSwitch™II system; La Jolla, CA) and tetracycline-based systems (see, *e.g.* Clontech's Tet On/Tet Off™ system; Palo Alto, CA). The arsenite-inducible system described is further depicted in Figures 1, 2 and 7.

The selection or construction of shuttle vectors and the selection and use of inducible systems are well known and thus other shuttle vectors appropriate for other bacteria can be readily provided by those skilled in the art, e.g., for use in other bacterial species.

Standard methodologies for expressing proteins from constructs, and isolating and manipulating those proteins, for example in cross-linking and affinity chromatography studies, may be found in various commonly available and known laboratory manuals. See, *e.g.*, Current Protocols in Protein Science, John Wiley & Sons, Secaucus, N.J., and Maniatis, T. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor University Press, Cold Spring, N.Y.

It has been found that certain phage or other viruses inhibit host cells, at least in part, by producing an antisense RNA which binds to and inhibits translation from a bacterial RNA seqeunce. Thus, in the case of potentially inhibitor RNA transcripts encoded by the phage genome, a strong indicator of a possible inhibitory function is provided by the identification of phage sequence which is the identical to or fully complementary (or with only a small percentage of mismatch, *e.g.*, <10%, preferably less than 5%, most preferably less than 3%, to a bacterial sequence. This approach is convenient in the case of bacteria that have been essentially completely sequenced, as the comparison can be performed by computer using public database information.

The inhibitory effect of the transcript can be confirmed using expression of the phage sequence in a host bacterium. If needed, such inhibitory can also be tested by transfecting the cells with a vector that will transcribe the phage sequence to form RNA in such manner that the RNA produced will not be translated into a polypeptide. Inhibition under such conditions provides a strong indication that the inhibition is due to the transcript rather than to an encoded polypeptide.

In an alternative, the expression of an ORF in a host bacterium is found to be inhibitory, but the inhibition is found to be due to an RNA product of the genomic coding region. For antisense inhibition, the sequence of the bacterial target nucleic acid sequence can be identified by inspection of the phage sequence, and the full sequence of the relevant coding region for the bacterial product can be found from a database of the bacterial genomic sequence or can be isolated by standard techniques (*e.g.*, a clone in a genomic library can be isolated which contains the full bacterial ORF, and then sequenced).

In either case, the identification of a target which is inhibited by an RNA transcript produced by a phage provides both the possible inhibition of bacteria naturally containing the same target nucleic acid sequence, as well as the ability to use the target sequence in screening for other types of compounds which will act directly on the target nucleic acid sequence or on a polypeptide product expressed or regulated, at least in part, by the target of the inhibitory phage RNA.

In some cases it will be found that the target of an inhibitory phage RNA or protein has previously been found to be a target of an inhibitory phage RNA or protein has previously been found to be a target for an antibacterial agent. In such cases, the phage inhibitor can still provide useful information if it is found that the phage-encoded product acts at a different site than the previously identified antibacterial agent or inhibitor, *i.e.*, acts at a phage-specific site. For many targets, action at a different site provides highly beneficial characteristics and/or information. For example, an alternate site of inhibitor action can at least partially overcome a resistance mechanism in a bacterium. As an illustration, in many cases, resistance is due, in large part, to altered binding characteristics of the immediate target to the antibacterial agent. The altered binding is due to a structural change which prevents or destabilizes the binding. However, the structural change is frequently quite local, so that compounds which bind at different local sites will b unaffected or affected to a much lesser degree. Indeed, in some cases the local sites will be on a different molecule and so may be completely unaffected by the local structural change creating resistance to the original agent(s). An example of resistance due to altered binding is

provided by methicillin-resistant *Staphylococcus aureus*, in which the resistance is due to an altered penicillin-binding protein.

In other cases, a new site of action can have improved accessibility as compared to a site acted on by a previously identified agent. This can, for example, assist in allowing effective treatment at lower doses, or in allowing access by a larger range of types of compounds, potentially allowing identification of more potential active agents.

Another advantage is that the structural characteristics of a different site of action will lead to identification and/or development of inhibitors with different structures and different pharmacological parameter. This can allow a greater range of possibilities when selecting an antibacterial agent.

Yet further, different sites often produce different inhibitory characteristics in the target organism. This is commonly the case for multi-domain target proteins. Thus, inhibition targeting an alternate site can produce more efficacious action, *e.g.*, faster killing, slower development of resistance, lower numbers of surviving cells, and different secondary effects (for example, different nutrient utilization).

Staphylococcus aureus phage 77

As indicated above, the present invention is concerned, in part, with the use of bacteriophage 77 coding sequences and the encoded polypeptides or RNA transcripts to identify bacterial targets for potential new antibacterial agents.

As described, phage 77 ORFs 17, 19, 43, 102, 104, and 182 have been found to have bacteria inhibiting function. Identification of ORFs 17, 19, 43, 102, 104, and 182 and products from the phage which inhibit the host bacterium both provides an inhibitor compound and allows identification of the bacterial target affected by the phage-encoded inhibitor. Such a target is thus identified as a potential target for development of other antibacterial agents or inhibitors and the use of those targets to inhibit those bacteria. As indicated above, even if such a target is not initially identified in a particular bacterium, such a target can still be identified if a homologous target is identified in another bacterium. Usually, but not necessarily, such another bacterium would be a genetically closely related bacterium. Indeed, in some cases, an inhibitor encoded by phage 77 ORF 17, 19, 43, 102, 104, or 182 can also inhibit such a homologous bacterial cellular component.

Possible bacterial target sequences are described herein by reference to sequence source sites. In preferred embodiments, the sequence encoding the target corresponds

to a *S. aureus* nucleic acid sequence available from numerous sources including *S. aureus* sequences deposited in GenBank, *S. aureus* sequences found in European Patent Application No. 97100110.7 to Human Genome Sciences, Inc. filed January 7, 1997, *S. aureus* sequences available from TIGR at http://www.tigr.org/tdb/mdb/mdb.html, and *S. aureus* sequences available from the Oklahoma University *S. aureus* sequencing project at the following URL: http://www.genome.ou.edu/staph_new.html. Such possible targets are particularly applicable to *S aureus* phages 77, 3A, 96, and 44 AHJD.

The amino acid sequence of a polypeptide target is readily provided by translating the corresponding coding region. For the sake of brevity, the sequences are not reproduced herein. Also, in preferred embodiments, a target sequence corresponds to a *S. aureus* coding sequence corresponding to a sequence listed in Table 15 herein. The listing in Table 15 describes *S. aureus* sequences currently listed with GenBank. Again, for the sake of brevity, the sequences are described by reference to the database accession numbers instead of being written out in full herein. In cases where an entry for a coding region is not complete, the complete sequence can be readily obtained by routine methods, e.g., by isolating a clone in a phage host *S. aureus* genomic library, and sequencing the clone insert to provide the relevant coding region. The boundaries of the coding region can be identified by conventional sequence analysis and/or by expression in a bacterium in which the endogenous copy of the coding region has been inactivated and using subcloning to identify the functional start and stop codons for the coding region.

Staphyloccus aureus phage 44 AHJD

The present invention also can utilize the identification of naturally occuring DNA sequence elements within *Staphylococcus aureus* bacteriophage 44AHJD which encode proteins with antimicrobial activity.

Such identification can utilize bioinformatics identification of specific proteins (ORFs) utilized by *Staphylococcus aureus* bacteriophage 44AHJD during the viral life cycle, resulting in a slowing or arrest of growth of the bacterial host, or in death, of the *Staphylococcus aureus* host including lysis of the infected bacteria. Thus, some of the bacteriophage 44AHJD DNA sequences encoding these proteins (ORFs) are predicted to encode antimicrobial functions. Information derived from these DNA sequences and translated ORFs can, in turn, be utilized to develop inhibitory compounds by peptidomimetics that can also function as antimicrobials. In addition, the identification of the host bacterial proteins that are targeted and inhibited by the

antimicrobial bacteriophage ORFs can themselves provide novel targets for drug discovery.

The methodology described above is used to identify and characterize DNA sequences from *Staphylococcus* sp. bacteriophage 44 AHJD that have antimicrobial activity. As described in the Examples, the *Staphylococcus aureus* propagating strain (PS 44A), obtained from the Felix d'Herelle Reference Centre (#HER 1101), was used as a host to propagate its phage 44AHJD, also obtained from the Felix d'Herelle Reference Centre (#HER 101). By sequencing, we found that bacteriophage 44AHJD consists of 16,668 bp (Table 16) predicted to encode 73 ORFs greater than 33 amino acids (Tables 17 & 18). Computational analysis of the predicted protein products of *Staphylococcus aureus* bacteriophage 44AHJD identified homolgs in public sequence databases as listed inTable 19 and 20, along with the accompanying list of related proteins.

From this analysis, it is apparent that 3 genes (ORF 3, 7, and 8) are related to structural proteins found in other bacteriophages. These include genes predicted to encode a tail protein (ORF 3), an upper collar/connector protein of the phage virion (ORF 7), and a lower collar protein (ORF 8). Bioinformatics has also identified one gene whose product is likely involved in phage DNA synthesis. One gene (ORF 1) shows significant homology to DNA polymerases of a number of bacteriophages, bacteria and fungi, and the product of this gene is likely responsible for replicating the genetic material of bacteriophage 44AHJD. ORF 2 encodes a protein with homology to the *din*C gene of *Bacillus subtilis* that encodes a protein involved in teichoic acid biosynthesis. Teichoic acid is a polyphosphate polymer found in some, but not all, Gram positive organisms (and not in Gram negative organisms), where it is attached to the peptidoglycan layer. The phage protein may thus be involved in the synthesis of this material for incorporation into the cell wall, allowing enhanced lysis by the phage lysis enzymes or, as many enzymes can function in "reverse reactions", may be involved in its degradation allowing for penetration of the peptidoglycan and phage genome entry into the cell following adsorption. The similarity between *Staphylococcus aureus* bacteriophage 44AHJD and *E. coli* phage T7 indicates that they may share similar mechanisms of replication and growth. Both phages belong to the Pododviridae Family of bacteriophages and are members of the "T7-like" Genus of this Family (Ackermann and DuBow; VIth ICTV Report).

Two genes, ORF 9 and 12, were identified with the potential to encode antimicrobial protein products. The homology alignments are shown in Tables 19 and 20. The predicted product of ORF 9 is related to a class of genes which encodes lysozyme-like functions, enzymes which cleave linkages in the mucopolysaccharide cell wall structure of a variety of micro-organisms, including that from the *Staphylococcus aureus* bacteriophage Twort. ORF 12 of *Staphylococcus aureus* bacteriophage 44AHJD shows homology to a set of lysis proteins from several bacteriophages. These lysis proteins are also referred to as holins, and represent phage-encoded lysis functions required for transit of the phage murein hydrolases (lysozyme) to the periplasm, where it can digest the cell wall and thus lyse the bacterium.

Thus, in particular embodiments, the present invention provides a nucleic acid sequence isolated from *Staphylococcus aureus* bacteriophage 44AHJD comprising at least a portion of one of the genes described above with antimicrobial activity. For example, ORF 1 encodes a DNA polymerase function. This polymerase may utilize host-derived accessory proteins for its activity when replicating the phage template, sequestering such proteins from use by the bacterial polymerase, resulting in inhibition of DNA replication, cell division, and cell growth. Alternatively, ORF 9 directly encodes a polypeptide with antimicrobial activity. ORF 9 is predicted to encode an amidase, a protein known to act as a cell wall degrading enzyme. ORF 12 likely encodes a holin function required for transit of the phage amidase (gene *9* product) to the periplasm. When this type of gene product from Bacillus phage phi 29 (gene 14), was cloned in *Escherichia coli*, cell death ensued (Steiner et al., 1993). Thus, production of proteins from Bacillus phage phi 29 gene 14 in *E. coli* resulted in cell death, whereas production of protein from Bacillus phage phi 29 gene 14 concomitantly with the phi 29 lysozyme or unrelated murein-degrading enzymes led to lysis, suggesting that membrane-bound protein 14 induces a nonspecific lesion in the cytoplasmic membrane (Steiner et al., 1993).

The present invention also provides the use of the *Staphylococcus* bacteriophage 44 AHJD antimicrobial ORFs or ORF products as pharmacological agents, either wholly or in part and derivatives, as well as the use of corresponding peptidomimetics, developed from amino acid or nucleotide sequence knowledge derived from *Staphylococcus* bacteriophage 44 AHJD killer ORFs.

Enterococcus phage 182

Bacteriophage 182 was obtained from the Felix D'Herelle phage collection (Ste. Foy, Quebec) and infects *Enterococcus sp.* Group D. The genome of *Enterococcus* bacteriophage 182 consists of 17,833 bp (Table 21) and is predicted to encode 80 ORFs greater than 33 amino acids (Tables 22 and 23). Computational analysis of the predicted protein products of *Enterococcus* bacteriophage 182 was performed in order to identify protein products related to those deposited in public databases. Bacteriophage 182 protein products which detected sequences with significant sequence similarity in public databases are listed in Table 24 and 26, along with the accompanying list of related proteins.

From this analysis, it is apparent that 5 genes (ORF 001, 004, 007, 009, and 011) are related to structural proteins of several *Bacillus* phages – *Bacillus* bacteriophage PZA, phi-29, and B103. These include genes predicted to encode a tail protein (ORF 001), a head protein (ORF 004), and upper collar protein (ORF 007), a lower collar protein (ORF 009), and a pre-neck appendage protein (ORF 011). Two gene products are predicted to encode genes which direct phage morphogenesis – these are ORF 005 and 019.

Bioinformatics has also identified three genes whose products are likely involved in phage DNA synthesis. One gene, ORF 002 shows significant homology to DNA polymerases of a number of bacteriophages, and the product of this gene is likely responsible for replicating the genetic material of bacteriophage 182. ORF 006 encodes a protein with homology to the encapsidation proteins of several other bacteriophages, including *Bacillus* phage phi-29 (P11014), PZA (P07541), and B103 (X99260) and *Streptococcus* phage CP-1 (Z47794). These gene products catalyze the *in vivo* and *in vitro* genome-encapsidation reaction (Garvey et al., 1985). Proteins involved in genome packaging have been shown to have additional activities that affect biochemical reactions in other phages and their hosts. For example, the coat protein of the RNA bacteriophage MS2 interacts with viral RNA to translationally repress replicase synthesis (Pickett and Peabody, 1993). This protein-RNA interaction also plays a role in genome encapsidation, enveloping a single copy of the viral genome in a protein shell composed of many molecules of coat protein. In addition, the bacteriophage λ terminase enzyme can be lethal to *E. coli* when expressed,

suggesting cleavage of packaging sites in the bacterial chromosome. Also present within bacteriophage 182 is a gene, ORF 010, that encodes a protein that is related to the terminal proteins of *Bacillus* phage Nf (P06812), *Bacillus* phage GA-1 (X96987) and *Bacillus* phage B103 (X99260). DNA terminal proteins are linked to the 5' ends of both strands of the genome and are essential for DNA replication playing a role in initial priming of DNA replication. The similarity between *Enterococcus* bacteriophage 182 and Bacillus phages phi-29, PZA, and B103 indicates that they may share similar mechanisms of replication and growth. Protein-primed DNA replication is a well described phenomenon, and in the phi-29-like phages, the ends of the DNA serve as origins and termini of replication (Gutiérrez et al., 1986; Yoshikawa et al., 1985).

There is also a gene (ORF 015) that encodes a protein showing homology to an early protein product of *Bacillus* bacteriophage PZA and the single-strand nucleic acid binding protein of bacteriophage B103.

Two genes, ORF 008 and 014, were identified with the potential to encode anti-microbial protein products. The homology alignments are shown in Tables 24 & 26 and biochemical features of the predicted polypeptides shown in Table 25. The predicted product of ORF 008 is related to a class of genes which encodes lysozyme-like functions, enzymes which cleave linkages in the mucopolysaccharide cell wall structure of a variety of micro-organisms. ORF 014 of *Enterococcus* 182 shows homology to a set of lysis proteins from *Bacillus* bacteriophage phi-29, PZA, and B103. These lysis proteins are also referred to as holins and represent phage encoded lysis functions required for transit of the phage murein hydrolases (lysozyme) to the periplasm, where it can digest the outer cell wall and thus lyse the bacterium.

Thus, the present invention provides a nucleic acid sequence obtained from *Enterococcus* bacteriophage 182 comprising at least a portion of a phage 182 ORF, preferably an inhibitory ORF, and more preferably at least a portion of one of the genes described above with anti-microbial activity. For example, ORF 002 encodes a DNA polymerase function. This polymerase may utilize host-derived accessory proteins for its activity when replicating the phage template, sequestering such proteins from use by the bacterial polymerase, resulting in inhibition of DNA replication, cell division, and cell growth. Alternatively, ORFs 008 or 014 directly encode polypeptides with anti-microbial activity. ORF 008 is predicted to encode an

autolytic lysozyme, a protein known to have anti-microbial activity (Martin *et al.*, 1998). ORF 014 likely encodes a holin function required for transit of the phage murein hydrolases to the periplasm. When the related product from *Bacillus* phage phi 29 (gene 14), was cloned in *Escherichia coli*, cell death ensued (Steiner *et al.*, 1993). Thus, production of proteins from *Bacillus* phage phi 29 gene 14 in *E. coli* resulted in cell death, whereas production of protein from Bacillus phage phi 29 gene 14 concomitantly with the phi 29 lysozyme or unrelated murein-degrading enzymes led to lysis, suggesting that membrane-bound protein 14 induces a nonspecific lesion in the cytoplasmic membrane (Steiner *et al.*, 1993).

The present invention also provides the use of the *Enterococcus* bacteriophage 182 anti-microbial ORFs as pharmacological agents, either wholly or in part and derivatives, as well as the use of corresponding peptidomimetics, developed from amino acid or nucleotide sequence knowledge derived from *Enterococcus* bacteriophage 182 killer ORFs. This can be done where the structure of the peptidomimetic compound corresponds to the structure of the active portion of a product of an ORF. In this analysis, the peptide backbone is transformed into a carbon based hydrophobic structure that can retain cytostatic or cytocidal activity for the bacterium. This is done by standard medicinal chemistry methods, measuring growth inhibition of the various molecules in liquid cultures or on solid medium. These mimetics also represent lead compounds for the development of novel antibiotics. In this context, "corresponds" means that the peptidomimetic compound structure has sufficient similarities to the structure of the active portion of a product of one of the *Enterococcus* ORFs listed, that the peptidomimetic will interact with the same molecule as the product of the ORF, and preferably will elicit at least one cellular response in common which relates to the inhibition of the cell by the phage protein.

To validate the identity of an ORF as a killer ORF, it is preferably expressed in the host or other test bacterial organism and the effect of this expression on bacterial growth and replication is assessed. Therefore, all individual ORFs identified herein, e.g., those identified above, can be expressed, preferably overexpressed, in a suitable host bacterium e.g., a host *Enterococcus* and the effect of this expression or overexpression on host metabolism and viability can be measured.

Individual ORFs can be resynthesized from the phage genomic DNA by the polymerase chain reaction (PCR) using oligonucleotide primers flanking the ORF on

either side. Those skilled in the art are familiar with the design and synthesis of appropriate primer sequences. These single ORFs are preferably engineered so that they contain appropriate cloning sites at their extremities to allow their introduction into a new bacterial expression plasmid, allowing propagation in a standard bacterial host such as *E. coli,* but containing the necessary information for plasmid replication in the target microbe, *Enterococcus* sp. (hereafter referred to as a shuttle vector).

This shuttle vector also preferably contains regulatory sequences that allow inducible expression of the introduced ORF. As the candidate ORF may encode a killer function that will eliminate the host, it is highly advantageous that it not be expressed (or at least not expressed at a substantial level) prior to testing for activity; thus screening for such sequences in a constitutive fashion is less likely to be successful (lethality). In an example presented in Fig. 7, regulatory sequences from the *ars* operon are used to direct individual ORF expression in *Enterococcus.* The *ars* operon encodes a series of proteins which normally mediate the extrusion of arsenite and several other trivalent oxyanions from the cells when they are exposed to such toxic substances in their environment. The operon encoding this detoxifying mechanism is normally silent and only induced when arsenite-related compounds are present.

Therefore, individual phage ORFs can be expressed in *Enterococcus* or other suitable host in an inducible fashion by adding to the culture medium non-toxic arsenite concentrations during the growth of individual *Enterococcus* (or other host cells) clones expressing such individual phage ORFs. Toxicity of the phage killer ORF for the host is monitored by reduction or arrest of growth under induction conditions, as measured by optical density in liquid culture or after plating the induced cultures on solid medium. Subsequently, interference of the phage ORF with the host biochemical pathways ultimately leading to reducing or arresting host metabolism can be measured by pulse chase experiments using radiolabeled precursors of either DNA replication, RNA transcription, or protein synthesis.

Of course, other inducible regulatory sequences (e.g., promoters, operators, etc.) may be used (e.g., systems using positive induction of expression or systems using release of repression). A variety of such systems are known to those skilled in the art and can be utilized in the present invention.

Nucleic acid sequences of the present invention can be isolated using a method similar to those described herein or other methods known to those skilled in the art. In addition, such nucleic acid sequences can be chemically synthesized by well-known methods. Having the phage 182 ORFs, e.g., anti-bacterial ORFs of the present invention, portions thereof, or oligonucleotides derived therefrom as described, other anti-microbial sequences from other bacteriophage sources can be identified and isolated using methods described here or other methods, including methods utilizing nucleic acid hybridization and/or computer-based sequence alignment methods.

The invention also provides bacteriophage anti-microbial DNA segments from other phages based on nucleic acids and sequences hybridizing to the presently identified inhibitory ORF under high stringency conditions or sequences which are highly homologous. The bacteriophage anti-microbial DNA segment from bacteriophage 182 can be used to identify a related segment from another unrelated phage based on stringent conditions of hybridization or on being a homolog based on nucleic acid and/or amino acid sequence comparisons. As with the phage 182 inhibitory sequences, such homologous coding sequences and products can be used as antimicrobials, to construct active portions or derivatives, to construct peptidomimetics, and to identify bacterial targets.

Enterococcus sequences are listed in Table 27 by accession number, providing identification of possible targets of *Enterococcus* phage inhibitory ORF products, *e.g.*, from phage 182.

Streptococcus pneumoniae

As indicated in the Summary above, the present invention is concerned with the use of *Streptococcus* sp. bacteriophage Dp-1 coding sequences and the encoded polypeptides or RNA transcripts to identify bacterial targets for potential new antibacterial agents.

Streptococcus pneumoniae is an important cause of community-acquired pneumonia and a major cause of otitis media, sinusitis, and meningitis in children and adults. In Spain and other Mediterranean countries, the majority of *S. pneumoniae* are relatively resistant to penicillin (Klugman, 1990; Fenoll et al., 1991; Jorgensen et al., 1990). These strains also have decreased susceptibility to broad-spectrum cephalosporins, which are frequently used in the empiric treatment of meningitis and

other serious invasive bacterial infections. High-level resistance of pneumococci has been encountered in Hungary where 70% of children who were colonized with *S. pneumoniae* carried penicillin resistant strains that were also resistant to tetracycline, erythromycin, trimethoprim/sulfamethoxazole, and 30% resistant to chloramphenicol (Neu, 1992). The resistance of pneumococci to macrolides such as erythromycin averages 20-25% in France, ~20% in Japan, and <10% in Spain (Neu, 1992).

The antimicrobial susceptibilities and distribution of serotypes of the 42 isolates of *S. pneumoniae* in southern Taiwan from invasive infections have been recently determined (Hseuh et al., 1996). Resistance rates among these isolates were: erythromycin, 61.9%; clindamycin, 47.6%; chloramphenicol, 19%; and tetracycline, 73.8%. Resistance to three or more classes of antibiotics was found in 33.3% of the isolates. Bacteremic pneumonia and primary bacteremia accounted for 64.3% of the infections and mortality was 42.6%. Given the severity of these infections despite adequate antibiotic therapy, there is clearly a need for introduction of new therapeutic options to prevent mortality due to invasive *S. pneumoniae* infections.

Pneumococcal phages belong to four families and they present a great variety in morphology, including lytic and temperate phages (for a review, see Garcia et al., 1997). Examples of lytic phages are Cp-1 and Dp-1, whereas examples of temperate phages are HB-3, EJ-1, and HB-746. The complete nucleotide sequence and functional organization of Cp-1 has been reported (Martin et al., 1996). Cp-1 has a 19,345 bp double-stranded DNA genome, with a terminal protein covalently linked to its 5' ends, that replicates by a protein primed mechanism. The phage contains 29 ORFs, 23 on one strand and 6 on the opposite. When these predicted proteins were compared to sequences compiled in GenBank EMBL databases, to ORFs showed significant similarity to proteins of bacteriophage 29 that infects *B. subtilis* (Martin et al., 1996). The similar proteins corresponded to those involved in DNA replication (terminal protein and DNA polymerase), structural and morphogenic proteins (major head, collar, connector, tail, and encapsidation proteins), and proteins involved in lysis function (holin and lysozyme). In its strategy of lysis, the holin gene product inserts itself into the cell membrane, allowing access of the lysozyme to the peptidoglycan. Expression of the Cp-1 holin protein in *E. coli* results in cell death after 2-hours of induction, but did not lead to lysis (Garcia et al., 1997). Cells harboring a plasmid construction with holin and lysozyme genes together did lyse after induction and the

viability loss was similar to that of the culture expressing holin alone. Cloning of these lytic genes in *S. pneumoniae* showed that both genes had the same effect as in *E. coli*. That is, holin itself did not lyse the culture but the viability loss was noticeable, whereas both holin and lysozyme together were capable of lysing M31, an amidase deleted mutant (Garcia et al., 1997).

Recently, a small portion (~4 kbp) of a second *S. pneumoniae* phage, Dp-1, has been sequenced (Sheehan et al., 1997). This portion contains the genes coding for the lytic system (Sheehan et al., 1997) and shows a modular organization similar to that described for Cp-1. However, in this case, a single chimeric protein appears to be made in which the N-terminal domain is highly similar to that of the murein hydrolase coded by a gene found in the phage BK5-T that infects *Lactococcus lactis*, and the C-terminal domain is homologous to holins. Thus, both functions appear to have been combined in a novel chimeric protein.

Bacteriophage Dp-1 was obtained from Dr. P. Garcia (Departamento de Microbiologia Molecular, Centro de Departamento de Investigaciones Biologicas, Consejo Superior de Investigaciones Cientificas, Velazquez, Madrid, Spain). We found that Dp-1 has a double-stranded DNA genome of 56,506 bp, predicted to encode 85 ORFs greater than 33 amino acids and with upstream Shine-Dalgarno motifs for translation initiation (Tables 28 & 30, and Fig. 6). Computational analysis of the predicted protein products of *Streptococcus* bacteriophage Dp-1 protein products, which detected homologs in public databases, are listed inTable 31, along with the accompanying list of related proteins.

From this analysis, it is apparent that several predicted genes of Dp-1 encode polypeptides that are related to structural proteins. ORFs 001, 002, 004, and 030 are predicted to encode tail proteins, minor structural proteins, and minor capsid proteins (Table 31). We also note the identification of several gene products that are likely involved in DNA synthesis. These include ORF 3 which encodes DNA polymerase, ORF 8 which encodes a SWI/SNF helicase-related protein, ORF 10 encodes a protein showing homology to recA, and ORF 13 encodes a dnaZX-like ORF.

In *E. coli*, RapA encodes an RNA polymerase (RNAP)-associated protein with ATPase activity and which is a homolog of the eukaryotic SWI/SNF family, a set of proteins whose members are involved are involved in transcription activation, nucleosome remodeling, and DNA repair. RapA forms a stable complex with RNAP,

as if it were a subunit of RNAP and it is possible that the ORF 8 product behaves similarly or in a dominant-negative fashion to inhibit the activity of RapA. Mutation of the essential *E. coli* dnaZX results in a block in DNA chain elongation during replication (Maki et al., 1988). The dnaZX gene has only one open reading frame for a 71-kDa polypeptide from which the two distinct DNA polymerase III holoenzyme subunits, tau (71 kDa) and gamma (47 kDa), are produced. The tau subunit is the precursor of the gamma subunit, and the gamma subunit is produced by a –1 frameshift causing early termination of translation (Tsuchihashi et al., 1990). These proteins show single-strand DNA binding properties that is ATPase (and dATPase) dependent and are thought to increasing the processivity of the core DNA polymerase enzyme (Lee et al., 1987).

There are several Dp-1 ORFs which encode proteins predicted to play a role in cellular metabolic pathways. These include polypeptides involved in coenzyme PQQ synthesis (ORFs 20, 29, 38). Pyrrolo-quinoline quinone (PQQ) is the non-covalently bound prosthetic group of many quinoproteins catalysing reactions in the periplasm of Gram-negative bacteria. Most of these involve the oxidation of alcohols or aldose sugars. Interestingly, ORFs 20, 29, and 30 also show homology to the exoenzyme S regulon (Frank, 1997). Proteins encoded by the *P. aeruginosa* exoenzyme S regulon may be involved in a contact-mediated translocation mechanism to transfer anti-host factors directly into eukaryotic cells disrupting eukaryotic signal transduction through ADP-ribosylation (Frank, 1997).

There is also a protein with similarity to GTP cyclohydrolase I (ORF 21) and ORF 41 which shows homology to dUTPase (Table 31). GTP cyclohydrolase I is an enzyme that catalyzes the first reaction in the pathway for the biosynthesis of the pteridine, a cofactor of the monooxygenases of the aromatic amino acids. Disruption of the homologous gene in *Saccharomyces cerevisiae* leads to a recessive conditional lethality due to folinic acid auxotrophy, that can be complemented with the mammalian or bacterial GTP cyclohydrolase I enzymes (Nardese et al., 1996; Mancini et al., 1999).

ORF 16 shows high homology to autolysin. This region of the phage sequence was previously reported (Sheehan et al., 1997) and encompasses ~ 4 kbp of our sequence. The sequence published by (Sheehan et al., 1997) is shown in Table 32.

Thus, the present invention provides a nucleic acid sequence obtained from *Streptococcus* bacteriophage Dp-1 comprising at least a portion of a phage Dp-1 ORF, preferably an inhibitory ORF, and more preferably at least a portion of one of the genes described above with anti-microbial activity. For example, ORF 013 encodes a

protein with homology to the gamma subunit of DNA polymerase (dnaX gene). This protein may act in a dominant-negative fashion to sequester the host DNA polymerase for its own replication, thus inhibiting host DNA replication. The dnaX gene product is essential for *E. coli* replication (Kodaira et al., 1983).

In certain preferred embodiments of the present invention, the bacterial target of a bacteriophage inhibitor ORF product, e.g., an inhibitory protein or polypeptide, is encoded by a *Streptococcus* nucleic acid coding sequence from a host bacterium for bacteriophage Dp-1. As above, possible target sequences are described herein by reference to sequence source sites. The sequence encoding the target preferably corresponds to a *Streptococcus* nucleic acid sequence available from The Institute for Genomic Research (TIGR), or available from GenBank or other public database. The TIGR *Streptococcus* sequences are publicly available at The Institute for Genomics Research at URL: http://www.tigr.org

The amino acid sequence of a polypeptide target is readily provided by translating the corresponding coding region. For the sake of brevity, the sequences are not reproduced herein. Also, in preferred embodiments, a target sequence corresponds to a *Streptococcus pneumoniae* coding sequences corresponding to a sequence listed in Table 33 herein. Sequences for other Streptococcal species are also available from TIGR and./or from GenBank. The listing in Table 33 describes *Streptococcus* sequences currently deposited in GenBank. Again, for the sake of brevity, the sequences are described by reference to the GenBank entries instead of being written out in full herein. In cases where the TIGR or GenBank entry for a coding region is not complete, the complete sequence can be readily obtained by routine methods, *e.g.*, by isolating a clone in a phage Dp-1 host *Streptococcus* sp. genomic library, and sequencing the clone insert to provide the relevant coding region. The boundaries of the coding region can be identified by conventional sequence analysis and/or by expression in a bacterium in which the endogenous copy of the coding region has been inactivated and using subcloning to identify the functional start and stop codons for the coding region.

In the various aspects of this invention involving Dp-1 sequences, preferably the sequence is preferably not contained in the sequence described in Sheehan et al., 1997 (Table 32).

Validating Identified Inhibitory Phage ORFs

A fifth step involves validating the identified phage inhibitor ORF by independent methods, and delineating further possible smaller segments of the ORFs

that have inhibitory activity. Several methods exist to validate the role of the identified ORF as an inhibitor ORF.

One example utilizes the creation of a mutant variant of the phage ORF in which the candidate ORF carries a partial or complete loss-of-function mutation that is measurable as compared with the non-mutant ORF. Comparison of the effects of expression of the loss of function mutant with the normal ORF provides confirmation of the identification of an inhibitor ORF where the loss-of-function mutant provides a measurably lower level of inhibition, preferably no inhibition. The loss of function may be conditional, *e.g.*, temperature sensitive.

Once validation of the inhibitor ORF is achieved, a bi-directional deletion analysis can be carried out using the same experimental system to identify the minimal polypeptide segment that has inhibitor activity. This may be carried out by a variety of means, *e.g.*, by exonuclease or PCR methodologies, and is used to determine if a relatively small segment of the ORF (*i.e.*, the product of the ORF) still possesses inhibitory activity when isolated away from its native sequence. If so, a portion of the ORF encoding this "active portion" can be used as a template for the synthesis of novel anti-microbial agents and further allowing derivation of the peptide sequence, *e.g.*, using modified peptides and/or peptidomimetics.

In creation of certain peptidomimetics, the peptide backbone is transformed into a carbon-based hydrophobic structure that can retain inhibitor activity against the bacterium. This is done by standard medicinal chemistry methods, typically monitored by measuring growth inhibition of the various molecules in liquid cultures or on solid medium. These mimetics can also represent lead compounds for the development of novel antibiotics.

Recently, a major effort has been undertaken by the pharmaceutical industry and their biotechnology partners for the sequencing of bacterial pathogen genomes. The rationale is that the systematic sequencing of the genome will identify all of the bacterial proteins and therefore this proteome will be the target for designing novel inhibitor antibiotics. Although systematic, this approach has several major problems. The first is that analysis of primary amino acid sequences of bacterial proteins does not immediately reveal which protein will be essential for viability of the bacterium, and target validation is thus a major issue. The second problem is one of redundancy, as several biochemical pathways are either structurally duplicated in bacteria (different isoforms of the same enzyme), or functionally duplicated by the presence of salvage pathways in the event of a metabolic block in one pathway (different nutritional conditions). The third is that even a valid target may not be structurally or

functionally amenable to inhibition by small molecules because of inaccessibility (sequestration of target).

Therefore, there is considerable interest within the pharmaceutical and biotechnology industry in identifying key targets for drug discovery amongst the mass of novel targets generated by large-scale genomic sequencing projects.

On the other hand, and underscoring the instant invention, the phages herein described have, over millions of years, evolved specific mechanisms to target such key biochemical pathways and proteins. In the few cases where inhibition by phages has been elucidated (*e.g.*, see ref. 3), such bacterial targets are invariably rate-limiting in their respective biochemical pathways, are not redundant, and/or are readily accessible for inhibition by the phage (or by another inhibitory compound). Therefore, the sixth step of this invention involves identifying the host biochemical pathways and proteins that are targeted by the phage inhibitory mechanisms.

Identifying, Validating, and Characterizing Bacterial Host Target Proteins and Affected Pathways

A rationale for this step is that the inhibitor ORF product from the phage physically interacts with and/or modifies certain microbial host components to block their function. Exemplary approaches which can be used to identify the host bacterial pathways and proteins that interact with, and preferably also are inhibited by, phage ORF product(s) are described below.

One approach is a genetic screen to determine physiological protein:protein interaction, for example, using a yeast two hybrid system. In this assay, the phage ORF is fused to the carboxyl terminus of the yeast Gal4 activation domain II (amino acids 768-881) to create a bait vector. A cDNA library of cloned *S. aureus* sequences which have been engineered into a plasmid where the *S. aureus* sequences are fused to the DNA binding domain of Gal4 is also generated. These plasmids are introduced alone, or in combination, into yeast strain Y190 - previously engineered with chromosomally integrated copies of the *E. coli lacZ* and the selectable HIS3 genes, both under Gal4 regulation (Durfee, T., Becherer, K., Chen, P.-L., Yeh, S.-H., Yang, Y., Kilburn, A.E., Lee, W.-H., and Elledge, S.J. (1993). *Genes & Dev.* 7, 555-569). If the two proteins expressed in yeast interact, the resulting complex will activate transcription from promoters containing Gal4 binding sites. A *lacZ* and His3 gene, each driven by a promoter containing Gal4 binding sites, have been integrated into the genome of the host yeast system used for measuring protein-protein interactions. Such a system provides a physiological environment in which to detect potential protein interactions. This system has been extensively used to identify novel protein-protein

interaction partners and to map the sites required for interaction (for example, to identify interacting partners of translation factors (Qiu, H., Garcia-Barrio, M.T., and Hinnebusch, A.G. (1998). *Mol & Cell Biology* 18, 2697-2711), transcription factors (Katagiri, T., Saito, H., Shinohara, A., Ogawa, H., Kamada, N., Nakamura ,Y., and Miki, Y. (1998). Genes, *Chromosomes & Cancer* 21, 217-222), and proteins involved in signal transduction (Endo, T.A., Masuhara, M., Yokouchi, M., Suzuki, R., Sakamoto, H., Mitsui, K., Matsumoto, A., Tanimura, S., Ohtsubo, M., Misawa, H., Miyazaki, T., Leonor N., Taniguchi, T., Fujita, T., Kanakura, Y., Komiya, S., and Yoshimura, A. *Nature.* 387, 921-924). This approach has also been used in many published reports to identify interaction between mammalian viral and mammalian cell proteins.

For example, the non-structural protein NS1 of parvovirus is essential for viral DNA amplification and gene expression and is also the major cytopathic effector of these viruses. A yeast two-hybrid screen with NS1 identified a novel cellular protein of unknown function that interacts with NS-1, called SGT, for small glutamine-rich tetratricopeptide repeat (TPR)-containing protein (Cziepluch C. Kordes E. Poirey R. Grewenig A. Rommelaere, J, and Jauniaux JC. (1998) *J Virol.* 72, 4149-4156). In another screen, the adenovirus E3 protein was recently shown to interact with a novel tumor necrosis factor alpha-inducible protein and to modulate some of the activities of E3 (Li Y. Kang J. and Horwitz M.S. (1998). *Mol & Cell Biol.* 18, 1601-1610). In yet another recent screen, the herpes simplex virus 1 alpha regulatory protein ICP0 was found to interact with (and stabilize) the cell cycle regulator cyclin D3 (Kawaguchi Y. Van Sant C. and Roizman B. (1997). *J Virol.* 71,7328-7336).

Another two-hybrid system for identifying protein:protein interactions is commercially available from STRATEGENE™ as the CYTO-TRAP™ system (Chang et al., *Strategies Newsletter* 11(3), 65-68 (1998)(from Stratagene)). The system is a yeast-based method for detecting protein:protein interactions *in vivo*, using activation of the Ras signal transduction cascade by localizing a signal pathway component, human Sos (hSos), to its activation site in the yeast plasma membrane. The system uses a temperature-sensitive *Saccharomyces cerevisiae* mutant, strain cdc25H, which contains a point mutation at amino acid residue 1328 of the cdc25 gene. This gene encodes a guanyl nucleotide exchange factor which binds and activates Ras, leading to cell growth. The mutation in the cdc25 gene prevents host growth at 37°C, but at a permissive temperature of 25°C, growth is normal. The system utilizes the ability of (hSos) to complement the cdc25 defect and activate the yeast Ras signaling pathway. Once (hSos) is expressed and localized to the plasma membrane, the cdc25H yeast strain grows at 37°C. Localizing hSos to the plasma

membrane occurs through a protein:protein interaction. A protein of interest, or bait, is expressed as a fusion protein with hSos. The library, or target proteins are expressed with the myristylation membrane-localization signal. The yeast cells are then incubated under restrictive conditions (37°C). If the bait and the target protein interact, the hSos protein is recruited to the membrane, activating the Ras signaling pathway and allowing the cdc25H yeast strain to grow at the restrictive temperature.

The protein targets of phage inhibitory ORFs can also be identified using bacterial genetic screens. One approach involves the overexpression of a phage inhibitory protein in mutagenized bacterial host species, followed by plating the cells and searching for colonies that can survive the antimicrobial activity of the inhibitory ORF. These colonies are then grown, their DNA extracted, and cloned into an expression vector that contains a replicon of a different incompatibility group from the plasmid expressing the original ORF. This library is then introduced into a wild-type host bacterium in conjunction with an expression vector driving synthesis of the phage ORF, followed by selection for surviving bacteria. Thus, bacterial DNA fragments from the survivors presumably contain a DNA fragment from the original mutagenized host bacterial genome that can protect the cell from the antimicrobial activity of the inhibitory phage ORF. This fragment can be sequenced and compared with that of the bacterial host to determine in which gene the mutation lies. This approach enables one to determine the targets and pathways that are affected by the killing function.

A second approach is based on identifying protein:protein interactions between the phage ORF product and bacterial *S. aureus,* e.g., proteins using a biochemical approach based, for example, on affinity chromatography. This approach has been used, for example, to identify interactions between lambda phage proteins and proteins from their *E. coli* host (Sopta, M., Carthew, R.W., and Greenblatt, J. (1985) *J. Biol. Chem.* 260, 10353-10369). The phage ORF is fused to a peptide tag (*e.g.* glutathione-S-transferase ("GST"), 6xHIS, ("HIS") and/or calmodulin binding protein ("CPB")) within a commercially available plasmid vector that directs high level expression on induction of a suitably responsive promoter driving the fusion's expression. The translated fusion protein is expressed in *E. coli*, purified, and immobilized on a solid phase matrix via, for example the tag. Total cell extracts from the host bacterium, *e.g.*, *S. aureus*, are then passed through the affinity matrix containing the immobilized phage ORF fusion protein; host proteins retained on the column are then eluted under different conditions of ionic strength, pH, detergents etc., and characterized by gel electrophoresis and other techniques. Appropriate controls are run to guard against nonspecific binding to the resin. Target proteins thus

recovered should be enriched for the phage protein/peptide of interest and are subsequently electrophoretically or otherwise separated, purified, sequenced, or biochemically analyzed. Usually sequencing entails individual digestion of the proteins to completion with a protease (*e.g.*-trypsin), followed by molecular mass and amino acid composition and sequence determination using, for example, mass spectrometry, *e.g.*, by MALDI-TOF technology (Qin, J., Fenyo, D., Zhao, Y., Hall, W.W., Chao, D.M., Wilson, C.J., Young, R.A. and Chait, B.T. (1997). *Anal. Chem.* 69, 3995-4001).

The sequence of the individual peptides from a single protein are then analyzed by the bioinformatics approach described above to identify the *S. aureus* protein interacting with the phage ORF. This analysis is performed by a computer search of the *S. aureus* genome for an identified sequence. Alternatively, all tryptic peptide fragments of the *S. aureus* genome can be predicted by computer software, and the molecular mass of such fragments compared to the molecular mass of the peptides obtained from each interacting protein eluted from the affinity matrix. The responsible gene sequence can be obtained, for example by using synthetic degenerate nucleic acid sequences to pull out the corresponding homologous bacterial sequence. Alternatively, antibodies can be generated against the peptide and used to isolate nascent peptide/mRNA transcript complexes, from which the mRNA can be reverse transcribed, cloned, and further characterized using the procedures discussed herein.

A variety of other binding assay methods are known in the art and can be used to identify interactions between phage proteins and bacterial proteins or other bacterial cell components. Such methods that allow or provide identification of the bacterial component can be used in this invention for identifying putative targets.

Validation of the interaction between the phage ORF product and the bacterial proteins or other components can be obtained by a second independent assay (*e.g.*, co-immunoprecipitation or protein-protein crosslinking experiments (Qiu, H., Garcia-Barrio, M.T., and Hinnebusch, A.G. (1998). *Mol & Cell Biology* 18, 2697-2711; Brown, S. and Blumenthal, T. (1976). *Proc. Natl. Acad. Sci. USA* 73, 1131-1135)).

Finally, the essential nature of the identified bacterial proteins is preferably determined genetically by creating a constitutive or inducible partial or complete loss-of-function mutation in the gene encoding the identified interacting bacterial protein. This mutant is then tested for bacterial survival and replication.

The protein target of the phage inhibitor function can also be identified using a genetic approach. Two exemplary approaches will be delineated here. The first approach involves the overexpression of a predetermined phage inhibitor protein in mutagenized host bacteria, *e.g.*, *S. aureus*, followed by plating the cells and searching

for colonies that can survive the inhibitor. These colonies will then be grown, their DNA extracted and cloned into an expression vector that contains a replicon of a different incompatibility group, and preferably having a different selectible marker than the plasmid expressing the phage inhibitor. Thus, host DNA fragments from the mutant that can protect the cell from phage ORF inhibition can be sequenced and compared with that of the bacterial host to determine in which gene the mutation lies. This approach allows rapid determination of the targets and pathways that are affected by the inhibitor.

Alternatively, the bacterial targets can be determined in the absence of selecting for mutations using an approach known as "multicopy suppression". In this approach, the DNA from the wild type host is cloned into an expression vector that can coexist, as previously described, with one containing a predetermined phage inhibitor. Those plasmids that contain host DNA fragments and genes that protect the host from the phage inhibitor can then be isolated and sequenced to identify putative targets and pathways in the host bacteria.

Regardless of the specific mode of identification, screening assays may additionally utilize gene fusions to specific "reporter genes" to identify a bacterial gene(s) whose expression is affected when the host target pathway is affected by the phage inhibitor. Such gene fusions can be used to search a number of small molecule compounds for inhibitors that may affect this pathway and thus cause cell inhibition. This approach will allow the screening of a large number of molecules on petri dishes or 96-well format by monitoring for a simple color change in the bacterial colonies. In this manner, we can validate host targets and classes of compounds for further study and clinical development. These inhibitors also represent lead compounds for the development of other antibiotics.

Bioinformatics and comparative genomics are preferably then applied to the identified bacterial gene products to predict biochemical function. The biochemical activity of the protein can be verified *in vitro* in cell free assays or *in vivo* in intact cells. *In vitro* biochemical assays utilizing cell-free extracts or purified protein are established as a basis for the screening and development of inhibitors.

These inhibitors, preferably small molecule inhibitors, may comprise peptides, antibodies, products from natural sources such as fungal or plant extracts or small molecule organic compounds. In general, small molecule organic compounds are preferred. These compounds may, for example, be identified within large compound libraries, including combinatorial libraries. For example, a plurality of compounds, preferably a large number of compounds can be screened to determine whether any of the compounds binds or otherwise disrupts or inhibits the identified bacterial target.

Compounds identified as having any of these activities can then be evaluated further in cell culture and/or animal model systems to determine the pharmacological properties of the compound, including the specific anti-microbial ability of the compound.

For mixtures of natural products, including crude preparations, once a preparation or fraction of a preparation is shown the have an anti-microbial activity, the active substance can be isolated and identified using techniques well known in the art, if the compound is not already available in a purified form.

Identified compounds possessing anti-microbial activity and similar compounds having structural similarity can be further evaluated and, if necessary, derivatized according to synthesis and/or modification methods available in the art selected as appropriate for the particular starting molecule.

Derivatization of identified anti-microbials

In cases where the identified anti-microbials above might represent peptidal compunds, the *in vivo* effectiveness of such compounds may be advantageously enhanced by chemical modification using the natural polypeptide as a starting point and incorporating changes that provide advantages for use, for example, increased stability to proteolytic degradation, reduced antigenicity, improved tissue penetration, and/or improved delivery characteristics.

In addition to active modifications and derivative creations, it can also be useful to provide inactive modifications or derivatives for use as negative controls or introduction of immunologic tolerance. For example, a biologically inactive derivative which has essentially the same epitopes as the corresponding natural antimicrobial can be used to induce immunological tolerance in a patient being treated. The induction of tolerance can then allow uninterrupted treatment with the active anti-microbial to continue for a significantly longer period of time.

Modified anti-microbial polypeptides and derivatives can be produced using a number of different types of modifications to the amino acid chain. Many such methods are known to those skilled in the art. The changes can include, for example, reduction of the size of the molecule, and/or the modification of the amino acid sequence of the molecule. In addition, a variety of different chemical modifications of the naturally occurring polypeptide can be used, either with or without modifications to the amino acid sequence or size of the molecule. Such chemical modifications can, for example, include the incorporation of modified or non-natural amino acids or non-amino acid moieties during synthesis of the peptide chain, or the post-synthesis modification of incorporated chain moieties.

The oligopeptides of this invention can be synthesized chemically or through an appropriate gene expression system. Synthetic peptides can include both naturally occurring amino acids and laboratory synthesized, modified amino acids.

Also provided herein are functional derivatives of anti-microbial proteins or polypeptides. By "functional derivative" is meant a "chemical derivative," "fragment," "variant," "chimera," or "hybrid" of the polypeptide or protein, which terms are defined below. A functional derivative retains at least a portion of the function of the protein, for example reactivity with a specific antibody, enzymatic activity or binding activity.

A "chemical derivative" of the complex contains additional chemical moieties not normally a part of the protein or peptide. Such moieties may improve the molecule's solubility, absorption, biological half-life, and the like. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, and the like. Moieties capable of mediating such effects are disclosed in Alfonso and Gennaro (1995). Procedures for coupling such moieties to a molecule are well known in the art. Covalent modifications of the protein or peptides are included within the scope of this invention. Such modifications may be introduced into the molecule by reacting targeted amino acid residues of the peptide with an organic derivatizing agent that is capable of reacting with selected side chains or terminal residues, as described below.

Cysteinyl residues most commonly are reacted with alpha-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with diethylprocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0.

Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing primary amine- containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride;

trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine alpha-amino group.

Tyrosyl residues are well-known targets of modification for introduction of spectral labels by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizol and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction carbodiimide (R'-N-C-N-R') such as 1-cyclohexyl-3-(2-morpholinyl(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Derivatization with bifunctional agents is useful, for example, for cross-linking component peptides to each other or the complex to a water-insoluble support matrix or to other macromolecular carriers. Commonly used cross-linking agents include, for example, 1,1-bis (diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobi-functional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[p-azidophenyl) dithiolpropioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Patent Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains (Creighton, T.E.,

Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)), acetylation of the N-terminal amine, and, in some instances, amidation of the C-terminal carboxyl groups.

Such derivatized moieties may improve the stability, solubility, absorption, biological half life, and the like. The moieties may alternatively eliminate or attenuate any undesirable side effect of the protein complex. Moieties capable of mediating such effects are disclosed, for example, in Alfonso and Gennaro (1995).

The term "fragment" is used to indicate a polypeptide derived from the amino acid sequence of the protein or polypeptide having a length less than the full-length polypeptide from which it has been derived. Such a fragment may, for example, be produced by proteolytic cleavage of the full-length protein. Preferably, the fragment is obtained recombinantly by appropriately modifying the DNA sequence encoding the proteins to delete one or more amino acids at one or more sites of the C-terminus, N-terminus, and/or within the native sequence.

Another functional derivative intended to be within the scope of the present invention is a "variant" polypeptide that either lacks one or more amino acids or contains additional or substituted amino acids relative to the native polypeptide. The variant may be derived from a naturally occurring polypeptide by appropriately modifying the protein DNA coding sequence to add, remove, and/or to modify codons for one or more amino acids at one or more sites of the C-terminus, N-terminus, and/or within the native sequence.

A functional derivative of a protein or polypeptide with deleted, inserted and/or substituted amino acid residues may be prepared using standard techniques well-known to those of ordinary skill in the art. For example, the modified components of the functional derivatives may be produced using site-directed mutagenesis techniques (as exemplified by Adelman et al., 1983, *DNA* 2:183; Sambrook et al., 1989) wherein nucleotides in the DNA coding sequence are modified such that a modified coding sequence is produced, and thereafter expressing this recombinant DNA in a prokaryotic or eukaryotic host cell, using techniques such as those described above. Alternatively, components of functional derivatives of complexes with amino acid deletions, insertions and/or substitutions may be conveniently prepared by direct chemical synthesis, using methods well-known in the art.

Insofar as other anti-microbial inhibitor compounds identified by the invention described herein may not be peptidal in nature, other chemical techniques exist to allow their suitable modification, as well, and according the desirable principles discussed above.

Administration and Pharmaceutical Compositions

For the therapeutic and prophylactic treatment of infection, the preferred method of preparation or administration of anti-microbial compounds will generally vary depending on the precise identity and nature of the anti-microbial being delivered. Thus, those skilled in the art will understand that administration methods known in the art will also be appropriate for the compounds of this invention.

The particularly desired anti-microbial can be administered to a patient either by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s). In treating an infection, a therapeutically effective amount of an agent or agents is administered. A therapeutically effective dose refers to that amount of the compound that results in amelioration of one or more symptoms of bacterial infection and/or a prolongation of patient survival or patient comfort.

Toxicity, therapeutic and prophylactic efficacy of anti-microbials can be determined by standard pharmaceutical procedures in cell cultures and/or experimental organisms such as animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. Compounds that exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

For any compound identified and used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. Such information can be used to more accurately determine useful doses in organisms such as plants and animals, preferably mammals, and most preferably humans. Levels in plasma may be measured, for example, by HPLC or other means appropriate for detection of the particular compound.

The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition (see *e.g.* Fingl et. al., in The Pharmacological Basis of Therapeutics, 1975, Ch. 1 p.1).

It should be noted that the attending physician would know how and when to terminate, interrupt, or adjust administration due to toxicity, organ dysfunction, or other systemic malady. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding

toxicity). The magnitude of an administered dose in the management of the disorder of interest will vary with the severity of the condition to be treated and the route of administration. The severity of the condition may, for example, be evaluated, in part, by standard prognostic evaluation methods. Further, the dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above also may be used in veterinary or phyto medicine.

Depending on the specific infection target being treated and the method selected, such agents may be formulated and administered systemically or locally, i.e., topically. Techniques for formulation and administration may be found in Alfonso and Gennaro (1995). Suitable routes may include , for example, oral, rectal, transdermal, vaginal, transmucosal, intestinal, parenteral, intramuscular, subcutaneous, or intramedullary injections, as well as intrathecal, intravenous, or intraperitoneal injections.

For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Use of pharmaceutically acceptable carriers to formulate identified anti-microbials of the present invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular those formulated as solutions, may be administered parenterally, such as by intravenous injection. Appropriate compounds can be formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Agents intended to be administered intracellularly may be administered using techniques well known to those of ordinary skill in the art. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are efficiently

delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, small organic molecules may be directly administered intracellularly.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated for oral administration may be in the form of tablets, dragees, capsules, or solutions, including those formulated for delayed release or only to be released when the pharmaceutical reaches the small or large intestine.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levitating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active anti-microbial compounds in water-soluble form. Alternatively, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

The above methodologies may be employed either actively or prophylactically against an infection of interest.

Computer-related Aspects and Embodiments

In addition to the provision of compounds as chemical entities, nucleotide sequences, or fragments thereof at least 95%, preferably at least 97%, more preferably at least 99%, and most preferably at least 99.9% identical to phage inhibitor sequences can also be provided in a variety of additional media to facilitate various uses.

Thus, as used in this section, "provided" refers to an article of manufacture, rather than an actual nucleic acid molecule, which contains a nucleotide sequence of the present invention; *e.g.*, a nucleotide sequence of an exemplary bacteriophage or a sequence encoding a bacterial target or a fragment thereof, preferably a nucleotide sequence at least 95%, more preferably at least 99% and most preferably at least 99.9% identical to such a bacteriophage or bacterial sequence, for example, to a polynucleotide of an unsequenced phage listed in Table 1, preferably of bacteriophage 77 (*S. aureus* host) or bacteriophage 3A (*S.aureus* host) or bacteriophage 96 (*S. aureus* host). Such an article provides a large portion of the particular bacteriophage genome or bacterial gene and parts thereof (*e.g.*, a bacteriophage open reading frame (ORF)) in a form which allows a skilled artisan to examine and/or analyze the sequence using means not directly applicable to examining the actual genome or gene or subset thereof as it exists in nature or in purified form as a chemical entity.

In one application of this aspect, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer

readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create an article of manufacture which includes one or more computer readable media having recorded thereon a nucleotide sequence or sequences of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can, for example, be presented in a word processing test file, formatted in commercially available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form a nucleotide sequence of an unsequenced bacteriophage, such as an exemplary bacteriophage listed in Table 1 or of a sequence encoding a bacterial target or a fragment thereof, preferably a nucleotide sequence at least 95%, more preferably at least 99% and most preferably at least 99.9% identical to such a bacteriophage or bacterial sequence, for example, to a polynucleotide of bacteriophage 77 (*S. aureus* host) or bacteriophage 3A (*S.aureus* host) bacteriophage

96 (*S. aureus* host), bacteriophage 44AHJD (*S. aureus* host), bacteriophage Dp-1 (*Streptococcus pneumoniae* host), or bacteriophage 182 (*Enterococcus* host) the present invention enables the skilled artisan to routinely access the provided sequence information for a wide variety of purposes.

Those skilled in the art understand that software can implement a variety of different search or analysis software which implement sequence search and analysis algorithms, *e.g.*, the BLAST (Altschul et al., J. Mol. Biol. 215:403410 (1990) and BLAZE (Brutlag et al., Comp. Chem 17:203-207 (1993)) search algorithms. For example, such search algorithms can be implemented on a Sybase system and used to identify open reading frames (ORFs) within the bacteriophage genome which contain homology to ORFs or proteins from other viruses, e.g, other bacteriophage, and other organisms, *e.g.*, the host bacterium. Among the ORFs discussed herein are protein encoding fragments of the bacteriophage genomes which encode bacteria-inhibiting proteins or fragments.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described. Such systems are designed to identify, among other things, useful fragments of the bacteriophage genomes.

As used herein, "a computer-based system" refers to the hardware, software, and data storage media used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input device, output device, and data storage medium or media. A skilled artisan will readily recognize that any of the currently available general purpose computer-based system are suitable for use in the present invention, as well as a variety of different specialized or dedicated computer-based systems.

As stated above, the computer-based systems of the present invention comprise data storage media having stored therein a nucleotide sequence of the present invention and the necessary hardware and software for supporting and implementing a search and/or analysis program.

As used herein, "data storage media" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search program" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means.

Search means are used to identify fragments or regions of the present gnomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches and/or sequence analyses can be adapted for use in the present computer-based systems.

As used herein in connection with sequence searches and analyses, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. Also, the target sequence length is preferably selected to include sequence corresponding to a biologically relevant portion of an encoded product, for example a region which is expected to be conserved across a range of source organisms. Preferably the sequence length of a target polypeptide sequence is from 5-100 amino acids, more preferably 7-50 or 7-100 amino acids, and still more preferably 10-80 or 10-100 amino acids. Preferably the sequence length of a target polynucleotide sequence is from 15-300 nucleotide residues, more preferably from 21-240 or 21-300, and still more preferably 30-150 or 30-300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length. Likewise, it may be desirable to search and/or analyze longer sequences.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output devices can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output device ranks fragments of the bacteriophage or bacterial sequences possessing varying degrees of homology to the

target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing methods and/or devices and/or formats can be used to compare a target sequence or target motif with the sequence stored in data storage media to identify sequence fragments of the bacteriophage or bacterium in question. One skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search program for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill, or later developed, also may be employed in this regard.

Figure 6 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well-known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the sequence (such as search tools, comparing tools, etc.) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

The data storage medium in which the sequence is embodied and the central processor need not be part of a single stand-alone computer, but may be separated so long as data transfer can occur. For example, the processor or processors being utilized for a search or analysis can be part of one general purpose computer, and the data storage medium can be part of a second general purpose computer connected to a network, or the data storage medium can be part of a network server. As another example the data storage medium can be part of a computer system or network accessible over telephone lines or other remote connection method.

EXAMPLES

Example 1. Growth of *Staph A* bacteriophage 77 and purification of genomic DNA.

The *Staphylococcus aureus* propagating strain (PS 77; ATCC #27699) was used as a host to propagate its respective phage 77 (ATCC # 27699-B1). Two rounds of plaque purification of phage 77 were performed on soft agar essentially as described in Sambrook et al (1989). Briefly, the PS 77 strain was grown overnight at 37°C in Nutrient broth [NB: 0.3% Bacto beef extract, 0.5% Bacto peptone (Difco Laboratories) and 0.5% NaCl (w/v)].The culture was then diluted 20x in NB and incubated at 37°C until the OD_{540}= .2 (early log phase) with constant agitation. In order to obtain single plaques, phage 77 was subjected to 10-fold serial dilutions using phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin (w/v)) and 10 µl of each dilution was used to infect 0.5 ml of the cell suspension in the presence of 400 µg/ml $CaCl_2$. After incubation of 15 min at room temperature (RT), 2 ml of melted soft agar kept at 45°C (NB supplemented with 0.6% agar) was added to the mixture and poured onto the surface of 100 mm nutrient agar plates (0.3% Bacto Beef extract, 0.5% Bacto peptone, 0.5% NaCl and 1.5% Bacto agar (w/v)). After overnight incubation at 30°C, a single plaque was isolated, resuspended in 1 ml of phage buffer by end over end rotation for 2 hrs at 20°C, and the phage suspension was diluted and used for a second infection as described above. After overnight incubation at 30°C, a single plaque was isolated and used as a stock.

The propagation procedure for bacteriophage 77 was modified from the agar layer method of Swanstörm and Adams (1951). Briefly, the PS 77 strain was grown to stationary phase overnight at 37°C in Nutrient broth. The culture was then diluted twenty-fold in NB and incubated at 37°C until the OD_{540}= .2. The suspension ($15x10^7$ Bacteria) was then mixed with $15x10^5$ plaque forming units (pfu) to give a ratio of 100-bacteria/phage particle in the presence of 400 µg/ml of $CaCl_2$. After incubation for 15 min at 20°C, 7.5 ml of melted soft agar (NB plus 0.6% agar) were added to the mixture and poured onto the surface of 150 mm nutrient agar plates and incubated 16 hrs at 30°C. To collect the phage plate lysate, 20 ml of NB were added to each plate and the soft agar layer was collected by scrapping off with a clean microscope slide followed by shaking of the agar suspension for 5 min to break up the agar. The mixture was then centrifuged for 10 min at 4,000 RPM (2,830xg) in a JA-10 rotor (Beckman) and the supernatant fluid (lysate) was collected and subjected to a treatment with 10 µg /ml of DNase I and RNase A for 30 min at 37°C. To precipitate the phage particles, the phage suspension was adjusted to 10% (w/v) PEG 8000 and

0.5 M of NaCl followed by incubation at 4°C for 16 hrs. The phage was recovered by centrifugation at 4,000 rpm (3,500xg) for 20 min at 4°C on a GS-6R table top centrifuge (Beckman). The pellet was resuspended with 2 ml of phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin). The phage suspension was extracted with 1 volume of chloroform and further purified by centrifugation on a cesium chloride step gradient as described in Sambrook et al. (1989), using a TLS 55 rotor centrifuged in an Optima TLX ultracentrifuge (Beckman) for 2 h at 28,000 rpm (67,000xg) at 4°C. Banded phage was collected and ultracentrifuged again on an isopycnic cesium chloride gradient (1.45 g/ml) at 40,000 rpm (64,000xg) for 24 h at 4°C using a TLV rotor (Beckman). The phage was harvested and dialyzed for 4 h at room temperature against 4 L of dialysis buffer consisting of 10 mM NaCl, 50 mM Tris-HCl [pH 8] and 10 mM $MgCl_2$. Phage DNA was prepared from the phage suspension by adding 20 mM EDTA, 50 mg/ml Proteinase K and 0.5% SDS and incubating for 1 h at 65°C, followed by successive extractions with 1 volume of phenol, 1 volume of phenol-chloroform and 1 volume of chloroform. The DNA was then dialyzed overnight at 4°C against 4 L of TE (10 mM Tris pH 8.0, 1mM EDTA).

Example 2. DNA sequencing of Bacteriophage 77 genome

Four micrograms of phage 77 DNA was diluted in 200 μl of TE (10 mM Tris, [pH 8.0], 1 mM EDTA) in a 1.5 ml eppendorf tube and sonication was performed (550 Sonic Dismembrator™, Fisher Scientific). Samples were sonicated under an amplitude of 3 μm with bursts of 5 s spaced by 15 s cooling in ice/water for 3 to 4 cycles. The sonicated DNA was then size fractionated by electrophoresis on 1% agarose gels utilizing TAE (1 x TAE is: 40 mM Tris-acetate, 1 mM EDTA [pH 8.0]) as the running buffer. Fractions ranging from 1 to 2 kbp were excised from the agarose gel and purified using a commercial DNA extraction system according to the instructions of the manufacturer (Qiagen), with a final elution of 50 μl of 1 mM Tris (pH 8.5).

The ends of the sonicated DNA fragments were repaired with a combination of T4 DNA polymerase and the Klenow fragment of E. coli DNA polymerase I, as follows. Reactions were performed in a reaction mixture (final volume, 100 μl) containing sonicated phage DNA, 10 mM Tris-HCl [pH 8.0], 50 mM NaCl, 10 mM $MgCl_2$, 1 mM DTT, 50 μg/ml BSA, 100 μM of each dNTP and 15 units of T4 DNA polymerase (New England Biolabs) for 20 min at 12°C followed by addition of 12.5 units of Klenow large fragment (New England Biolabs) for 15 min at room temperature. The reaction was stopped by two phenol/chloroform extractions and the

DNA was precipitated with ethanol and the final DNA pellet was resuspended in 20 µl of H_2O.

Blunt-ended DNA fragments were cloned by ligation directly into the *Hinc* II site of pKSII+ vector (New England Biolabs) dephosphorylated by treatment with calf intestinal alkaline phosphatase (New England Biolabs)-treated pKS II+ vector (Stratagene). A typical ligation reaction contained 100 ng of vector DNA, 2 to 5 µl of repaired sonicated phage DNA (50-100 ng) in a final volume of 20 µl containing 800 units of T4 DNA ligase (New England Biolabs) and was incubated overnight at 16°C. Transformation and selection of bacterial clones containing recombinant plasmids was performed in *E. coli* DH10β according to standard procedures (Sambrook et al., 1989).

Recombinant clones were picked from agar plates into 96-well plates containing 100 µl LB and 100 µg/ml ampicillin and incubated at 37°C. The presence of phage DNA insert was confirmed by PCR amplification using T3 and T7 primers flanking the *Hinc* II cloning site of the pKS II+ vector. PCR amplification of foreign insert was performed in a 15 µl reaction volume containing 10 mM Tris (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.02% gelatin, 1 µM primer, 187.5 µM each dNTP, and 0.75 units *Taq* polymerase (BRL). The thermocycling parameters were as follows: 2 min initial denaturation at 94°C for 2 min, followed by 20 cycles of 30 sec denaturation at 94°C, 30 sec annealing at 57°C, and 2 min extension at 72°C, followed by a single extension step at 72°C for 10 min. Clones with insert sizes of 1 to 2 kbp were selected and plasmid DNA was prepared from the selected clones using QIAprep™ spin miniprep kit (Qiagen).

The nucleotide sequence of the extremities of each recombinant clone was determined using an ABI 377-36 automated sequencer with two types of chemistry: ABI prism Big Dye™ primer or ABI prism Big Dye™ terminator cycle sequencing ready reaction kit (Applied Biosystems). To ensure co-linearity of the sequence data and the genome, all regions of phage genome were sequenced at least once from both directions on two separate clones. In areas that this criteria was not initially met, a sequencing primer was selected and phage DNA was used directly as sequencing template employing ABI prism Big Dye™ terminator cycle sequencing ready reaction kit.

Example 3. Bioinformatic management of primary nucleotide sequence from Phage 77.

Phage 77 sequence contigs were assembled using Sequencher™ 3.1 software (GeneCodes). To close contig gaps, sequencing primers were selected near the edge of

the contigs. Phage DNA was used directly as sequencing template employing ABI prism BIG DYE™ terminator cycle sequencing ready reaction kit. The complete sequence of bacteriophage 77 is shown in Table 2.

A software program was developed and used on the assembled sequence of bacteriophage 77 to identify all putative ORFs larger than 33 codons. Other ORF identification software can also be utilized, preferably programs which allow alternative start codons. The software scans the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon; I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG, GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI (http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code.

When an appropriate start codon is encountered, a counting mechanism is employed to count the number of codons (groups of three nucleotides) between this start codon and the next stop codon downstream of it. If a threshold value of 33 is reached, or exceeded, then the sequence encompassed by these two codons (start and stop codons) is defined as an ORF. This procedure is repeated, each time starting at the next nucleotide following the previous stop codon found, in order to identify all the other putative ORFs. The scan is performed on all three reading frames of both DNA strands of the phage sequence.

Sequence homology (BLAST) searches for each ORF are then carried out using an implementation of BLAST programs, although any of a variety of different sequence comparison and matching programs can be utilized as known to those skilled in the art. Downloaded public databases used for sequence analysis include:
i) non-redundant GenBank (ftp://ncbi.nlm.nih.gov/blast/db/nr.Z),
ii) Swissprot (ftp://ncbi.nlm.nih.gov/blast/db/swissprot.Z);
iii) vector (ftp://ncbi.nlm.nih.gov/blast/db/vector.Z);
iv) pdbaa databases (ftp://ncbi.nlm.nih.gov/blast/db/pdbaa.Z);
v) *S. aureus* NCTC 8325 (ftp://ftp.genome.ou.edu/pub/staph/staph-1k.fa);
vi) streptococcus pyogenes (ftp://ftp.genome.ou.edu/pub/strep/strep-1k.fa);
vii) *Streptococcus pneumoniae* (ftp://ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);
viii) *Mycobacterium tuberculosis* CSU#9 (ftp://ftp.tigr.org/pub/data/m_tuberculosis/TB_091097.Z) and
ix) pseudomonas aeruginosa (http://www.genome.washington.edu/pseudo/data.html).

The results of the homology searches performed on the ORFs is shown in Table 5.

Example 4. Subcloning of Bacteriophage 77 ORFs into a Staph A inducible expression system.

The shuttle vector pT0021, in which the firefly luciferase (*lucFF*) expression is controlled by the *ars* (arsenite) promoter/operator (Tauriainen et al., 1997), was modified in the following fashion. Two oligonucleotides corresponding to a short antigenic peptide derived from the heamaglutinin protein of influenza virus (HA epitope tag) were synthesized (Field et al., 1988). The sense strand HA tag sequence (with *BamHI*, *SalI* and *HindIII* cloning sites) is: 5'-gatcccggtcgaccaagcttTACCCATACGACGTCCCAGACTACGCCAGCTGA-3' (where upper case letters denote the nucletotide sequence of the HA tag); the antisense strand HA tag sequence (with a *HindIII* cloning site) is: 5'-agctTCAGCTGGCGTAGTCTGGGACGTCGTATGGGTAaagcttggtcgaccgg-3' (where upper case letters denote the sequence of the HA tag). The two HA tag oligonucleotides were annealed and ligated into pT0021 vector which had been digested with *BamHI* and *HindIII*. This manipulation resulted in replacement of the *lucFF* gene by the HA tag. This modified shuttle vector containing the *arsenite* inducible promoter, the *arsR* gene, and HA tag was named pTHA. A diagram outlining our modification of pT0021 to generate pTHA is shown in Fig. 1A.

Each ORF, encoded by Bacteriophage 77, larger than 33 amino acids and having a Shine-Dalgarno sequence upstream of the initiation codon was selected for functional analysis for bacterial inhibition. In total, 98 ORFs were selected and screened as detailed below. A list of these is presented in Table 3. Each individual ORF, from initiation codon to last codon (excluding the stop codon), was amplified from phage genomic DNA using the polymerase chain reaction (PCR). For PCR amplification of ORFs, each sense strand primer targets the initiation codon and is preceded by a *BamHI* restriction site ($^{5'}$cg<u>ggatcc</u>$^{3'}$) and each antisense oligonucleotide targets the pentultimate codon (the one before the stop codon) of the ORF and is preceded by a *Sal* I restriction site ($^{5'}$gc<u>gtcgac</u>cg$^{3'}$). The PCR product of each ORF was gel purified and digested with *BamHI* and *SalI*. The digested PCR product was then gel purified using the Qiagen kit as described, ligated into *BamHI* and *SalI* digested pTHA vector, and used to transform *E. coli* bacterial strain DH10β(as described above). As a result of this manipulation, the HA tag is set inframe with the ORF and is positioned at the carboxy terminus of each ORF (pTHA/ORF clones). Recombinant pTHA/ORF clones were picked and their insert sizes were confirmed by PCR analysis

using primers flanking the cloning site. The names and sequences of the primers that were used for the PCR amplification were: HAF: $^{5'}$TATTATCCAAAACTTGAACA$^{3'}$; HAR: $^{5'}$CGGTGGTATATCCAGTGATT$^{3'}$. The sequence integrity of cloned ORFs was verified directly by DNA sequencing using primers HAF and HAR. In cases where verification of ORF sequence could not be achieved by one pass with the sequencing primers, additional internal primers were selected and used for sequencing.

Staphylococcus aureus strain RN4220 (Kreiswirth et al., 1983) was used as a recipient for the expression of recombinant plasmids. Electoporation was performed essentially as previously described (Schenk and Laddaga, 1992). Selection of recombinant clones was performed on Luria-Broth agar (LB-agar) plates containing 30 μg/ml of kanamycin.

For each ORF introduced in the pTHA plasmid, 3 independent transformants were isolated and used to individually inoculate cultures in 5 ml of TSB containing 30μg/ml kanamycin, followed by growth to saturation (16 hrs at 30°C). An aliquot of this stationary phase culture was used to generate a frozen glycerol stock of the transformant (stored at - 80°C). The remaining culture was used for plasmid DNA extraction. Bacterial cells were harvested by centrifugation at 3000 x g at 22°C for 5 min. The pellet was resuspended in 200 μl 25% sucrose containing 25U/ml of lysostaphin and incubated for 15 min at 37°C. Then, 400μl of alkaline SDS solution (3% SDS, 0.2N NaOH) were added, well mixed and incubated for 7 min at room temperature. After the alkaline SDS treatment, 300μl of ice-cold 3M sodium acetate pH 4.8 were added, and the mix is immediately spun at 13000g for 15 min at room temperature. The supernatant was transferred to a new 1.5 ml conical centrifuge tube and 650μl of isopropanol (stored at room temperature) were added. The mix was then centrifuged at 13,000 x g for 5 min. The supernatant fluid was discarded, the pellet washed with 70% ethanol, and resuspended in 320 μl sterile distilled water.

The presence of individual phage 77 ORF DNA inserts in the plasmid was verified by PCR amplification using 1.5 μl transformant miniprep DNA in a PCR with primers flanking the cloning site of ORF in pTHA vector (HAF and HAR). The composition of the PCR reaction and the cycling parameters are identical to those employed for library screening described above.

Example 5. Functional assay for bacterial inhibitory activity of bacteriophage 77 ORFs.

The anti-microbial activity of individual phage 77 ORFs was monitored by two growth inhibitory assays, one on solid agar medium, the other in liquid medium.

In general, Staphylococcus bacteria transformed with expression plasmids containing individual ORFs were grown in normal TSA medium and stored in 19% glycerol. At pre-determined times, arsenite was added to the culture to induce transcription of the phage 77 ORFs cloned immediately downstream from an arsenite-inducible promoter in the pTHA expression plasmid.

The effect of ORF induction on bacterial growth characteristics was then monitored and quantitated. The growth inhibition assay on solid medium was performed by streaking pTHA/ORF containing *S. aureus* transformant onto LB-Kn and TSA-Kn plates containing increasing concentrations of sodium arsenite (0; 2.5; 5; and 7.5 μM). Arsenite is used to induce the expression of cloned DNA in pTHA vector. In parallel, 3 μl of 1/10 and 1/100 dilutions of the frozen cultures of the pTHA/ORF transformants were spotted as single drops onto LB-Kn and TSA-Kn plates containing increasing concentration of sodium arsenite (0; 2.5; 5; and 7.5 μM). The plates were then incubated 16 hrs at 37°C, and the effect of arsenite-induced ORF expression on bacterial growth was monitored and quantitated by comparing the extent to that seen in control plates. As positive controls for growth inhibition,the *holin/lysin* genes of the *Sthaphylococcus aureus* phage Twort (Loessner et al., 1998) was subcloned into the pTHA *ars* inducible vector and used.

For the growth inhibition assay in liquid medium, stationary phase cultures were prepared by inoculating 2.5ml TSB-Kn with frozen *S. aureus* RN4220 transformants containing phage 77 ORFs cloned in pTHA vector followed by incubation for 16 hrs at 37°C. These cultures were then diluted 1/100 in the same medium, and the bacteria were allowed to grow for 2 hrs at 37°C to reach early log phase. 150 μl of such culture were then mixed with 2.35 ml TSB-Kn medium with or without arsenite (the final concentration of arsenite in the medium was 0 or 5 μM arsenite). After 3.5 hrs incubation at 37°C with shaking at 250 rpm, 100 μl of bacterial culture was removed from each tube for OD_{565} measurement. Serial ten-fold dilutions of the culture in buffered saline solution (0.85% NaCl) were then spotted onto TSB-Kn plates. The plates were incubated at 37°C 16 hrs and the number of surviving colonies counted the following day. The growth inhibitory property of individual ORFs was then quantitated by comparing CFU numbers under normal or arsenite-induction conditions. A schematic flow of the inhibition analysis is shown in Fig. 3 (also applicable to inhibition analysis for the other phage and bacteria pointed out herein). Inhibition results are shown in Figures 4A-C.

<u>Example 6: Itentification of Cecropin Signature Motif in *Staphylococcus aureus* Bacteriophage 3A ORF</u>

The genome for *S. aureus* bacteriophage 3A was determined and the sequence was analyzed essentially as described for bacteriophage 77 in the examples above. Upon blast analysis of the identified open reading frames of phage 3A, the presence of an amino acid sequence corresponding to a cecropin signature motif was observed. This motif (WDGHKTLEK) is located at position aa 481-489. Cecropins were originally identified in proteins from the cecropia moth and are recognized as potent antibacterial proteins that constitute an important part of the cell-free immunity of insects. Cecropins are small proteins (31-39 amino acid residues) that are active against both Gram-positive and Gram-negative bacteria by disrupting the bacterial membranes. Although the mechanisms by which the cecropons cause cell death are not fully understood, it is generally thought to involve channel formation and membrane destabilization.

The identification of a motif corresponding to a known inhibitor suggests that the product of ORF002 is also an inhibitory compound. Such inhibitory activity can be confirmed as described herein or by other methods known in the art. Confirmation of the inhibitory activity would indicate that the ORF product could serve as the basis for construction of mimetic compounds and other inhibitors directed to the target of the ORF002 product.

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Example 7. Growth of *Staphylococcus aureus* bacteriophage 44AHJD:

Staphylococcus aureus propagating strain (PS 44A) (Felix d'Herelle Reference Centre #HER 1101) was used as a host to propagate its respective phage 44AHJD (Felix d'Herelle Reference Centre #HER 101). Two rounds of plaque purification of phage 44AHJD were performed on soft agar essentially as described in Sambrook *et al.* (1989). Briefly, the *Staphylococcus aureus* PS strain was grown overnight at 37°C in Nutrient Broth [NB: 3 g Bacto Beef Extract, 5 g Bactopeptone per liter, (Difco Laboratories # 0003-17-8), supplemented with 0.5% NaCl]. The culture was then diluted 20 fold in NB and incubated at 37°C until an OD_{540} of 0.2. In order to obtain single plaques, phage 44AHJD was subjected to 10-fold serial dilutions using the phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin) and 10 µl were used to infect 0.5 ml of the cell suspension in the presence of 400 µg/ml of

$CaCl_2$. After incubation of 15 min at room temperature, 2 ml of melted soft agar (NB supplemented with 0.6% of agar) were added to the mixture and poured onto the surface of 100 mm nutrient agar plates (3 g Bacto Beef extract, 5 g Bactopeptone, 0.5% NaCl and 15 g of Bacto agar per liter (Difco Laboratories # 0001-17-0). After overnight incubation at 37°C, a single plaque was isolated, resuspended in 1ml of phage buffer by end over end rotation for 2 h at room temperature and the phage suspension was diluted and used for a second infection as described above. After overnight incubation at 37°C, a single plaque was isolated and used as a stock.

Large scale purification of bacteriophage and preparation of phage DNA was as follows.

The propagation method was carried out by using the agar layer method described by Swanstörm and Adams (1951). Briefly, the PS 44A strain was grown to stationary phase overnight at 37°C in Nutrient Broth. The culture was then diluted 20x in NB and incubated at 37°C until the A_{540}= 0.2. The suspension ($15x10^7$ Bacteria) was then mixed with $15x10^5$ phage particles to give a ratio of 100-bacteria/phage particle in the presence of 400 µg/ml of $CaCl_2$. After incubation of 15 min at room temperature, 7.5 ml of melted soft agar were added to the mixture and poured onto the surface of 150 mm nutrient agar plates and incubated overnight at 37°C. To collect the lysate, 20 ml of NB were added to each plate and the soft agar layer was collected by scrapping off with a clean microscope slide and shaken vigorously for 5 min to break up the agar. The mixture was then centrifuged for 10 min at 4,000 rpm (2,830 xg) using a JA-10 rotor (Beckman) and the supernatant (lysate) is collected and subjected to a treatment with 10 µg/ml of DNase I and RNase A for 30 min at 37°C. To precipitate the phage particles, 10% (w/v) of PEG 8000 and 0.5 M of NaCl were added to the lysate and the mixture was incubated on ice for 16 h. The phage was recovered by centrifugation at 4,000 rpm (3,500 xg) for 20 min at 4°C on a GS-6R table top centrifuge (Beckman).

The pellet was resuspended with 2 ml of phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin). The phage suspension was extracted with 1 volume of chloroform and further purified by centrifugation on a preformed cesium chloride step gradient as described in Sambrook *et al.* (1989), using a TLS 55 rotor and centrifuged in an Optima TLX ultracentrifuge (Beckman) for 2 h at 28,000 rpm (67,000 xg) at 4°C. Banded phage was collected and ultracentrifuged again on an

isopycnic cesium chloride gradient (1.45 g/ml) at 40,000 rpm (64,000 x g) for 24 h at 4°C using a TLV rotor (Beckman). The phage was harvested and dialyzed for 4 h at room temperature against 4 L of dialysis buffer consisting of 10 mM NaCl, 50 mM Tris-HCl [pH 8] and 10 mM $MgCl_2$. Phage DNA was prepared from the phage suspension by adding 20 mM EDTA, 50 µg/ml Proteinase K and 0.5% SDS and incubating for 1 h at 65°C, followed by successive extractions with 1 volume of phenol, 1 volume of phenol-chloroform and 1 volume of chloroform. The DNA was then dialyzed overnight at 4°C against 4 L of TE (10 mM Tris-HCl [pH 8.0], 1mM EDTA).

Example 8. DNA sequencing of the Bacteriophage 44 AHJD genome.

Four mg of phage DNA was diluted in 200 µl of TE pH 8.0 in a 1.5 ml eppendorf tube and sonication was performed (550 Sonic Dismembrator, Fisher Scientific). Samples were sonicated under an amplitude of 3 µm with bursts of 5 s spaced by 15 s cooling in ice/water for 3 to 4 cycles and size fractionated on 1% agarose gels. The sonicated DNA was then size fractionated by gel electrophoresis. Fractions ranging from 1 to 2 kbp were excised from the agarose gel and purified using a coommercial DNA extraction system according to the instructions of the manufacturer (Qiagen) and eluted in 50 µl of 1mMTris-HCl [pH 8.5].

The ends of the sonicated DNA fragments were repaired with a combination of T4 DNA polymearse and the Klenow fragment of *E. coli* DNA polymerase 1 as follows. Reactions were performed in a final volume of 100 µl containing DNA, 10 mM Tris-HCl pH 8.0, 50 mM NaCl, 10 mM $MgCl_2$, 1 mM DTT, 5 µg BSA, 100 µM of each dNTP and 15 units of T4 DNA polymerase (New England Biolabs) for 20 min at 12°C followed by addition of 12.5 units of Klenow fragment (New England Biolabs) for 15 min at room temperature. The reaction was stopped by two phenol/chloroform extractions and the DNA was ethanol precipitated and resuspended in 20 µl of H_2O.

Cloning of the sonicated phage DNA into pKSII vector and transformation:

Blunt-ended DNA fragments were cloned by ligation directly into the *Hinc*II site of the pkSII vector (Stratagene) dephosphorylated with calf intestinal alkaline phosphatase (New England Biolabs). A typical reaction contained 100 ng of vector, 2

to 5 μl of repaired sonicated phage DNA (50-100 ng) in a final volume of 20 μl containing 800 units of T4 DNA ligase (New England Biolabs) overnight at 16°C. Transformation and selection of positive clones was performed in the host strain DH10 β of *E. coli* using ampicillin as a selective antibiotic as described in Sambrook *et al.* (1989).

Recombinant clones were picked from agar plates into 96-well plates containing 100 ml LB and 100 μg/ml ampicillin and incubated at 37°C. The presence of phage DNA insert was confirmed by PCR amplification using T3 and T7 primers flanking the *Hinc*II cloning site of the pKS vector. PCR amplification of the potential foreign inserts was performed in a 15 μl reaction volume containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.02% gelatin, 1 mM primer, 187.5 μM each dNTP, and 0.75 units *Taq* polymerase (BRL). The thermocycling parameters were as follows: 2 min initial denaturation at 94°C for 2 min, followed by 20 cycles of 30 sec denaturation at 94°C, 30 sec annealing at 58C, and 2 min extension at 72°C, followed by a single extension step at 72°C for 10 min. Clones with insert sizes of 1 to 2 kbp were selected and plasmid DNA was prepared from the selected clones using the QIAprep™ spin miniprep kit (Qiagen).
The nucleotide sequence of the extremities of each recombinant clone was determined using an ABI 377-36 automated sequencer with two types of chemistry: ABI prism BigDye™ primer cycle sequencing (21M13 primer: #403055)(M13REV primer: #403056) or ABI prism BigDye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). To ensure co-linearity of the sequence data and the genome, all regions of the phage genome were sequenced at least once from both directions on two separate clones. In areas that this criteria was not initially met, a sequencing primer was selected and phage DNA was used directly as sequencing template employing ABI prism BigDye™ terminator cycle sequencing ready reaction kit.

<u>Example 9. Bioinformatic management of primary nucleotide sequence.</u>

Sequence contigs were assembled using Sequencher™ 3.1 software (GeneCodes). To close contig gaps, sequencing primers were selected near the edge of the contigs. Phage DNA was used directly as sequencing template employing ABI

prism BigDye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). The complete sequence of *Staphylococcus aureus* bacteriophage 44AHJD is shown in Table 16.

A software program was used on the assembled sequence of bacteriophage 44AHJD to identify all putative ORFs larger than 33 codons. The software scans the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon; I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG, GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI(http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code. When an appropriate start codon is encountered, a counting mechanism is employed to count the number of codons (groups of three nucleotides) between this start codon and the next stop codon downstream of it. If a threshold value of 33 is reached, or exceeded, then the sequence encompassed by these two codons is defined as an ORF. This procedure is repeated, each time starting at the next nucleotide following the previous stop codon found, in order to identify all the other putative ORFs. The scan is performed on all three reading frames of both DNA strands of the phage sequence. The predicted ORFs for bacteriophage 44AHJD are listed in Tables 17 & 18.

Sequence homology searches for each ORF were carried out using an implementation of blast programs. Downloaded public databases used for sequence analysis include:

(i) non-redundant GenBank (ftp://ncbi.nlm.nih.gov/blast/db/nr.Z),

ii) Swissprot (ftp://ncbi.nlm.nih.gov/blast/db/swissprot.Z);

iii) vector (ftp://ncbi.nlm.nih.gov/blast/db/vector.Z);

iv) pdbaa databases (ftp://ncbi.nlm.nih.gov/blast/db/pdbaa.Z);

v) *Staphylococcus aureus* NCTC 8325 (ftp://ftp.genome.ou.edu/pub/staph/staph-1k.fa);

vi)*Staphylococcuspyogenes*(ftp://ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);

vii)PRODOM(ftp://ftp.toulouse.inra.fr/pub/prodom/current_release/prodom99_1.forblast.gz);

viii) DOMO (ftp://ftp.infobiogen.fr/pub/db/domo/);

ix) TREMBL (ftp://www.expasy.ch/databases/sp_tr_nrdb/fasta/)

The results of the homology searches performed on the ORFs of bacteriophage 44AHJD are shown in Tables 19 & 20.

Example 10. Sub-Cloning of Bacteriophage 44 AHJD ORFs.

Expression preferably utilizes a shuttle expression vector which is arranged such that expression of the exogenous bacteriophage 44 AHJD ORF sequence is inducible. For example, the shuttle vector pT0021, in which the firefly luciferase (*lucFF*) expression is controlled by the *ars* (arsenite) promoter/operator (Tauriainen et al., 1997), can be modified in the following fashion. Two oligonucleotides corresponding to a short antigenic peptide derived from the heamaglutinin protein of influenza virus (HA epitope tag) were synthesized (Field et al., 1988). The sense strand HA tag sequence (with *BamHI*, *SalI* and *Hind*III cloning sites) is: 5'-gatcccggtcgaccaagcttTACCCATACGACGTCCCAGACTACGCCAGCTGA-3' (where upper case letters denote the nucletotide sequence of the HA tag); the antisense strand HA tag sequence (with a *Hind*III cloning site) is: 5'-agctTCAGCTGGCGTAGTCTGGGACGTCGTATGGGTAaagcttggtcgaccgg-3' (where upper case letters denote the sequence of the HA tag). The two HA tag oligonucleotides were annealed and ligated into pT0021 vector which had been digested with *BamHI* and *Hind*III. This manipulation resulted in replacement of the *lucFF* gene by the HA tag. This modified shuttle vector containing the *arsenite* inducible promoter, the *arsR* gene, and HA tag was named pTHA. A diagram outlining our modification of pT0021 to generate pTHA is shown in Fig. 1A (another userful vector construct is shown in Fig. 1B).

Each ORF, encoded by Bacteriophage 44 AHJD, larger than 33 amino acids and having a Shine-Dalgarno sequence upstream of the initiation codon can be selected for functional analysis for bacterial inhibition. Each individual ORF, from initiation codon to last codon (excluding the stop codon), can be amplified from phage genomic DNA using the polymerase chain reaction (PCR). For PCR amplification of ORFs, each sense strand primer targets the initiation codon and is preceded by a *BamHI* restriction site ($^{5'}$cgggatcc$^{3'}$) and each antisense oligonucleotide targets the pentultimate codon (the one before the stop codon) of the ORF and is preceded by a *Sal* I restriction site ($^{5'}$gcgtcgaccg$^{3'}$). The PCR product of each ORF can be gel

purified and digested with *BamHI* and *SalI*. The digested PCR product can then be gel purified using the Qiagen kit as described, ligated into *BamHI* and *SalI* digested pTHA vector, and used to transform *E. coli* bacterial strain DH10β(as described above). As a result of this manipulation, the HA tag is set inframe with the ORF and is positioned at the carboxy terminus of each ORF (pTHA/ORF clones). Recombinant pTHA/ORF clones will be picked and their insert sizes were confirmed by PCR analysis using primers flanking the cloning site. The following primers can be used for PCR amplification: HAF: $^{5'}$TATTATCCAAAACTTGAACA$^{3'}$; HAR: $^{5'}$CGGTGGTATATCCAGTGATT$^{3'}$. The sequence integrity of cloned ORFs can be verified directly by DNA sequencing using primers HAF and HAR. In cases where verification of ORF sequence can not be achieved by one pass with the sequencing primers, additional internal primers will be selected and used for sequencing.

Staphylococcus aureus strain RN4220 (Kreiswirth et al., 1983) will be used as a recipient for the expression of recombinant plasmids. Electoporation will be performed essentially as previously described (Schenk and Laddaga, 1992). Selection of recombinant clones will be performed on Luria-Broth agar (LB-agar) plates containing 30 μg/ml of kanamycin.

Alternatively, a constitutive promoter can be used to drive expression of the introduced ORF, and compare cell growth to control bacterial cells containing the parental vector lacking any introduced phage ORF. Recombinant plasmids will be introduced into *Staphylococcus aureus* strain RN4220 (Kreiswirth et al., 1983) using electoporation as previously described (Schenk and Laddaga, 1992).

Cloning of ORFs with a Shine-Dalgarno sequence

ORFs with a Shine-Dalgarno sequence are selected for functional analysis of bacterial killing. Each ORF, from initiation codon to last codon (excluding the stop codon), can be amplified by PCR from phage genomic DNA. For PCR amplification of ORFs, each sense strand primer starts at the initiation codon and is preceded by a restriction site and each antisense strand starts at the last codon (excluding the stop codon) and is preceded by a different restriction site. The PCR product of each ORF will be gel purified and digested with the restriction enzymes with sites contained on the PCR oligonucleotides. The digested PCR product is then gel purified using the Qiagen kit, ligated into the modified shuttle vector, and used to transform bacterial strain DH10. Recombinant clones are then picked and their insert sizes confirmed by

PCR analysis using primers flanking the cloning site as well as restriction digestion. The sequence fidelity of cloned ORFs can be verified by DNA sequencing using the same primers as used for PCR. In the cases that the verification of ORFs can not be achieved by one path of sequencing using primers flanking the cloning site internal primers can be selected and used for sequencing. Recombinant plasmids can be introduced into *Staphylococcus aureus* strain RN4220 (Kreiswirth et al., 1983) using electoporation as previously described (Schenk and Laddaga, 1992).

Induction of gene expression from the *ars* promoter.

If an inducible promoter is used, e.g., the *ars* promoter, induction can be assessed, for example, in either of the two methods.

<u>1. Screening on agar</u> plates

The functional identification of killer ORFs can be performed by spreading an aliquot of *S. aureus* transformed cells containing phage 44 AHJD ORFs onto agar plates containing different concentrations of sodium arsenite (0; 2.5; 5; and 7.5 μM). The plates are incubated overnight at 37°C, after which a growth inhibition of the ORF transformants on plates that contain arsenite are compared to plates without arsenite.

<u>2. Quantification of growth inhibition in liquid medium</u>

Cells containing different recombinant plasmids can be grown for overnight at 37°C in LB medium supplemented with the appropriate antibiotic selection. These are then diluted to the mid log phase (OD_{540}=.2) with fresh media containing antibiotic and transferred to 96-well microtitration plates (100 μl/well). Inducer is then added at different final concentrations (ranging from 2.5 to 10 μM) and the culture incubated for an additional 2 hrs at 37°C. The effect of expression of the phage 44 AHJD ORFs on bacterial cell growth is then monitored by measuring the OD_{540} and comparing the rate of growth to the culture not containing inducer. [As positive controls for growth inhibition, the *kilA* gene of phage lambda (Reisinger, GR., Rietsch, A., Lubitz, W. and Blasi, U. 1993 *Virology* #193: 1033-1036), and the *holin/lysin* genes of the *Sthaphylococcus aureus* phage Twort (Loessner, MJ., Gaeng, S., Wendlinger, G., Maier, SK. and Scherer, S. 1998. *FEMS Microbiology Letters* #162:265-274) can be subcloned into the *ars* inducible vector. An aliquot of the induced and uninduced culture can also be plated out on agar plates containing an appropriate antibiotic selection but lacking inducer. Following incubation overnight at 37°C, the number of

colonies is counted. Any ORF showing bacteriostatic activity will show a lower, but detectable, number of colonies on the agar plates when grown in the presence of inducer as compared to when grown in the absence of inducer. Any ORF showing full bacteriocidal activity will show no colonies on the agar plates, when grown in the presence of inducer as compared to when grown in the absence of inducer.

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Example 11. Growth of *Enterococcus* bacteriophage 182 and purification of genomic DNA.

The *Enterococcus* propagating strain (PS) (*Enterococcus sp.* Group D, Felix d'Herelle Reference Centre #HER 1080) was used as host to propagate its respective phage 182 (Felix d'Herelle Reference Centre #HER 80). Two rounds of plaque purification of phage 182 were performed on soft agar essentially as described in Sambrook *et al.* (1989). Briefly, the *Enterococcus sp.* PS strain was grown overnight at 37°C in Tryptic Soy Broth [TSB: 17 g Bacto tryptone, 3 g Bacto soytone, 2.5 g Bacto dextrose, 5 g Sodium chloride, and 2.5 g Dipotassium phosphate per liter (Difco Laboratories (#0370-17-3)]. The culture was then diluted 20 fold in TSB and incubated at 37°C until the OD_{540}= 0.2 (early log phase) with constant agitation. In order to obtain single plaques, phage 182 was subjected to 10 fold serial dilutions using the phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin (w/v)) and 10 l of each dilution was used to infect 0.5 ml of the bacterial cell suspension. After incubation at 15 min at 37°C, 2 ml of melted soft agar (TSB supplemented with 0.6% agar) was added to the mixture and poured onto the surface of 100 mm Trytic Soy Agar plates [TSA: 15 g Tryptone peptone, 5 g Soytone peptone, 5 g Sodium chloride and 15 g of Agar per liter (Difco Laboratories #0369-17)]. After overnight incubation at 37°C, a single plaque was isolated, resuspended in 1 ml of phage buffer by end over end rotation for 2 hrs at room temperature, and the phage suspension was diluted and used for a second infection as described above. After overnight incubation at 37°C, a single plaque was isolated and used as a stock for all subsequent manipulations.

The propagation procedure for bacteriophage 182 was modified from the agar layer method of Swanstörm and Adams (1951). Briefly, the *Enterococcus* sp. PS strain was grown to stationary phase overnight at 37°C in TSB. The culture was then diluted 20 fold in TSB and incubated at 37°C until the A_{540}= 0.2. The suspension ($15x10^7$ Bacteria) was then mixed with $15x10^5$ plaque forming units (pfu) to give a

ratio of 100-bacteria/pfu. After incubation of 15 min at 37°C, 7.5 ml of melted soft agar (TSB plus 0.6% agar) were added to the mixture and poured onto the surface of 150 mm TSA plates and incubated 16 hrs at 37°C. To collect the plate lysate, 20 ml of TSB were added to each plate and the soft agar layer was collected by scrapping off with a clean microscope slide followed by vigorous shaking of the agar suspension for 5 min to break up the agar. The mixture was then centrifuged for 10 min at 4,000 rpm (2,830 xg) using a JA-10 rotor (Beckman) and the supernatant fluid (lysate) is collected and subjected to a treatment with 10 µg /ml of DNase I and RNase A for 30 min at 37°C. To precipitate the phage particles, the phage suspension was adjusted to 10% (w/v) of PEG 8000 and 0.5 M of NaCl followed by incubation at 4°C for 16 hrs. The phage was recovered by centrifugation at 4,000 rpm (3,500 xg) for 20 min at 4°C on a GS-6R table top centrifuge (Beckman). The pellet was resuspended with 2 ml of phage buffer (1 mM $MgSO_4$, 5 mM $MgCl_2$, 80 mM NaCl and 0.1% Gelatin). The phage suspension was extracted with 1 volume of chloroform and further purified by centrifugation on a cesium chloride step gradient as described in Sambrook *et al.* (1989), using a TLS 55 rotor and centrifuged in an Optima TLX ultracentrifuge (Beckman) for 2 hrs at 28,000 rpm (67,000 xg) at 4°C. Banded phage was collected and ultracentrifuged again on an isopycnic cesium chloride gradient (1.45 g/ml) at 40,000 rpm (64,000 xg) for 24 hrs at 4°C using a TLV rotor (Beckman). The phages were harvested and dialyzed for 4 hrs at room temperature against 4 L of dialysis buffer consisting of 10 mM NaCl, 50 mM Tris-HCl [pH 8] and 10 mM $MgCl_2$. Phage DNA was prepared from the phage suspension by adding 20 mM EDTA, 50 g/ml Proteinase K and 0.5% SDS and incubating for 1 hr at 65°C, followed by successive extractions with 1 volume of phenol, 1 volume of phenol-chloroform and 1 volume of chloroform. The DNA was then dialyzed overnight at 4°C against 4 L of TE (10 mM Tris-HCl [pH 8.0], 1mM EDTA).

<u>Example 12. DNA sequencing of the Bacteriophage 182 genome.</u>

Four micrograms of phage DNA was diluted in 200 µl of TE (10 mM Tris, [pH 8.0], 1 mM EDTA) in a 1.5 ml eppendorf tube and sonication was performed (550 Sonic Dismembrator, Fisher Scientific). Samples were sonicated under an amplitude of 3 µm with bursts of 5 s spaced by 15 s cooling in ice/water for 3 to 4

cycles. The sonicated DNA was then size fractionated by electrophoresis on 1% agarose gels utilizing TAE (1 x TAE is: 40 mM Tris-acetate, 1 mM EDTA [pH 8.0]) as the running buffer. Fractions ranging from 1 to 2 kbp were excised from the agarose gel and purified using a commercial DNA extraction system according to the instructions of the manufacturer (Qiagen), with a final elution of 50 µl of 1 mM Tris [pH 8.5].

The ends of the sonicated DNA fragments were repaired with a combination of T4 DNA polymerase and the Klenow fragment *of E. coli* DNA polymerase I, as follows. Reactions were performed in a reaction mixture (final volume, 100 µl) containing sonicated phage DNA, 10 mM Tris-HCl [pH 8.0], 50 mM NaCl, 10 mM $MgCl_2$, 1 mM DTT, 50 µg/ml BSA, 100 µM of each dNTP and 15 units of T4 DNA polymerase (New England Biolabs) for 20 min at 12°C followed by addition of 12.5 units of the Klenow large fragment of DNA polymerase I(New England Biolabs) for 15 min at room temperature. The reaction was stopped by two phenol/chloroform extractions and the DNA was precipitated with ethanol and the final DNA pellet resuspended in 20 µl of H_2O.

Blunt-ended DNA fragments were cloned by ligation directly into the *Hinc* II site of the pKSII+ vector (New England Biolabs) dephosphorylated by treatment with calf intestinal alkaline phosphatase (New England Biolabs). A typical ligation reaction contained 100 ng of vector DNA, 2 to 5 µl of repaired sonicated phage DNA (50-100 ng) in a final volume of 20 µl containing 800 units of T4 DNA ligase (New England Biolabs) and was incubated overnight at 16°C. Transformation and selection of bacterial clones containing recombinant plasmids was performed in *E. coli* DH10β according to standard procedures (Sambrook *et al.,* 1989).

Recombinant clones were picked from agar plates into 96-well plates containing 100 µl LB and 100 µg/ml ampicillin and incubated at 37°C. The presence of phage DNA insert was confirmed by PCR amplification using T3 and T7 primers flanking the Hinc II cloning site of the pKS vector. PCR amplification of the potential foreign inserts was performed in a 15 µl reaction volume containing 10 mM Tris (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.02% gelatin, 1 µM primer, 187.5 µM each dNTP, and 0.75 units *Taq* polymerase (BRL). The thermocycling parameters were as follows: 2 min initial denaturation at 94°C for 2 min, followed by 20 cycles of 30 sec

denaturation at 94°C, 30 sec annealing at 58°C, and 2 min extension at 72°C, followed by a single extension step at 72°C for 10 min. Clones with insert sizes of 1 to 2 kbp were selected and plasmid DNA was prepared from the selected clones using the QIAprep™ spin miniprep kit (Qiagen).

The nucleotide sequence of the extremities of each recombinant clone was determined using an ABI 377-36 automated sequencer with two types of chemistry: ABI prism Big Dye™ primer cycle sequencing (21M13 primer: #403055)(M13REV primer: #403056) or ABI prism Big Dye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). To ensure co-linearity of the sequence data and the genome, all regions of the phage genome were sequenced at least once from both directions on two separate clones. In areas that this criteria was not initially met, a sequencing primer was selected and phage DNA was used directly as sequencing template employing ABI prism BigDye™ terminator cycle sequencing ready reaction kit.

Example 13. Bioinformatic management of primary nucleotide sequence.

Sequence contigs were assembled using Sequencher™ 3.1 software (GeneCodes). To close contig gaps, sequencing primers were selected near the edge of the contigs. Phage DNA was used directly as sequencing template employing ABI prism BigDye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). The complete sequence of *Enterococcus* bacteriophage 182 is shown in Table 21.

A software program was used on the assembled sequence of bacteriophage 182 to identify all putative ORFs larger than 33 codons. The software scans the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon; I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG, GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI(http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code. When an appropriate start codon is encountered, a counting mechanism is employed to count the number of codons (groups of three nucleotides) between this start codon and the

next stop codon downstream of it. If a threshold value of 33 is reached, or exceeded, then the sequence encompassed by these two codons is defined as an ORF. This procedure is repeated, each time starting at the next nucleotide following the previous stop codon found, in order to identify all the other putative ORFs. The scan is performed on all three reading frames of both DNA strands of the phage sequence. The predicted ORFs for bacteriophage 182 are listed in Tables 22 & 23. Sequence homology searches for each ORF were carried out using an implementation of BLAST programs. Downloaded public databases used for sequence analysis include:

(i) non-redundant GenBank (ftp://ncbi.nlm.nih.gov/blast/db/nr.Z),

ii) Swissprot (ftp://ncbi.nlm.nih.gov/blast/db/swissprot.Z);

iii) vector (ftp://ncbi.nlm.nih.gov/blast/db/vector.Z);

iv) pdbaa databases (ftp://ncbi.nlm.nih.gov/blast/db/pdbaa.Z);

v) staphylococcus aureus NCTC 8325 (ftp://ftp.genome.ou.edu/pub/staph/staph-1k.fa);

vi) streptococcus pyrogenes (ftp://ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);

vii) PRODOM (ftp://ftp.toulouse.inra.fr/pub/prodom/current_release/prodom99.1.forblast.gz);

viii) DOMO (ftp://ftp.infobiogen.fr/pub/db/domo/);

ix) TREMBL (ftp://www.expasy.ch/databases/sp_tr_nrdb/fasta/)

The results of the homology searches performed on the ORFs of bacteriophage 182 are shown in Tables 24 & 26.

Example 14. Sub-Cloning of Bacteriophage 182 ORFs.

Preparation of the shuttle expression vector

Expression preferably utilizes a shuttle expression vector which is arranged such that expression of the exogenous bacteriophage 182 ORF sequence is inducible. For example, the plasmid pND50 replicates in *E. coli*, *E. faecalis*, and *S. aureus* (Yamagishi, J., Kojima, T., Oyamada, Y., Fujimoto, K., Hattori, H., Nakamura, S., and Inoue, M. 1996. *Antimocrob. Agents Chemother.* 40, 1157-1163). This plasmid can be modified by conventional techniques to insert the inducible arsenite promoter, derived from the shuttle vector pT0021, in which the firefly luciferase (*lucFF*)

expression is controlled by the *ars* promoter/operator from a *S. aureus* plasmid (Tauriainen, S., Karp, M., Chang, W and Virta, M. (1997). Recombinant luminescent bacteria for measuring bioavailable arsenite and antimonite. *Appl. Environ. Microbiol.* 63:4456-4461). This modified shuttle vector will contain the *ars* promoter, *arsR* gene and a cloning site for introduction of individual phage ORFs downstream from a shine-delgarno sequence.

Other inducible regulatory sequences can be utilized instead of the arsenite-inducible system. An example is a nisin-inducible system The nisA promoter activity is dependent on the proteins NisR and NisK, which constitute a two-component signal transduction system that responds to the extracellular inducer nisin. The nisin sensitivity and inducer concentration required for maximal induction varies among the strains, but is functional in *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Enterococcus faecalis*, and *Bacillus subtilis*. Significant induction of the nisA promoter (10- to 60-fold induction) can be obtained in all of the species. A vector containing this promoter was published as Eichenbaum Z, Federle MJ, Marra D, de Vos WM, Kuipers OP, Kleerebezem M, and Scott JR (1998) *Appl Environ Microbiol* 64, 2763-2769. Other vectors, e.g., plasmids, can also be utilized which will allow replication and transciption in *Enterococcus*.

Alternatively, a constitutive promoter can be used (e.g,, the β-lactamase promoter is constitutive in *E. faecalis* – see ref. 1) to drive expression of the introduced ORF, and compare cell growth to control bacterial cells containing the parental vector lacking any introduced phage ORF. Recombinant plasmids are introduced into *E. faecalis* strain FA2-2 by electroporation, as previously described (Yamagishi, J., Kojima, T., Oyamada, Y., Fujimoto, K., Hattori, H., Nakamura, S., and Inoue, M. 1996. *Antimicrob. Agents Chemother.* 40, 1157-1163).

Cloning of ORFs with a Shine-Dalgarno sequence

ORFs with a Shine-Dalgarno sequence are selected for functional analysis of bacterial killing. Each ORF, from initiation codon to last codon (excluding the stop codon), will be amplified by PCR from phage genomic DNA. For PCR amplification of ORFs, each sense strand primer starts at the initiation codon and is preceded by a restriction site and each antisense strand starts at the last codon (excluding the stop codon) and is preceded by a different restriction site. The PCR product of each ORF will be gel purified and digested with the restriction enzymes with sites contained on

the PCR oligonucleotides. The digested PCR product is then gel purified using the Qiagen kit, ligated into the modified shuttle vector, and used to transform bacterial strain DH10β. Recombinant clones are then picked and their insert sizes confirmed by PCR analysis using primers flanking the cloning site as well as restriction digestion. The sequence fidelity of cloned ORFs will be verified by DNA sequencing using the same primers as used for PCR. In the cases that the verification of ORFs can not be achieved by one path of sequencing using primers flanking the cloning site internal primers will be selected and used for sequencing. Recombinant plasmids will be introduced into E. faecalis strain FA2-2 by electroporation, as previously described (Yamagishi, J., Kojima, T., Oyamada, Y., Fujimoto, K., Hattori, H., Nakamura, S., and Inoue, M. 1996. Antimicrob. Agents Chemother. 40, 1157-1163).

Induction of gene expression from the *ars* promoter.

If an inducible promoter is used, e.g., the ars promoter, induction can be assessed, for example, in either of the two methods.

1. Screening on agar plates

The functional identification of killer ORFs can be performed by spreading an aliquot of *E. faecalis* transformed cells containing phage 182 ORF onto agar plates containing different concentrations of sodium arsenite (0; 2.5; 5; and 7.5 μM). The plates are incubated overnight at 37°C, after which a growth inhibition of the ORF transformants on plates that contain arsenite are compared to plates without arsenite.

2. Quantification of growth inhibition in liquid medium

Cells containing different recombinant plasmids can be grown for overnight at 37°C in LB medium supplemented with the appropriate antibiotic selection. These are then diluted to the mid log phase (OD_{540}=.2) with fresh media containing antibiotic and transferred to 96-well microtitration plates (100 μl/well). Inducer is then added at different final concentrations (ranging from 2.5 to 10 μM) and the culture incubated for an additional 2 h at 37°C. The effect of expression of the phage 182 ORFs on bacterial cell growth is then monitored by measuring the OD_{540} and comparing the rate of growth to the culture not containing inducer. As positive controls for growth inhibition, the *kilA* gene of phage lambda (Reisinger, GR., Rietsch, A., Lubitz, W. and Blasi, U. 1993 *Virology* #193: 1033-1036), and the *holin/lysin* genes of the *Sthaphylococcus aureus* phage Twort (Loessner, MJ., Gaeng, S., Wendlinger, G.,

Maier, SK. and Scherer, S. 1998. *FEMS Microbiology Letters* #162:265-274) were subcloned into the *ars* inducible vector. An aliquot of the induced and uninduced culture can also be plated out on agar plates containing an appropriate antibiotic selection but lacking inducer. Following incubation overnight at 37°C, the number of colonies is counted. Any ORF showing bacteriostatic activity will show a lower, but detectable, number of colonies on the agar plates when grown in the presence of inducer as compared to when grown in the absence of inducer. Any ORF showing bacteriocidal activity will show no colonies on the agar plates, when grown in the presence of inducer as compared to when grown in the absence of inducer.

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Example 15. Growth of *Streptococcus* bacteriophage Dp-1 and purification of genomic DNA.

The *Streptococcus pneumoniae* R6 propagating strain (PS) (Tomasz, 1966) was used as host to propagate its respective phage Dp-1 (McDonnell et al., 1975). (Alternatively, *Streptococcus (Diplococcus) pneumoniae* R36A could be used. Strain R36A is available from ATCC as #11733 or 27336. *Streptococcus pneumoniae* is also available from Felix d'Herelle Reference Center in Quebec, Canada as catalog number HER 1054. Other *S. pneumoniae* strains are also available from ATCC.) Two rounds of plaque purification of phage Dp-1 were performed on soft agar essentially as described in Sambrook *et al.* (1989). Briefly, the *Streptococcus* R6 PS strain was grown overnight at 37°C in K-Cat media [K-Cat: 10 g Bacto casitone, 5 g Bacto tryptone, 1 g Yeast extract, 5g Potassium chloride, 0.2% Glucose, 30mM Potassium phosphate buffer [pH 8] and 250,000 Units Catalase per liter (Boehringer Mannheim #10683600). The culture was then diluted 20 fold in K-CAT and

incubated at 37°C until the OD_{540}= 0.2 (early log phase) with constant agitation. In order to obtain single plaques, Dp-1 phage was subjected to 10-fold serial dilutions using the phage buffer (100 mM Tris-HCl [pH 7.5], 100 mM NaCl and 10 mM $MgCl_2$)and 10 µl of each dilution was used to infect 0.5 ml of the cell suspension. After incubation of 15 min at 37°C, 2 ml of melted soft agar (K-CAT supplemented with 0.8% of agar) were added to the mixture and poured onto the surface of 100 mm K-CAT agar plates [K-CAT supplemented with 1.2 % of agar]. After solidification of the soft agar layer, an additional 5 ml of melted soft agar was added to visualize distinct plaques (Ronda et al., 1978). After overnight incubation at 37°C, a single plaque was isolated, resuspended in 1 ml of phage buffer by end over end rotation for 2 hrs at room temperature, and the phage suspension was diluted and used for a second infection as described above. After overnight incubation at 37°C, a single plaque was isolated and used as a stock for all subsequent manipulations.

The propagation procedure for bacteriophage Dp-1 was modified from the agar layer method of Swanstörm and Adams (1951). Briefly, the R6 strain of *Streptococcus pneumoniae* was grown to stationary phase overnight at 37°C in K-CAT. The culture was then diluted 20 fold in K-CAT and incubated at 37°C until the OD_{540}= 0.2. The suspension ($15x10^7$ Bacteria) was then mixed with $15x10^5$ plaque forming units (pfu) to give a ratio of 100-bacteria/pfu. After incubation of 15 min at 37°C, 7.5 ml of melted soft agar (K-CAT plus 0.8% agar) were added to the mixture and poured onto the surface of 150 mm K-CAT agar plates and incubated 16 hrs at 37°C. After solidification of the soft agar layer, 7.5 ml of melted soft agar were added to each plate. To collect the plate lysate, 20 ml of K-CAT media were added to each plate and the soft agar layers were collected by scrapping off with a clean microscope slide followed by vigorous shaking of the agar suspension for 5 min to break up the agar. The mixture was then centrifuged for 10 min at 4,000 rpm (2,830 xg) using a JA-10 rotor (Beckman) and the supernatant (lysate) was collected and subjected to a treatment with 10 µg /ml of DNase I and RNase A for 30 min at 37°C. To precipitate the phage particles, the phage suspension was adjusted to 10% (w/v) of PEG 8000 and 0.5 M of NaCl followed by incubation at 4°C for 16 hrs. The phage was recovered by centrifugation at 4,000 rpm (3,500 xg) for 20 min at 4°C on a GS-6R table top centrifuge (Beckman). The pellet was resuspended with 2 ml of phage buffer (100 mM Tris-HCl [pH 7.5], 100 mM NaCl and 10 mM $MgCl_2$). The phage suspension was extracted with 1 volume of chloroform and further purified by centrifugation on a cesium chloride step gradient as described in Sambrook et al. (1989), using a TLS-55 rotor and centrifuged in an Optima TLX ultracentrifuge (Beckman) for 2 hrs at 28,000 rpm (67,000 xg) at 4°C. Banded phage was collected and ultracentrifuged again on an

isopycnic cesium chloride gradient (1.45 g/ml) at 40,000 rpm (64,000 xg) for 24 hrs at 4°C using a TLV rotor (Beckman). The phage was harvested and dialyzed for 4 hrs at room temperature against 4 L of dialysis buffer consisting of 10 mM NaCl, 50 mM Tris-HCl [pH 8] and 10 mM $MgCl_2$. Phage DNA was prepared from the phage suspension by adding 20 mM EDTA, 50 µg/ml Proteinase K and 0.5% SDS and incubating for 1 hr at 65°C, followed by successive extractions with 1 volume of phenol, 1 volume of phenol-chloroform and 1 volume of chloroform. The DNA was then dialyzed overnight at 4°C against 4 L of TE (10 mM Tris-HCl [pH 8.0], 1mM EDTA).

Example 16. DNA sequencing of the Bacteriophage Dp-1 genome.

Four micrograms of phage DNA was diluted in 200 µl of TE (10 mM Tris, [pH 8.0], 1 mM EDTA) in a 1.5 ml eppendorf tube and sonication was performed (550 Sonic Dismembrator, Fisher Scientific). Samples were sonicated under an amplitude of 3 µm with bursts of 5 sec spaced by 15 sec cooling in ice/water for 3 to 4 cycles. The sonicated DNA was then size fractionated by electrophoresis on 1% agarose gels utilizing TAE (1 x TAE is: 40 mM Tris-acetate, 1 mM EDTA [pH 8.0]) as the running buffer. Fractions ranging from 1 to 2 kbp were excised from the agarose gel and purified using a commercial DNA extraction system according to the instructions of the manufacturer (Qiagen), with a final elution of 50 µl of 1 mM Tris [pH 8.5].

The ends of the sonicated DNA fragments were repaired with a combination of T4 DNA polymerase and the Klenow fragment *of E. coli* DNA polymerase I, as follows. Reactions were performed in a reaction mixture (final volume, 100 µl) containing sonicated phage DNA, 10 mM Tris-HCl [pH 8.0], 50 mM NaCl, 10 mM $MgCl_2$, 1 mM DTT, 50 µg/ml BSA, 100 µM of each dNTP and 15 units of T4 DNA polymerase (New England Biolabs) for 20 min at 12°C followed by addition of 12.5 units of the Klenow large fragment of DNA polymerase I (New England Biolabs) for 15 min at room temperature. The reaction was stopped by two phenol/chloroform extractions and the DNA was precipitated with ethanol and the final DNA pellet resuspended in 20 µl of H_2O.

Blunt-ended DNA fragments were cloned by ligation directly into the *Hinc* II site of the pKSII+ vector (New England Biolabs) dephosphorylated by treatment with calf intestinal alkaline phosphatase (New England Biolabs). A typical ligation reaction contained 100 ng of vector DNA, 2 to 5 µl of repaired sonicated phage DNA (50-100 ng) in a final volume of 20 µl containing 800 units of T4 DNA ligase (New England Biolabs) and was incubated overnight at 16°C. Transformation and selection

of bacterial clones containing recombinant plasmids was performed in *E. coli* DH10β according to standard procedures (Sambrook *et al.,* 1989).

Recombinant clones were picked from agar plates into 96-well plates containing 100 µl LB and 100 µg/ml ampicillin and incubated at 37°C. The presence of phage DNA insert was confirmed by PCR amplification using T3 and T7 primers flanking the *Hinc* II cloning site of the pKS vector. PCR amplification of the potential foreign inserts was performed in a 15 µl reaction volume containing 10 mM Tris (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.02% gelatin, 1 µM primer, 187.5 µM each dNTP, and 0.75 units *Taq* polymerase (BRL). The thermocycling parameters were as follows: 2 min initial denaturation at 94°C for 2 min, followed by 20 cycles of 30 sec denaturation at 94°C, 30 sec annealing at 58°C, and 2 min extension at 72°C, followed by a single extension step at 72°C for 10 min. Clones with insert sizes of 1 to 2 kbp were selected and plasmid DNA was prepared from the selected clones using the QIAprep™ spin miniprep kit (Qiagen).

The nucleotide sequence of the extremities of each recombinant clone was determined using an ABI 377-36 automated sequencer with two types of chemistry: ABI prism Big Dye™ primer cycle sequencing (21M13 primer: #403055)(M13REV primer: #403056) or ABI prism Big Dye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). To ensure co-linearity of the sequence data and the genome, all regions of the phage genome were sequenced at least once from both directions on two separate clones. In areas that this criteria was not initially met, a sequencing primer was selected and phage DNA was used directly as sequencing template employing ABI prism Big Dye™ terminator cycle sequencing ready reaction kit.

Example 17. Bioinformatic management of primary nucleotide sequence.

Sequence contigs were assembled using Sequencher™ 3.1 software (GeneCodes). To close contig gaps, sequencing primers were selected near the edge of the contigs. Phage DNA was used directly as sequencing template employing ABI prism BigDye™ terminator cycle sequencing ready reaction kit (Applied Biosystems; #4303152). The complete sequence of *Streptococcus* bacteriophage Dp-1 is shown in Table 28.

A software program was used on the assembled sequence of bacteriophage Dp-1 to identify all putative ORFs larger than 33 codons. The software scans the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon; I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG,

GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI(http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code. When an appropriate start codon is encountered, a counting mechanism is employed to count the number of codons (groups of three nucleotides) between this start codon and the next stop codon downstream of it. If a threshold value of 33 is reached, or exceeded, then the sequence encompassed by these two codons is defined as an ORF. This procedure is repeated, each time starting at the next nucleotide following the previous stop codon found, in order to identify all the other putative ORFs. The scan is performed on all three reading frames of both DNA strands of the phage sequence. The predicted ORFs for bacteriophage Dp-1 are listed in Tables 29 and 30, and Fig. 6.

Sequence homology searches for each ORF were carried out using an implementation of BLAST programs. Downloaded public databases used for sequence analysis include:

(i) non-redundant GenBank (ftp://ncbi.nlm.nih.gov/blast/db/nr.Z),

ii) Swissprot (ftp://ncbi.nlm.nih.gov/blast/db/swissprot.Z);

iii) vector (ftp://ncbi.nlm.nih.gov/blast/db/vector.Z);

iv) pdbaa databases (ftp://ncbi.nlm.nih.gov/blast/db/pdbaa.Z);

v) staphylococcus aureus NCTC 8325 (ftp://ftp.genome.ou.edu/pub/staph/staph-1k.fa);

vi) streptococcus pyogenes (ftp://ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);

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viii) DOMO (ftp://ftp.infobiogen.fr/pub/db/domo/);

ix) TREMBL (ftp://www.expasy.ch/databases/sp_tr_nrdb/fasta/)

The results of the homology searches performed on the ORFs of bacteriophage Dp-1 are shown in Table 31.

Example 18. Sub-Cloning of Bacteriophage Dp-1 ORFs.

Preparation of the shuttle expression vector

Expression preferably utilizes a shuttle expression vector which is arranged such that expression of the exogenous bacteriophage Dp-1 ORF sequence is inducible. For example, the plasmid pLSE4 replicates in *E. coli*, and *S. pneumoniae* (Diaz and Garcia, 1990). This plasmid can be modified by conventional techniques to insert the inducible arsenite promoter, derived from the shuttle vector pT0021, in which the

firefly luciferase (*lucFF*) expression is controlled by the *ars* promoter/operator from a *S. aureus* plasmid (Tauriainen, S., Karp, M., Chang, W and Virta, M. (1997). Recombinant luminescent bacteria for measuring bioavailable arsenite and antimonite. *Appl. Environ. Microbiol.* 63:4456-4461). This modified shuttle vector will contain the *ars* promoter, *arsR* gene and a cloning site for introduction of individual phage ORFs downstream from a shine-dalgarno sequence.

Other inducible regulatory sequences can be utilized instead of the arsenite-inducible system. An example is a nisin-inducible system The nisA promoter activity is dependent on the proteins NisR and NisK, which constitute a two-component signal transduction system that responds to the extracellular inducer nisin. The nisin sensitivity and inducer concentration required for maximal induction varies among the strains, but is functional in *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Enterococcus faecalis*, and *Bacillus subtilis*. Significant induction of the nisA promoter (10- to 60-fold induction) can be obtained in all of the species. A vector containing this promoter was published as Eichenbaum Z, Federle MJ, Marra D, de Vos WM, Kuipers OP, Kleerebezem M, and Scott JR (1998) *Appl Environ Microbiol* 64, 2763-2769. Other vectors, e.g., plasmids, can also be utilized which will allow replication and transcription in *Streptococcus*.

Alternatively, a constitutive promoter can be used to drive expression of the introduced ORF, and compare cell growth to control bacterial cells containing the parental vector lacking any introduced phage ORF. Recombinant plasmids are introduced into *S. pneumoniae* R6 as previously described (Diaz and Garcia, 1990)

Cloning of ORFs with a Shine-Dalgarno sequence

ORFs with a Shine-Dalgarno sequence are selected for functional analysis of bacterial killing. Each ORF, from initiation codon to last codon (excluding the stop codon), will be amplified by PCR from phage genomic DNA. For PCR amplification of ORFs, each sense strand primer starts at the initiation codon and is preceded by a restriction site and each antisense strand starts at the last codon (excluding the stop codon) and is preceded by a different restriction site. The PCR product of each ORF will be gel purified and digested with the restriction enzymes with sites contained on the PCR oligonucleotides. The digested PCR product is then gel purified using the Qiagen kit, ligated into the modified shuttle vector, and used to transform bacterial strain DH10β. Recombinant clones are then picked and their insert sizes confirmed by PCR analysis using primers flanking the cloning site as well as restriction digestion. The sequence fidelity of cloned ORFs will be verified by DNA sequencing using the same primers as used for PCR. In the cases that the verification of ORFs can not be achieved by one path of sequencing using primers flanking the cloning site

internal primers will be selected and used for sequencing. Recombinant plasmids will be introduced into *S. pneumoniae* R6 as previously described (Diaz and Garcia, 1990).

Induction of gene expression from the *ars* promoter.

If an inducible promoter is used, e.g., the ars promoter, induction can be assessed, for example, in either of the two methods.

1. Screening on agar plates

The functional identification of killer ORFs can be performed by spreading an aliquot of *S. pneumoniae* transformed cells containing phage Dp-1 ORFs onto agar plates containing different concentrations of sodium arsenite (0; 2.5; 5; and 7.5 μM). The plates are incubated overnight at 37°C, after which a growth inhibition of the ORF transformants on plates that contain arsenite are compared to plates without arsenite.

2. Quantification of growth inhibition in liquid medium

Cells containing different recombinant plasmids can be grown for overnight at 37°C in LB medium supplemented with the appropriate antibiotic selection. These are then diluted to the mid log phase (OD_{540}=.2) with fresh media containing antibiotic and transferred to 96-well microtitration plates (100 μl/well). Inducer is then added at different final concentrations (ranging from 2.5 to 10 μM) and the culture incubated for an additional 2 hrs at 37°C. The effect of expression of the phage Dp-1 ORFs on bacterial cell growth is then monitored by measuring the OD_{540} and comparing the rate of growth to the culture not containing inducer. [As positive controls for growth inhibition, the *kilA* gene of phage lambda (Reisinger, GR., Rietsch, A., Lubitz, W. and Blasi, U. 1993 *Virology* #**193**: 1033-1036), and the *holin/lysin* genes of the *Sthaphylococcus aureus* phage Twort (Loessner, MJ., Gaeng, S., Wendlinger, G., Maier, SK. and Scherer, S. 1998. *FEMS Microbiology Letters* #**162**:265-274) can be subcloned into the *ars* inducible vector. An aliquot of the induced and uninduced culture can also be plated out on agar plates containing an appropriate antibiotic selection but lacking inducer. Following incubation overnight at 37°C, the number of colonies is counted. Any ORF showing bacteriostatic activity will show a lower, but detectable, number of colonies on the agar plates when grown in the presence of inducer as compared to when grown in the absence of inducer. Any ORF showing full bacteriocidal activity will show no colonies on the agar plates, when grown in the presence of inducer as compared to when grown in the absence of inducer.

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All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The specific methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. For example, those skilled in the art will recognize that the invention may suitably be practiced using a variety of different bacteria, bacteriophage, and sequencing methods within the general descriptions provided.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising," "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is not intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group. For example, if there are alternatives A, B, and C, all of the following possibilities are included: A separately, B separately, C separately, A and B, A and C, B and C, and A and B and C. Thus, for example, for the bacteria and phage specified herein, the embodiments expressly include any subset or subgroup of those bacteria and/or phage. While each such subset or subgroup could be listed separately, for the sake of brevity, such a listing is replaced by the present description.

Thus, additional embodiments are within the scope of the invention and within the following claims.

Table 1

Phages against human and animal pathogenic bacteria

I. Pathogen name	Phage name	II. Catalog#	Origin/reference
Acinetobacter calcoaceticus	A3/2 A10/45 A36 B9GP B_9PP BS46 E13 E14 531		Felix d'Herelle Reference Centre,Quebec,Quebec
	Ap3 P78		J. Bacteriol 1984. 157: 179-183 J. Gen. Microbiol 1986.132: 2633-2636
Acinetobacter haemolyticus			Felix d'Herelle Reference Centre,Quebec,Quebec
Acinetobacter johnsonii			Felix d'Herelle Reference Centre.Quebec,Quebec
Acinetobacter sp.	BP1		J.Virol.1968.2:716-722
	G4, HP2, HP3 & HP4		Can.J.Microbiol.1966.12:1023-1030 & J.Virol.1974.13:46-52 & Arch.Virol.1994.135:345-354
	A1, A4, A9 & 196		Arch.Virol.1994.135:345-354
	HP1		Can.J.Microbiol.1966.12:1023-1030
	A19, A23, A29, A31, A33, A34, A3759 & 2845		J.Microsc (Paris) 1973.16:215-224 & CR.Hebdo Seances Acad.Sci.Ser D.Sci Natur(Paris)278:1907-1909 & Arch.Virol.1994.135:345-354 & Rev.Can.Biol.1970.29:317-320
Actinobacillus actinomycetecomitans			FEMS Microbiol Lett 1994. 119:329-337

			Infec. Immun. 1982. 35: 343-349
			Mol.Gen.Genet 1998.258: 323-325
	Aaφ247		Oral Micriol. Immunol 1997.12: 40-46
Actinomyces viscosus		43146-B1	The American Type Culture Collection
			Infect.Immun.1985.48:228-233
			Infect.Immun.1988.56:54-59
			Plasmid 1997.37:141-153
Aeromonas hydrophila	PM2** & PM3		FEMS Microbiol.Lett. 1990.57:277-282
	Aeh1 Aeh2 PM4 PM5 PM6 T7-ah		Felix d'Herelle Reference Centre,Quebec,Quebec

Aeromonas salmonicida	3 25 29 31 32 $40RR_{2.8}t$ 43 51 56 59.1 65 Asp37		Felix d'Herelle Reference Centre,Quebec,Quebec
	55R.1		Can. J. Microbiol. 1983. 29: 1458-1461
Alteromonas espejiana	PM2**	27025-B1	The American Type Culture Collection
Asticacaulis biprosthecum			Felix d'Herelle Reference Centre,Quebec,Quebec
Asticcacaulis excentricus	ϕAc21 ϕAc24	15261-B1 15261-B2 15261-B3	The American Type Culture Collection
Azotobacter vinelandii	A14 A21 A31 A41 PAV1	12518-B1 12518-B4 12518-B5 12518-B9 12518-B10 13705-B1	The American Type Culture Collection
Azotobacter sp.			Virology 1972.49:439-452
Bacteroides fragilis	Bf-1		Rev. Infect. Dis. 1979. 1: 325-336
	B40-8		FEMS Microbiol. Lett. 1991. 66: 61-67
	HSP40		Appl. Environ. Microbiol. 1989. 55: 2696-2701
	phiA1		Zentralbl.bakteriol.1972.222:57-63
Bdellovibrio bacteriovorus	MAC-1		J. Gen. Microbiol. 1987. 133: 3065-3070
Bdellovibrio sp.	VL-1		J.Virol.1973.12:1522-1533
Bordetella brochiseptica	214		Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13

Bordetella parapertussis			Felix d'Herelle Reference Centre,Quebec,Quebec
			Mol. Gen. Mikrobiol. Virusol. 1988.4: 22-25
			Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13
	41405		Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13
Brucella abortus			Felix d'Herelle Reference Centre,Quebec,Quebec
	10/I 24/II 212/XV	23448-B1 23448-B2 23448-B3 17385-B1 17385-B2	The American Type Culture Collection
	BK-2, TB & Fi**		Zh.Mikrobiol.Epidemiol.Immunobiol.1983.2: 48-52
	R/c & R/O		Dev. Biol. Stand. 1984.56: 55-62
Brucella canis	R/c		Dev. Biol. Stand. 1984.56: 55-62
Brucella melitensis	BK-2	23456-B1	The American Type Culture Collection
Brucella suis	Wb		Zentralbl.Veterinarmed.1975.22:866-867

	Fi** & TB		Zh.Mikrobiol.Epidemiol.Immunobiol.1983.2: 48-52
Brucella sp.			Can. J. Vet. Res. 1989.53: 319-325
			Res. Vet. Sci. 1988. 44: 45-49
	R		Zh.Mikrtobiol.Epidemiol.Immunobiol.1983.2: 48
Campylobacter coli *Campylobacter coli (Cont'd)*	 18 19 20	43133-B1 43134-B1 43135-B1 43136-B1	The American Type Culture Collection The American Type Culture Collection
Campylobacter jejuni	1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20	35918-B1 35919-B1 35920-B1 35921-B1 35918-B2 35920-B2 35922-B2 35923-B1 35924-B1 35925-B1 35925-B2 35922-B2 35924-B2 35922-B3 43133-B1 43134-B1 43135-B1 43136-B1	The American Type Culture Collection
Campylobacter (Helicobacter) pylori	HP1		J. Med. Microbiol.1993. 38: 245-249
Chlamydia psittaci	Chp1**		J. Gen. Virol. 1989. 70: 3381-3390
Clostridium acetobutylicum	CAK-1		J.Bacteriol.1993.175:3838-3843

Clostridium botulinum			Nucleic Acids Res.1990.18:1291
			Bioch.Biophys.res.Commun.1990.171.1304-1311
			Microbiol.immunol.1981.25:915-927
	CE β & CE γ		J.Vet.Med.Sci.1992.54:675-684
Clostridium difficile	41 & 56		J. Clini.Microbiol. 1985.21:251-254

Clostridium perfringens			Rev.Can.Biol.1977.36:205-215
			FEMS Microbiol.Lett. 1990.54:323-326
Clostridium sporogenes	 59 70 71 72S 72L	8074-B1 17886-B1 17886-B3 17886-B4 17886-B5 17886-B6	The American Type Culture Collection
Clostridium tetani	A & B		Rev.Can.Biol.1978.37:43-46
Corynebacterium diphteriae			Vopr.Virusol.1986.31:577-584
Corynebacterium pseudotuberculosis	NN	12319-B1	The American Type Culture Collection
Corynebacterium sp	DLC 2921/49	12052-B1	The American Type Culture Collection

Enterococcus faecalis	42	19948-B1	The American Type Culture Collection
Enterococcus faecium	124 133	19950-B1 19953-b2 19953-B1	The American Type Culture Collection

Escherichia coli		11303-B14	The American Type Culture Collection
		11303-B10	
		11303-B21	
		8677-B1	
		11303-B13	
		13706-B4	
Escherichia coli (Cont'd)		15766-B1	The American Type Culture Collection
		15766-B1	
		1242-B5	
		15669-B2	
		15767-B1	
		11303-B16	
		27-65-B1	
		25065-B2	
	C204	15669-B1	
	E1	15597-B1	
	f1**	21816-B1	
	f2**	23724-B9	
	FCZ	15593-B1	
	fd**	25404-B1	
		29746-B1	
		23631-B1	
		25868-B1	
		25298-B1	
		25298-B2	
		11303-B37	
		11303-B24	
		11303-B26	
	If1**	11303-B27	
		11303-B28	
		11303-B29	
		11303-B30	
		11303-B33	
		11303-B31	
		11303-B25	
		11303-B35	
		11303-B34	
	MS2**	11303-B36	
	MU9	11303-B32	
	Mu-1	13706-B5	
	Ox6	11303-B1	
	P1**	11303-B2	
	P4 sid_i **	11303-B3	
	Q-β**	11303-B4	
	R17**	35060-B1	
	Z1K/1	35060-B2	
	ZJ/2	35060-B3	
		11303-B5	
		11303-B6	
		11303-B7	
		11303-B38	
		12141-B1	

Escherichia coli (Cont'd)	 547 UV1 UV47 UV375 α3** λ ** λ C-17 λ sus P-3 λ sus R-5 λ sus J-6 λ sus O-8 λ sus A-11 λ ind$^-$ ϕ92 ϕR ϕV-1 ϕX174** ϕXcs70am-3	11303-B20 11303-B17 11303-B15 11303-B11 11303-B18 13706-B2 23724-B2 23724-B1 23724-B3 23724-B4 23724-B5 23724-B6 23724-B7 23724-B8 35860-B1 13706-B3 15597-B2 13706-B1 49696-B1	The American Type Culture Collection
	G4** & ϕK**		Biochim.Biophysica Acta.1992.1130:277-288
	BF23**		J.Bacteriol.1977.129:265-275
	Mu1		J.Ultrastruct.Res.1966.14:441-448
	Hp17		J.Mol.Biol.1991.218:705-721
	K3** & Ox2**		FEBS Lett.1987.215:145-150
	Rb18**, Rb51 & Rb69**		J.Bacteriol.1990.172:180-186
	H1**, H3, H8, K9, K18 & Ox1		Mol.Gen.Genet.1990.221:491-494
	M1**, TuIa** & TuIb**		J.Mol.Biol.1987.196:165-174
	K10		J.Bacteriol.1979.140:680-686
	Qsr'		J.Bacteriol.1985.162:256-262
	B278		J.Gen.Microbiol.1988.134:1333-1338
	phi 80**		FEMS Microbiol.Lett.1994.119:71-76
	phi m173		Genetika 1985.21:673-675
	tf-1		J.Gen.Microbiol.1987.133:953-960
	P4 & phiR73		Mol.Microbiol.1995.18:201-208
	I_2-2		J.Gen.Microbiol.1982.128:2797-2804
	PRD1		Virology 1990.177:445-451
	K3hx		Mol.Gen.Genet.1987.206:110-115
	933J**& 933W**		Infect.Immunity.1986.53:135-140
	H19-B**		J.Bacteriol.1987.169:4308-4312
	Tcp-111		Zentralbnl.Bakteriol.Mikrobiol.Hyg.1988.270: 41-51

	N4**		Vet.Microbiol.1992.30:203-212
	Phi 80 trp		Ann.Inst.Pasteur.1971.120:121-125
	Obeta 1		J.Bacteriol.1978.133:172-177
	P1CM		J.Gen.Microbiol.1978.107:73-83
	PA-2**		J.Bacteriol.1990.172:1660-1662
	186**		Mol.Gen.Genet.1982.187:87-95
	186.IX.B		Mol.Microbiol.1992.6:2629-2642
	21**		Virology 1983.129:484-489
	P4**		MicrobiolRev.1993.57:683-702
	82**		J.Biol.Chem.1987.262:11721-11725
	PSP3		J.Bacteriol.1996.178:5668-5675
	HK022**		Nucleic Acids Res.1994.22:354-356
	D108**		Nucleic Acids Res.1986.14:3813-3825
Escherichia coli (Cont'd)	Rb49		J.Mol.Biol.1997.267:237-249
	Ike**		J.Mol.Biol.1985.181:27-39
	P22dis		Mol.Gen.Genet.1978.166:233-243
	N15**		J.Bacteriol.1996.178:1484-1486
	If1**		Proc.R.Soc.Lond.B.Biol.Sci.1991.245:23-30
	Stx2Phi-I & Stx2Phi-II		Infect.Immun.1998.66:4100-4107
	18		Virology 1987.156:122-126
	X		J.Gen.Microbiol.1981.126:389-396
	AC3		Mol.Microbiol.1991.5:715-725

	BW-1 C-1 E920g Esc-7-11 H19J Haiti HK243 Iα K20 K30 KL_3 M Mu** O103 O157:H7 P1D pt1 PilHα PR64FS PR772 SS4 β4Q λvir** Ω8 09-1 92		Felix d'Herelle Reference Centre,Quebec,Quebec
Haemophilus influenzae	HP1**		Nucleic Acids Res. 1996.24:2360-2368
	S2**		Gene 1997. 196: 139-144
Halobacterium cutirubrum	S45		Felix d'Herelle Reference Centre,Quebec,Quebec
Halobacterium halobium			Felix d'Herelle Reference Centre,Quebec,Quebec
			Can.J.Microbiol.1982.28:916-921
Halobacterium salinarium			Biol.Chem.Hoppe Seyler 1994.375:747-757

Klebsiella oxytoca	tf-1		J.Gen.Microbiol.1987.133:953-960
Klebsiella pneumoniae	60 92	23356-B1 23357-B1	The American Type Culture Collection
	K19Q		Felix d'Herelle Reference Centre,Quebec,Quebec
	FC3-1 & FC3-9		Can.J.Microbiol.1991.37:270-275
	FC3-10		FEMS Microbiol.Lett.1991.67:291-297
Klebsiella sp.	K11**		Mol.Gen.Genet. 1990.221:283-286
Leptospira sp.	LE1, LE3 & LE4		Res.Microbiol.1990.141:1131-1138
Listeria monocytogenes	243	23074-B1	The American Type Culture Collection
	197,1313 & 9425		Appl.Environ.Microbiol.1997.63:3374-3377
	H387 & H387-A		Appl.Environ.Microbiol.1993.59:2914-2917
	5775,6223 &12682		APMIS.1993.101:160-167
	2389, 2671, 4211 & 2685		Intervirology 1994.37:31-35 & Zentralbl.Bakteriol.Mikrobiol.Hyg.1986.261:12-28
	4b, 4ab, 4g & 3c		Ann.Microbiol (Paris) 1977.128:185-198
	A118, A500 & A511**		Mol.Microbiol. 1995.16:1231-1241-992
	1, 3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 17, 19 & 20		Ann.Microbiol. (Paris) 1979.130B:179-189
	1/2a, 1/2b, 3c, 4ab, 6a & 6b		Clin.Invest.Med.1984.7:229-232
	ϕLMUP35 2685		Felix d'Herelle Reference Centre,Quebec,Quebec
Listeria innocua	4211		Felix d'Herelle Reference Centre,Quebec,Quebec
Micrococcus luteus	 N3 N4 N8	4698-B1 4698-B4 4698-2 4698-B3	The American Type Culture Collection
Micrococcus luteus	N17		Can.J.Microbiol. 1979.25:1027-1035
Mycobacterium smegmatis	BK-3 Bo1** Bo 6 Bo 6II Bo 6III Mc-2 Mc-4 NN Phagus lacticola R1	27203-B1 27204-B1 27205-B1 27205-B2 27205-B3 607-B6 607-B7 11727-B1 11759-B1 607-B1	The American Type Culture Collection

	Legendre Leo Roy Sedge	HER 317 HER 330 HER 333 HER 335 HER 334 HER 331 HER 316	Felix d'Herelle Refrence Centre,Quebec,Quebec
			Mol.Microbiol.1993.7:395-405
			J.Mol.Biol.1998.279:143-164
			Proc.Natl.Acad.Sci USA.1988.84:2833-2837
			Mol.Biol.Rep. 1981.30:11-15
			Proc.Natl.Acad.Sci.USA 1997.94:10961-10966
	29M, 31M, 122, 154, 37, 29D, 46, 139,110, 141, 74D, AG1 & DS6A		Arch.Virol.1993.133:39-49 & Am.Rev.Respir.Dis.1975.112:17-22
Mycobacterium fortuitum	Bo 4 Bo 7	23052-B1 27207-B1 27207-B2	The American Type Culture Collection

Mycobacterium leprae			Ann.Microbiol. (Paris) 1982.133:93-97
Mycobacterium tuberculosis	DS6A	25618-B1 25618-B2 4243-B1	The American Type Culture Collection
	110, 139 & 33D		Arch.Virol.1993.133:39-49
	AG1,GS4E, BG1, PH & BK1		The Biology of Mycobacteria.Academic Press,Toronto 1982 (Ratledge & Stanford) 1982.309-351
Mycobacterium sp	Phagus pellegrini NN B1	11760-B1 11761-B1 23239-B1	The American Type Collection Culture

	TM4, ph60, ph72, PhAE39, phAE40 & Bxb1		Microbiology 1995.141:1173-1181
	C2		Experentia 1969.25:1112-1113
	18 & I15		J.Gen.Virol.1987.68:949-956
	63		Gruzlica 1968.36:617-622
	phlei & butyricum		J.Gen.Virol.1975.29:235-238
	MyF3P-59a		Z.Allg.Mikrobiol.1968.8:29-37
	Bo2a		J.Gen.Virol.1973.20:75-87
	D4,D28 & D32		J.Exptl.Med.1966.123:327-340
	HC		J.Bacteriol.1963.86:608-609
Mycobacterium vaccae	B5	15483-B1	The American Type Culture Collection
Mycobacterium phlei	 NN Bo 2 Bo 2h Bo 3	11728-B1 11758-B1 27086-B2 27086-B1	The American Type Culture Collection
Mycoplasma arthritidis	MAV1**		Infect.Immunity.1995.63:4016-4023
Mycoplasma hyorhinis	Hr-1		Arch.Virol.1983.77:81-85
Mycoplasma pneumoniae	Br-1		Arch.Virol.1983.75:1-15
Mycoplasma pulmonis			Plasmid 1995. 33: 41-49
Mycoplasma sp.			J.Gen.Microbiol.1985:131:3117-3126
			J. Virol.1986.59:584-590
			Gene 1994. 141: 1-8

		Microbios 1990. 64: 111-125
		Infection& Immunity 1995. 63: 4016-4023
		Med.Biol.1982.60:116-120
MV-L2 &		Arch.Virol.1979.61:289-296
		Acta.Virol.1978.22:443-450
		J.Gen.Virol.1979.42:315-322
		Virology 1973.55:118-126

			Science 1971.173:725-727
Neisseria perflava			J.Clin.Microbiol.1976. 4:87-91
Nocardia erythrypolis	φC		J.Gen.Virol.1974.23:247-254
	φEC		J.Bacteriol.1976.126:1104-1107
Pasteurella multocida	B225		Arch.Exp.Veterinarmed.1981.35:433-436
	B939a		Am.J.Vet.Res.1978.39:1565-1566
	Nos.115, 32, 967 & 1075		Vet.Med.Nauki. 1977.14:33-36
Propionibacterium acnes	NN	29399-B1	The American Type Collection Culture

Pseudomonas aeruginosa		12175-B1	The American Type Culture Collection
	2	12175-B2	
	2A	12175-B3	
	2B	12175-B4	
	11	14205-B1	
	16	14206-B1	
	24	14207-B1	
	27	14208-B1	
	44	14209-B1	
	73	14210-B1	
	95	14211-B1	
	109	14212-B1	
	113	14213-B1	
	249	14214-B1	
	B3	15692-B1	
	Hoff 2	14203-B1	
	Hoff 3	14204-B1	
	Pa	12055-B1	
	Pb	12055-B2	
	PB-1	15692-B3	
	Pc	12055-B3	
	Pf	25102-B1	
	PP7**	15692-B2	
	7 & 31		Felix d'Herelle Reference Centre,Quebec,Quebec
	Pf3**		J.Virol.1983.47:221-223
	φ-MC		Can.J.Microbiol.1969.15:1179-1186
	Pf1**		J.Mol.Biol.1991.218:349-364
	PR4**		J.Gen.Virol.1979.43:583-592
	A7		J.Bacteriol.1992.174:2407-2411
	KF1		J.Biochem.1983.93:61-71
	∅CTX**		Mol.Microbiol.1993.4:1703-1709
	f2**		J.Virol.1977.24:135-141

	φKZ, 21, φNZ, PMN17, PTB80, 68, PB-1, E79, 16, 109, 352, 1214, F8, 71, 337, M4, φC17, SL2, B17, Li-24, φmnP78, PS17**, φ1, 73, M6, Li-2, 7, φmnF82, PTB2, PTB20, PTB42, φKF77, 31, PTB21, 119x, φPLS27, B3, 258, Hw12, PM57, PM62, PM105, 148, PM681, 198, 218, 222, 242, 246, PC131, φC11, SL5, D3112**, Jb19, F7, PM69, PM13, PM61, PM113, φ240, 249 & 269		dd

Pseudomonas aeruginosa (Cont'd)	297, 309, 318, 11,		Arch.Virol.1993.131:141-151

Pseudomonas cepacia			Felix d'Herelle Reference Centre,Quebec,Quebec
Pseudomonas fragi	wy	27362-B1 27363 B1	The American Type Culture Collection
Pseudomonas phaseolicola	ϕ6		Felix d'Herelle Reference Centre,Quebec,Quebec
Pseudomonas putida	gh-1	12633-B1	The American Type Culture Collection
Pseudomonas syringae	ϕ6	40492-B1 21781-B1	The American Type Culture Collection
Pseudomonas sp.	PPs-G3	49780-B1	The American Type Culture Collection
Salmonella bareilly	Sab 2		Felix d'Herelle Reference Centre,Quebec,Quebec
Salmonella enteritidis	1, 2,3 & 6		Epidemiol.Infect.1995.114:227-236
	2a, 3a, 4a, 5a, 6a, 7a, 8a, 9a, 15, 19, 20 &21**		Vet.Med.Nauki.1975.12:55-60
Salmonella newington	Epsilon 34		J.Struct.Biol. 1995.115:283-289
Salmonella newport	16-19	27869-B1 27869-B2	The American Type Culture Collection
			Felix d'Herelle Reference Centre,Quebec,Quebec
Salmonella paratyphi	Paratyphoid A	19940-B1 12176-B1	The American Type Culture Collection
	Jersey		Felix d'Herelle Reference Centre,Quebec,Quebec
Salmonella senftenberg	SasL1, SaL2, Sal 3, SaL4, SaL5 & SasL6		Indian J.Med.Res. 1997.105:47-52
Salmonella typhimurium	P22** SL-1	19585-B1 40282	The American Type Culture Collection
	MB78**		J.Virol. 1982.41: 1038-1043
	SE1		J.Gen.Microbiol.1986.132:1035-1041
	LT2		Virology 1971.45:835-636
	ES18**		Virology 1970.42:621-632
	L**		J.Virol.1985.56:1034-1036

	P1CM clr-100		Mol.Gen.Genet.1975.138:113-126
	F22		Genet.Res.1986.48:139-143
	Fels 1		J.Gen.Virol.1978.38:263-272
	Fels 2		Genet.Res.1986.48:139-143
	Px		Mol.Gen.Genet.1970.108:184-202
	P1kc		Virology 1974.60:503-514
	A3 & A4		J.Bacteriol. 1987.169:1003-1009
	HT		Genet.Res.1976.27:315-322
Salmonella typhimurium (Cont'd)	IRA		J.Basic Microbiol. 1990.30:707-716
	Mud1		Mol.Gen.Genet. 1986.202:327-330
	P22 (cir4-1, cir5-1 & cir6-1)		Mol.Gen.Genet.1984.198:105-109
	BF23**		Mol.Gen.Genet.1976.147:195-202
	Kb1		J.Bacteriol.1974.117:907-908
	P221dis		J.Gen.Virol.1978.41:367-376
	PRD1**		Virology 1990.177:445-451
	I_2-2**		J.Gen.Microbiol.1982.128:2797-2804
	tf-1		J.Gen.Microbiol.1987.133:953-960
	X**		J.Gen.Microbiol.1981.126:389-396
Salmonella typhosa/typhi	8 23 25 46 53 163 175 ViI ViVI	19937-B1 19938-B1 19939-B1 19942-B1 19943-B1 19946-B1 19947-B1 27870-B1 27870-B2	The American Type Culture Collection
	O1		Felix d'Herelle Refrence Centre,Quebec,Quebec
	ViII		Chung Hua Liu Hsing Ping H.T.C.1992.13:288
	j2		J.Gen.Microbiol.1983.129:3395-33400
Salmonella sp.	P3 P4** P9a P9c P10 102 Chi (χ) R34	25957-B1 25957-B2 25957-B3 25957-B4 25957-B5 19945-B1 9842-B1 97541	The American Type Culture Collection
	MG40		Virology 1968.34:521-530
	P14		Microb.Pathog.1990.8:393-402
	PSP3		Virology 1992.188:414
	Ike**		Zentralbl.Bakteriol.1976.234:294-304
	P27 & 9NA		J.Virol.1986.12:921-931
Sphaerotilus natans	SN1		Appl.Environ.Microbiol.1979.37:1025-1030

Shigella dysenteriae	 P2 ϕ-80	23351-B1 11456b 11456a-B1	The American Type Culture Collection
Shigella flexeneri	D20	12661-B1	The American Type Culture Collection
	SfII**		Mol.Microbiol.1997.26:939-950
	SfV**		Gene 1997.22:217-227
	Sf6**		Mol.Microbiol.1995.18:201-208
	SfX		Gene 1993.129:99-101
Shigella sonnei	C16**		
	Ufa		Mol..Biol (Mosk) 1977.11:323-331
Shigella sp	37	23354-B1	The American Type Culture Collection
Spiroplasma citri	SpV1		Plasmid 1993.29:193-205
Spiroplasma sp.	SpV1-R8A2B		Nucleic Acids Res. 1990.18:1293
	SpV3		Isr.J.Med.Sci.1987.23:429-433
	Sp V4		J.Bacteriol.1987.169:4950-4961
Staphylococcus albus			Staphylococci & Staphylococcal Infections.1997. Vol1:503-508 (Karger,Basel)

Staphylococcus aureus		27702-B1	The American Type Culture Collection
		27703-B1	
		27704-B1	
		23360-B1	
		23361-B1	
	15	27705-B1	
	17	27712-B1	
	29	27690-B1	
	42D**	27691-B1	
	42E	27692-B1	
	47	27693-B1	
	52	27694-B1	
	52A	27695-B1	
	53	27696-B1	
	54	27697-B1	
	55	27698-B1	
	71	27699-B1	
	75	27693-B2	
	77	27700-B1	
	79	27701-B1	
	80	27706-B1	
	81	27707-B1	
	83A	27708-B1	
	84	33742	
	85**	33741-B1	
	88	15565	
	92	19685-B1	
	5504'	11987-B1	
	K	11988-B1	
	P1	15752-B1	
	P14		
	UC18		

	Twort**	HER 101 HER 239 HER 283 HER 49	Felix d'Herelle Reference Centre,Quebec,Quebec
	ϕ11**		J.Bacteriol.1988.170:2409-2411
	ϕ13** & ϕ42**		J.Gen..Microbiol.1989.135:1679-1697
	L54a**		J.Bcteriol.1986.166:385-391
	80α**		Can.J.Microbiol.1996.43:612-616
	94,95 & 96		J.Clin.Microbiol.1988.26:2395-2401
	φ131,A_3 & A_5		Staphylococci & Staphylococcal Infections.1997. Vol1:503-508 (Karger,Basel)
	Phi PVL**		Gene 1998.215:57-67
Staphylococcus carnosus	BaSTC2		Felix d'Herelle Reference Centre,Quebec,Quebec
Staphylococcus epidermidis	1a, 2b, 3a, 4b, 5a, 6b, 7b, 8c, 9a, 10a, 11b,12a & 13b		Can.J.Microbiol.1988.34:1358-1361
	41, 63, 118II, 138, 245, 336, 392 & 550		Res.Virol.1994.145:111-121
Staphylococcus saprophyticus	1154A, 1405, 1314, 1139 & 1259		Res.Virol.1990.141: 625-635 & Res.Virol.1994.145:111-121
Staphylococcus sp.	Phi 812, Phi 131, SK311 & U16		Virology 1998.246:241-252
Streptococcus faecalis	VD13	HER44	Felix d'Herelle Reference Centre,Quebec,Quebec
Streptococcus faecium	PE1		Zentralbl.Bakteriol.1975.231:421-425
Streptococcus oralis	Cp-1** & Cp-7**		FEMS Microbiol.Lett.1989.65:187-192

Streptococcus pneumoniae	Cp-1**	HER223	Felix d'Herelle Reference Centre,Quebec,Quebec
	Cp-1**, Cp-5**, Cp-7**, Cp-9**, ω-1 & ω-2		J.Virol.1981.40:551-559 & Eur.J.Biochem.1979.101:59-64 & Microbial Drug Resistance 1997.3:165-176
	HB-623 & HB-746		J.Virol.1990.64:5149-5155
	EJ -1**		J.Bacteriol.1992.174:5516-5525
	Dp-2 & Dp-4		J.Virol.1978.26:221-225
	Dp-1		Virology 1975.63:577-582
	ω-3 & ω-8		J.Virol.1976.19:659-667
	304		J.Bacteriol.1980.141:1298-1304
	HB-1,HB-2, HB-3**, HB-4, HB-5 & HB-6		J.Bacteriol.1979.138:618-624
Streptococcus pyogenes	T12**		Mol. Microbiology. 1997#23:719-728
	A-1 A-6 A-25 Kjem	12202-B1 12203-B1 12204-B1 14918	The American Type Culture Collection
Streptococcus sp./Enterococcus	1 182 VD1884	HER 339 HER 80 HER 323	Felix d'Herelle Refrence Centre,Quebec,Quebec
	1A 1B NN 42 118 120	12169-B1 12170-B1 21597-B1 19948-B1 19951-B2 19952-B1	The American Type Culture Collection
Veillonella rodentium	N2		Antonie Van Leeuwenhoek 1989.56:263-271
Vibrio cholerae	Psi 92		Intervirology 1993.36:237-244
	VCB-1,2,3 & 4		J.Infetion 1998.36:131
	CP-T1**		J.Virol.1984.51:163-169
	VSK		FEMS Microbiol.Lett.1996.145:17-22
	Phi138		J.Virol.1986.57:960-967
	Phi149		J.Virol.1985.140:217-223
	Fs-2**		Microbiology 1998.144:1901-1906

	e4 e5 X29 β κ 13 14 16 24 32 57		Felix d'Herelle Reference Centre,Quebec,Quebec
Vibrio cholerae (Cont'd)	138 145 149 163 N-4 S-5 S-20 M-4 D-10 I II III IV V	14100-B1 14100-B2 14100-B30 14100-B4 51352-B1 51352-B2 51352-B3 51352-B4 51352-B5 51352-b6 51352-B7 51352-B8 51352-B9 51352-B10	The American Type Culture Collection
Vibrio costicola	UTAK		Felix d'Herelle Reference Centre,Quebec,Quebec
Vibrio eltor	e_4		J.Gen.Virol.1987.68:1411-1416
Vibrio natrigens	nt1,nt6		Felix d'Herelle Reference Centre,Quebec,Quebec
Vibrio parahaemolyticus	KVP40** VF33 VP1 ϕ60 ϕHAWI-5 ϕPEL8C-1		Felix d'Herelle Reference Centre,Quebec,Quebec
Vibrio sp.	α3a		Felix d'Herelle Reference Centre,Quebec,Quebec
	NN ph1	11985-B1 51582-B1	The American Type Culture Collection
	Phi149		J.Virol.1987.61:3999-4006
Veillonella rodentium	N2		Antonie V.Leeuwenhoek.1989.56:263-271

Yersinia enterocolitica	1 2 3 4 5 6 7 8 9 ϕYeO3-12		Felix d'Herelle Reference Centre,Quebec,Quebec
	I, IV & VIII		Zentralbl.Bakteriol.Mikrobiol.Hyg.1982.253:102
Yersinia pestis	R S Y	23208-B1 11593-B1 23053-B1	The American Type Culture Collection
	II		Zh.Mikrobiol.Epidemiol.Immunobiol.1990.11:9
Yersinia pseudotuberculosis	PST**	23207-B1	The American Type Culture Collection
Yersinia sp.	RD2		Mol.Gen.Mikrobiol.Virusol.1990.8:18-21

xxxx)

Table 2

>Bacteriophage 77, complete genome sequence, 41708 nucleotides

1 gatcaaaata cttggggaac ggttagggag taaacttcgc gataatttta aaaattcatg
61 tataaccccc ctcttataac cattttaagg caggtgatga aatggagatt atagtcgatg
121 aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
181 ataaattaaa agtagttgat ggtttaatta ttcaagcagc aaggctacgt gtaatgcttg
241 attacatgtg ggaagacata aaagaaaaag gtgattatga tttatttact caatctgaaa
301 aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
361 catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
421 aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
481 gtggaaacaa ggaaagataa ttttaaataa agaaagaatt gatctcttta attatctaca
541 aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
601 caaatttatt gaaaaatggt attttccaac attaccattt caaaggttta tcatagctaa
661 tatatttctt atagataaaa atacagatga agctttcttt acagaatttg ctattttcat
721 gggacgtgga ggcgggaaaa acggtctaat aagtgctatt agtgattttc tttctacgcc
781 cttacacgga gttaaagaat atcacatctc cattgttgct aatagtgaag atcaagcaaa
841 aacatcgttt gatgaaatca gaaccgtttt aatggataac aaacgaaata agacgggtaa
901 aacgccaaaa gctccttatg aagttagtaa agcaaaaata ataaaccgtg caactaaatc
961 ggttattcga tataacacat caaacacaaa aaccaaagac ggtggacgtg aggggtgtgt
1021 tatttttgat gaaattcatt atttctttgg tcctgaaatg gtaaacgtca aacgtggtgg
1081 attaggtaaa aagaaaaata gaagaacgtt ttatataagt actgatggtt ttgttagaga
1141 gggttatatc gatgcaatga agcacaaaat tgcaagtgta ttaagtggca aggttaaaaa
1201 tagtagattg tttgcttttt attgtaagtt agacgatcca aaagaagttg atgacagaca
1261 gacgtgggaa aaggcgaacc caatgttaca taaaccgtta tcagaatacg ctaaaacact
1321 gctaagcacg attgaagaag aatataacga tttaccattc aaccgttcaa ataagcccga
1381 attcatgact aagcgaatga atttgcctga agttgacctt gaaaaagtaa tagcaccatg
1441 gaaagaaata ctagcgacta atagagagat accaaattta gataatcaaa tgtgtattgg
1501 tggtttagac tttgcaaaca ttcgagattt tgcaagtgta gggctattat tccgaaaaaa
1561 cgatgattac atttggttag gacattcgtt tgtaagacaa gggtttttgg atgatgtcaa
1621 attagaacct cctattaaag aatgggaaaa aatgggatta ttgaccattg tcgatgatga
1681 tgtcattgaa attgaatata tagttgattg gtttttaaag gctagagaaa aatatgggct
1741 tgaaaaagtc atagctgata attatagaac tgatattgta agacgtgcgt ttgaggatgc
1801 tggcataaaa cttgaagtac ttagaaatcc aaaagcaata catggattac ttgcaccacg
1861 tatcgataca atgtttgcga aacataacgt aatatatgga gacaatcctt tgatgcgttg
1921 gtttactaat aatgttgctg taaaaatcaa gccggatgga aataaagagt atatcaaaaa
1981 agatgaagtc agacgtaaaa cggatggatt catggctttt gttcacgcat tatatagagc
2041 agacgatata gtagacaaag acatgtctaa agcgcttgat gcattaatga gtatagattt
2101 ctaatagagg aggtgagaca tgagtattct agaaaagata tttaaaacta ggaaagatat
2161 aacatatatg cttgatttag atatgataga agatctatca caacaagcgt atgtgaaacg
2221 tttagcgatt gatagttgta ttgaatttgt tgcgcgagct gtcgctcaaa gtcattttaa
2281 agtattggaa ggtaatagaa ttcaaaagaa tgatgtttac tacaagttaa atataaaacc
2341 aaatactgac ttatcaagcg atagtttttg gcaacaagtt atatataaac taatttatga
2401 taacgaggtt ttaatcgtag taagtgacag caaagaatta cttatcgcag atagctttta
2461 cagagaagag tacgctttgt atgatgatat attcaaagat gtaacggtta aagattatac
2521 ttatcaacgt actttcacaa tgcaagaggt catatattta aagtacaaca acaataaagt
2581 gacacacttt gtagaaagtc tattcgaaga ttacgggaaa atattcggaa gaatgatagg
2641 tgcacaatta aaaaactatc aaataagagg gattttgaaa tctgcctcta gcgcatatga
2701 cgaaaagaat atagaaaaat tacaagcgtt cacaaataaa ttattcaata cttttaataa
2761 aaatcaacta gcaatcgcgc ctttgataga aggttttgat tatgaggaat tatctaatgg
2821 tggtaagaat agtaacatgc ctttttctga attgagtgag ctaatgagag atgcaataaa
2881 aaatgttgcg ttgatgattg gtatacctcc aggtttgatt tacggagaaa cagctgattt
2941 ggaaaaaaac acgcttgtat ttgagaagtt ctgtttaaca cctttattaa aaaagattca
3001 gaacgaatta aacgcgaaac tcataacaca aagcatgtat ttgaaagata caagaataga
3061 aattgtcggt gtgaataaaa aagacccact tcaatatgct gaagcaattg acaaacttgt
3121 aagttctggt tcatttacaa ggaatgaggt gcggattatg ttaggtgaag aaccatcaga
3181 caatcctgaa ttagacgaat acctgattac taaaaactac gaaaaagcta acagtggtga
3241 aaatgatgaa aaagaaaaag atgaaaacac tttgaaaggt ggtgatgaag atgaaagcgg
3301 agattaaagg cgtcatcgtt tccaacgaag ataaatgggt ttacgaaatg cttggtatgg
3361 attcgacttg tcctaaagat gttttaacac aactagaatt tagtgatgaa gatgttgata
3421 ttataattaa ctcaaatggt ggtaacctag tagctggtag tgaaatatat acacatttaa
3481 gagctcataa aggcaaagtg aatgttcgta tcacagcaat agcagcaagt gcggcatcgc
3541 ttatcgcaat ggctggtgac cacatcgaaa tgagtccggt tgctagaatg atgattcaca

3601 atccttcaag tattgcgcaa ggagaagtga aagatctaaa tcatgctgca gaaacattag
3661 aacatgttgg tcaaataatg gctgaggcat atgcggttag agctggtaaa aacaaacaag
3721 aacttataga aatgatggct aaggaaacgt ggctaaatgc tgatgaagcc attgaacaag
3781 gttttgcgga tagtaaaatg tttgaaaacg acaatatgca aattgtagca agcgatacac
3841 aagtgttatc gaaagatgta ttaaatcgtg taacagcttt ggtaagtaaa acgccagagg
3901 ttaacattga tattgacgca atagcaaata aagtaattga aaaaataaat atgaaagaaa
3961 aggaatcaga aatcgatgtt gcagatagta aattatcagc aaatggattt tcaagattcc
4021 tttttaata caaaaatagg aggtcataaa atgactataa atttatcgga aacattcgca
4081 aatgcgaaaa acgaatttat taatgcagta aacaacggtg aaccgcaaga aagacaaaat
4141 gaattgtacg gtgacatgat taaccaacta tttgaagaaa ctaaattaca agcaaaagca
4201 gaagctgaaa gagtttctag tttacctaaa tcagcacaaa ctttgagtgc aaaccaaaga
4261 aatttcttta tggatatcaa taagagtgtt ggatataaag aagaaaaact tttaccagaa
4321 gaaacaattg atagaatctt cgaagattta acaacgaatc atccattatt agctgactta
4381 ggtattaaaa atgctggttt gcgtttgaag ttcttaaaat ccgaaacttc tggcgtggct
4441 gtttggggta aaatctatgg tgaaattaaa ggtcaattag atgctgcgtt cagtgaagaa
4501 acagcaattc aaaataaatt gacagcgttt gttgttttac caaaagattt aaatgatttt
4561 ggtcctgcgt ggattgaaag atttgttcgt gttcaaatcg aagaagcatt tgcagtggcg
4621 cttgaaactg cgttcttaaa aggtactggt aaagaccaac cgattggctt aaaccgtcaa
4681 gtacaaaaag gtgtatcggt aactgatggt gcttatccag agaaagaaga acaaggtacg
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32521 tacttaaagt tttttcacta atgtaaaact ttgaagcttc tagagcagga cctagaagag
32581 aaaattgtgg ttcttgtaaa ttatttttag gtacagaaga tatttctttt ttaaattgtt
32641 ctttgaattt ttcaaattct acttctcttt gataaataac tttatccaca taaaggtgga
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32761 cttcaataat tttatcaata cctttaccta aaataggatc cataattatt cacccccaat
32821 ctaacgcaat agcgataata aaattatacc agaaaggaga atcaacatga ctgaccaacc
32881 aagttactac tcaataatta cagcaaatgt cagatacgat aaccgactta ctgacagcga
32941 aaagttactt tttgcagaaa taacatcttt aagtaacaaa tacggatact gcacagcaag
33001 taatggttac tttgcaactt tatacaacgt tgttaaggaa actatatctc gtagaatttc
33061 gaaccttacc aactttggtt atctaaaaat cgaaattatc aaagaaggta atgaagttaa
33121 acaaaggaag atgtacccct tgacgcaaac gtcaatacct attgacgcaa aaatcaatac
33181 ccctattgat aattctgtca atacccctat tgacgcaaat gtcaaagaga atattacaag
33241 tattaataat acaagtaata acaatataaa tagaatagat atattgtcgg gcaacccgac
33301 agcatcttct ataccctata aagaaattat cgattactta aacaaaaaag cgggcaagca
33361 ttttaaacac aatacagcta aaacaaaaga ttttattaaa gcaagatgga atcaagattt
33421 taggttggag gattttaaaa aggtgattga tatcaaaaca gctgagtggc taaacacgga
33481 tagcgataaa taccttagac cagaaacact tttggcagt aaatttgagg ggtacctcaa
33541 tcaaaaaata caaccaactg gcacggatca attggaacgc atgaagtacg acgaaagtta
33601 ttgggattag gggatatta tgaaaccact attcagcgaa aagataaacg aaagcttgaa
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33721 cgacttatat aagtttgctc ctactaaaaa acacccgaat ggttacgagt ataaagacgg
33781 ttgcaaatgt gaaatctatg aggaatataa gcgaaacaag caacggaaga taaacaacat
33841 attcaatcaa tcaaacgtta atccgtcttt aagagatgca acagtcaaaa actacaagcc
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33961 tacaaaagaa ccaaaatcat taatattgca aggttcatac ggaactggta aaagccacct
34021 agcatacgct atcgcaaaag cagtcaaagc taaagggcat acggttgctt ttatgcacat
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34141 cgagctagtc agattgctaa gtgatattga tttacttgta ctagatgata tgggtgtaga
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34321 tataaattcg agaatgaaaa aaagagcaag aaaagtaaga gtaatcggag acgatttcag
34381 ggagcgagat gcatggtaac caaagaattt ttaaaaacta aacttgagtg ttcagatatg
34441 tacgctcaga aactcataga tgaggcacag ggcgatgaaa ataggttgta cgacctattt
34501 atccaaaaac ttgcagaacg tcatacacgc cccgctatcg tcgaatatta aggagtgtta
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34621 atcaagtata aagacaacgt aaatgaggtt tattcgctca caggagccca tttcagcgac
34681 gaaaagaaaa ttatgactga tagtgaccta aaacgattca aaggcgctca cgggcttcta
34741 tatgagcaag aattaggttt acaagcaacg atatttgata tttagaggtg gacgatgagt
34801 aaatacaacg ctaagaaagt tgagtacaaa ggaattgtat ttgatagcaa agtagagtgt
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35581 aaaagattaa acaagcgaga ctcgaacgtg aattggaaag agagcgaaag aaagaggctg
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35701 actggttcga tgtcacttat aaccaaatgt tcaagaaatg gagtgaagca taatgagcat
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35881 accacaatta gcattcgcaa taggtaatgc aattaaatac ttgtctagag caccgttaaa
35941 gaatggtcat gaggatttag caaaggcgaa gttttacgtc gatagagtat ttgacttgtg
36001 ggagtgatga ccatgacaga tagcggacgt aaagaatact taaaacattt tttcggctct
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36241 ctaactttat tttaaaaggg cggaaacaat gaaaatcaaa attgaaaaag aaatgaattt
36301 acctgaactt atccaatggg cttgggataa ccccaagtta tcaggtaata aaagattcta
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36481 aaaatcaaag ttaaaaaaga aatgagatta gatgaattaa ttaaatgggc gcgagaaaat
36541 ccggatctat cacaaggaaa aatatttttt tcaacaggat ttagtgatgg attcgttcgt
36601 tttcatccaa atacaaataa gtgttcgacg tcaagtttta ttccaattga tatccccttc
36661 atagttgata ttgaaaaaga agtaacggaa gagactaagg ttgataggtt gattgaatta
36721 ttcgagattc aagaaggaga ctataactct acactatatg agaacactag tataaaagaa
36781 tgtttatatg gcagatgtgt gcctaccaaa gcattctaca tcttaaacga tgacctaact
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36961 tgatttcaac aggttataaa agtttcaatg aagtaaaact attacaatac acaggattta
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37201 tgctattgga ggttatgaga tgacgttcac cttatcagat gaacaatata aaaatctttg
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37321 caagaagcaa cgagatgagc ttattgggga tatagcgaag ttacgagatt gtaacaaaga
37381 tctagagaag aaagcaagcg catgggatag gtattgcaag agcgttgaaa aagatttaat
37441 aaacgaattc ggtaacgatg atgaaagagt taaattcgga atggaattaa acaataaaat
37501 ttttatggag gatgacacaa atgaataatc gcgaaaaaat cgaacagtcc gttattagtg
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38161 agaagagttt accaaatcaa caaaggcgat aaactagctc aattggttat cgtgcctata
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38641 atggttatat ttacgcaagt actataatca agaaaccaac gtatattaaa acagatacga
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39361 gtattagaca acaaacaagt cattgaaaat tccgacttat tattcaaaaa gaaatttgat
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40261 tattataaat gaatatcaaa aagatatatc ttatttaaaa aatataatta ataaaatgaa

40321 tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaaat
40381 aaacgattat aatctttatc ttgataaatt tgaagaacag tttagtcaaa agtttaaaat
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41161 tgtaagtccg cattaaaaca gtttattatg ttagtatcag attaatattt aaagttatta
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41401 cgattctata agtctaaaga atggcaaata acaagaaaaa gagtgctaga aagagataat
41461 tatgaatgtc aacaatgtaa gagagacggc aagttaacga catatgacaa aagcaagcgt
41521 aagtcgttgg atgtagatca tatattatcg ctagaacatc atccggagtt tgctcatgac
41581 ttaaacaatt tagaaacact gtgtattaaa tgtcacaaca aaaaagaaaa gagatttata
41641 aaaaaagaaa ataaatggaa agacgaaaaa tggtaaatac cccgggtca aaaaaatcaa
41701 aagcgatc

Table 3

	Name	Position		Name	Position
1	77ORF005	19572..21026	48	77ORF052	1762..2013
2	77ORF006	3976..5196	49	77ORF053	37521..37757
3	77ORF007	21871..23076	50	77ORF054	22818..23060
4	77ORF008	2120..3307	51	77ORF055	17546..17788
5	77ORF009	31946..32803	52	77ORF058	18892..19122
6	77ORF010	26092..26889	53	77ORF059	34564..34785
7	77ORF011	24441..25208	54	77ORF064	29574..29795
8	77ORF012	29788..30576	55	77ORF065	28528..28746
9	77ORF013	33620..34399	56	77ORF066	27494..27703
10	77ORF014	27760..28512	57	77ORF069	38341..38547
11	77ORF015	3291..4028	58	77ORF070	36269..36475
12	77ORF016	32867..33610	59	77ORF071	40498..40701
13	77ORF017	23269..23982	60	77ORF072	38735..38938
14	77ORF018	31169..31840	61	77ORF073	30945..31148
15	77ORF019	39851..40501	62	77ORF074	38544..38738
16	77ORF020	6926..7570	63	77ORF075	13673..13870
17	77ORF021	37762..38304	64	77ORF077	25357..25605
18	77ORF022	30605..31156	65	77ORF079	29089..29280
19	77ORF023	26903..27346	66	77ORF080	35204..35389
20	77ORF024	10700..11140	67	77ORF085	24060..24242
21	77ORF025	9707..10147	68	77ORF092	39706..39876
22	77ORF026	40729..41145	69	77ORF094	32226..32393
23	77ORF027	6518..6925	70	77ORF096	13606..13773
24	77ORF028	34795..35199	71	77ORF098	7092..7256
25	77ORF029	6117..6521	72	77ORF102	29051..29212
26	77ORF030	36478..36879	73	77ORF104	34393..34551
27	77ORF031	39151..39546	74	77ORF109	18282..18434
28	77ORF032	33892..34266	75	77ORF112	39543..39692
29	77ORF033	5758..6120	76	77ORF117	27361..27501
30	77ORF034	7886..8236	77	77ORF118	38390..38530
31	77ORF035	19258..19560	78	77ORF120	36059..36199
32	77ORF036	36876..37223	79	77ORF124	33699..33833
33	77ORF037	102..446	80	77ORF128	14221..14355
34	77ORF038	34908..35219	81	77ORF130	15675..15806
35	77ORF039	37220..37528	82	77ORF133	8414..8542
36	77ORF040	41377..41676	83	77ORF140	13113..13235
37	77ORF041	35454..35753	84	77ORF147	7029..7148
38	77ORF042	5490..5774	85	77ORF149	30668..30787
39	77ORF043	29304..29564	86	77ORF151	31837..31953
40	77ORF044	18481..18768	87	77ORF155	30278..30391
41	77ORF045	5216..5500	88	77ORF157	4044..4157
42	77ORF046	25663..25935	89	77ORF167	20692..20799
43	77ORF047	11159..11425	90	77ORF175	35717..35821
44	77ORF048	28776..29039	91	77ORF176	6836..6940
45	77ORF049	36013..36255	92	77ORF178	35390..35491
46	77ORF050	35753..36007	93	77ORF179	8318..8419
47	77ORF051	38931..39167	94	77ORF182	29268..29564

Table 4

77ORF017 sequence

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23982     atgacgcataatatagaaaaacgcattaataaattaaaaacttct
1    M  T  H  N  I  E  K  R  I  N  K  L  K  T  S
23937     ggaaatccaaaatttaaaaagttagattcagatattcactattta
16   G  N  P  K  F  K  K  L  D  S  D  I  H  Y  L
23892     ctcaagagatttgaaggtgaaaaaaaccataaaggtttttatcca
31   L  K  R  F  E  G  E  K  N  H  K  G  F  Y  P
23847     aagtttaaacaaggagaaatagtttttgtagatttcggtataaac
46   K  F  K  Q  G  E  I  V  F  V  D  F  G  I  N
23802     gttaataaagaatttctaattcacactttgcaatagtgatgaat
61   V  N  K  E  F  S  N  S  H  F  A  I  V  M  N
23757     aaaaatgattctaatacggaggatatagtaaatgttattccctta
76   K  N  D  S  N  T  E  D  I  V  N  V  I  P  L
23712     tcctctaaagaaaacaaaaagtatttaaagatgaattttgatttg
91   S  S  K  E  N  K  K  Y  L  K  M  N  F  D  L
23667     aaatgggagtattatttaagattgtttttaaatttaattagcgcg
106  K  W  E  Y  Y  L  R  L  F  L  N  L  I  S  A
23622     caaaataattcagctatattaaaagaagttttcgataaaaaatac
121  Q  N  N  S  A  I  L  K  E  V  F  D  K  K  Y
23577     caaaaaaacaacacagaattcatcactaaagattattttattgaa
136  Q  K  N  N  T  E  F  I  T  K  D  Y  F  I  E
23532     tttatatctgatagtttagaaattgaaaataaattaaataaaatt
151  F  I  S  D  S  L  E  I  E  N  K  L  N  K  I
23487     gacagaaacattaataacatagtatcagcaattgataaggtaaaa
166  D  R  N  I  N  N  I  V  S  A  I  D  K  V  K
23442     aaattaaaaggtaatagttacgcttgcataaattctttccagccg
181  K  L  K  G  N  S  Y  A  C  I  N  S  F  Q  P
23397     attagtaagtttcgcataagaaaagttttaccccaaaaaattaaa
196  I  S  K  F  R  I  R  K  V  L  P  Q  K  I  K
23352     aatccagtaatagattcttcggatattatgttactgataaataga
211  N  P  V  I  D  S  S  D  I  M  L  L  I  N  R
23307     attaataataatatattgcagatccctgatataagatga 23269
226  I  N  N  N  I  L  Q  I  P  D  I  R  *
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Physico-chemical parameters of ORF 77ORF017

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1       MTHNIEKRIN KLKTSGNPKF KKLDSDIHYL LKRFEGEKNH KGFYPKFKQG EIVFVDFGIN
61      VNKEFSNSHF AIVMNKNDSN TEDIVNVIPL SSKENKKYLK MNFDLKWEYY LRLFLNLISA
121     QNNSAILKEV FDKKYQKNNT EFITKDYFIE FISDSLEIEN KLNKIDRNIN NIVSAIDKVK
181     KLKGNSYACI NSFQPISKFR IRKVLPQKIK NPVIDSSDIM LLINRINNNI LQIPDIR
```

Number of amino acids: 237
Average molecular weight (Daltons): 27887.38
Mean amino acid weight (Daltons): 117.67
Monoisotopic molecular weight (Daltons): 27869.83
Mean amino acid monoisotopic weight (Daltons): 117.59

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	5	2.11%	7.58%	Cys	C	1	0.42%	1.66%
Asp	D	14	5.91%	5.28%	Glu	E	13	5.49%	6.37%
Phe	F	16	6.75%	4.09%	Gly	G	6	2.53%	6.84%
His	H	4	1.69%	2.24%	Ile	I	29	12.24 %	5.81%
Lys	K	33	13.92 %	5.95%	Leu	L	19	8.02%	9.42%
Met	M	4	1.69%	2.37%	Asn	N	30	12.66 %	4.45%
Pro	P	7	2.95%	4.9%	Gln	Q	6	2.53%	3.97%
Arg	R	8	3.38%	5.16%	Ser	S	17	7.17%	7.12%
Thr	T	5	2.11%	5.67%	Val	V	11	4.64%	6.58%
Trp	W	1	0.42%	1.23%	Tyr	Y	8	3.38%	3.18%

Number of acidic (negative) amino acids (ED): 27
11.39%
Number of basic (positive) amino acids (KR): 41
17.30%
Total charge (KRED): 68
28.69%
Net charge (KR - ED): 14
5.91%
Theoritical pI: 10.01
Total linear charge density: 0.30
Average hydrophobicity: -5.37
Ratio of hydrophilicity to hydrophobicity: 1.41
Percentage of hydrophilic amino acid: 57.81%
Percentage of hydrophobic amino acid: 42.19%
Ratio of %hydrophilic to %hydrophobic: 1.37

77ORF019 sequence

```
39851     atgaacgagcaaataataggaagcatatatactttagcaggaggt
1    M  N  E  Q  I  I  G  S  I  Y  T  L  A  G  G
39896     gttgtgctttattcagttaaagagattttaggtattttacagat
16   V  V  L  Y  S  V  K  E  I  F  R  Y  F  T  D
39941     tctaacttacaacgtaaaaaaatcaatttagaacaaatatatccg
31   S  N  L  Q  R  K  K  I  N  L  E  Q  I  Y  P
39986     atatatttagattgttttaaaaaggctaaaaagatgattggagct
46   I  Y  L  D  C  F  K  K  A  K  K  M  I  G  A
40031     tatattattccaacagaacagcatgaattttttagatttttttgat
61   Y  I  I  P  T  E  Q  H  E  F  L  D  F  F  D
40076     attgaagtctttaataatttagataagcaaagtaaaaaagcgtat
76   I  E  V  F  N  N  L  D  K  Q  S  K  K  A  Y
40121     gaaaatgttattggatttagacaaatgattaatttatcaaataga
91   E  N  V  I  G  F  R  Q  M  I  N  L  S  N  R
40166     gttaaggcaatggaagattttaagatgagtttcaacaatgaattt
106  V  K  A  M  E  D  F  K  M  S  F  N  N  E  F
40211     agtacaaatcagatttttttaatccttcttttgttatggaaaca
121  S  T  N  Q  I  F  F  N  P  S  F  V  M  E  T
40256     attgctattataaatgaatatcaaaaagatatatcttatttaaaa
136  I  A  I  I  N  E  Y  Q  K  D  I  S  Y  L  K
40301     aatataattaataaaatgaatgaaaatagagcttataatcatatt
151  N  I  I  N  K  M  N  E  N  R  A  Y  N  H  I
40346     gatagttttatcacttcagagtaccgacgaaaaataaacgattat
166  D  S  F  I  T  S  E  Y  R  R  K  I  N  D  Y
40391     aatctttatcttgataaatttgaagaacagtttagtcaaaagttt
181  N  L  Y  L  D  K  F  E  E  Q  F  S  Q  K  F
40436     aaaataaacagaacttcgataaaagaaagaattattattaattta
196  K  I  N  R  T  S  I  K  E  R  I  I  I  N  L
40481     aacaagaggagatttaaatga 40501
211  N  K  R  R  F  K  *
```

Physico-chemical parameters of ORF 77ORF019

```
1     MNEQIIGSIY TLAGGVVLYS VKEIFRYFTD SNLQRKKINL EQIYPIYLDC FKKAKKMIGA
61    YIIPTEQHEF LDFFDIEVFN NLDKQSKKAY ENVIGFRQMI NLSNRVKAME DFKMSFNNEF
121   STNQIFFNPS FVMETIAIIN EYQKDISYLK NIINKMNENR AYNHIDSFIT SEYRRKINDY
181   NLYLDKFEEQ FSQKFKINRT SIKERIIINL NKRRFK
```

Number of amino acids:	216
Average molecular weight (Daltons):	26026.06
Mean amino acid weight (Daltons):	120.49
Monoisotopic molecular weight (Daltons):	26009.34
Mean amino acid monoisotopic weight (Daltons):	120.41

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	7	3.24%	7.58%	Cys	C	1	0.46%	1.66%
Asp	D	10	4.63%	5.28%	Glu	E	16	7.41%	6.37%
Phe	F	19	8.80%	4.09%	Gly	G	5	2.31%	6.84%
His	H	2	0.93%	2.24%	Ile	I	28	12.96 %	5.81%
Lys	K	22	10.19 %	5.95%	Leu	L	12	5.56%	9.42%
Met	M	7	3.24%	2.37%	Asn	N	23	10.65 %	4.45%
Pro	P	3	1.39%	4.9%	Gln	Q	10	4.63%	3.97%
Arg	R	11	5.09%	5.16%	Ser	S	13	6.02%	7.12%
Thr	T	7	3.24%	5.67%	Val	V	7	3.24%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	13	6.02%	3.18%

Number of acidic (negative) amino acids (ED):	26 12.04%
Number of basic (positive) amino acids (KR):	33 15.28%
Total charge (KRED):	59 27.31%
Net charge (KR - ED):	7 3.24%
Theoritical pI:	9.52
Total linear charge density:	0.28
Average hydrophobicity:	-4.84
Ratio of hydrophilicity to hydrophobicity:	1.37
Percentage of hydrophilic amino acid:	54.17%
Percentage of hydrophobic amino acid:	45.83%
Ratio of %hydrophilic to %hydrophobic:	1.18

77ORF043 sequence

```
29304     atgtattacgaaataggcgaaatcatacgcaaaaatattcatgtt
1    M  Y  Y  E  I  G  E  I  I  R  K  N  I  H  V
29349     aacggattcgattttaagctattcattttaaaaggtcatatgggc
16   N  G  F  D  F  K  L  F  I  L  K  G  H  M  G
29394     atatcaatacaagttaaagatatgaacaacgtaccaattaaacat
31   I  S  I  Q  V  K  D  M  N  N  V  P  I  K  H
29439     gcttatgtcgtagatgagaatgacttagatatggcatcagactta
46   A  Y  V  V  D  E  N  D  L  D  M  A  S  D  L
29484     tttaaccaagcaatagatgaatggattgaagagaacacagacgaa
61   F  N  Q  A  I  D  E  W  I  E  E  N  T  D  E
29529     caggacagactaattaacttagtcatgaaatggtag 29564
76   Q  D  R  L  I  N  L  V  M  K  W  *
```

Physico-chemical parameters of ORF 77ORF043

```
1       MYYEIGEIIR KNIHVNGFDF KLFILKGHMG ISIQVKDMNN VPIKHAYVVD ENDLDMASDL
61      FNQAIDEWIE ENTDEQDRLI NLVMKW
```

Number of amino acids: 86
Average molecular weight (Daltons): 10186.68
Mean amino acid weight (Daltons): 118.45
Monoisotopic molecular weight (Daltons): 10180.02
Mean amino acid monoisotopic weight (Daltons): 118.37

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	3	3.49%	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	10.47 %	5.28%	Glu	E	7	8.14%	6.37%
Phe	F	4	4.65%	4.09%	Gly	G	4	4.65%	6.84%
His	H	3	3.49%	2.24%	Ile	I	11	12.79 %	5.81%
Lys	K	6	6.98%	5.95%	Leu	L	6	6.98%	9.42%
Met	M	5	5.81%	2.37%	Asn	N	8	9.30%	4.45%
Pro	P	1	1.16%	4.9%	Gln	Q	3	3.49%	3.97%
Arg	R	2	2.33%	5.16%	Ser	S	2	2.33%	7.12%
Thr	T	1	1.16%	5.67%	Val	V	6	6.98%	6.58%
Trp	W	2	2.33%	1.23%	Tyr	Y	3	3.49%	3.18%

Number of acidic (negative) amino acids (ED): 16
18.60%
Number of basic (positive) amino acids (KR): 8
9.30%
Total charge (KRED): 24
27.91%
Net charge (KR - ED): -8
9.30%
Theoritical pI: 4.38
Total linear charge density: 0.30
Average hydrophobicity: -2.80
Ratio of hydrophilicity to hydrophobicity: 1.19
Percentage of hydrophilic amino acid: 48.84%
Percentage of hydrophobic amino acid: 51.16%
Ratio of %hydrophilic to %hydrophobic: 0.95

77ORF102 sequence

```
29051     atgagcaacatttataaaagctacctagtagcagtattatgcttc
1    M  S  N  I  Y  K  S  Y  L  V  A  V  L  C  F
29096     acagtcttagcgattgtacttatgccgtttctatacttcactaca
16   T  V  L  A  I  V  L  M  P  F  L  Y  F  T  T
29141     gcatggtcaattgcgggattcgcaagtatcgcaacattcatgtac
31   A  W  S  I  A  G  F  A  S  I  A  T  F  M  Y
29186     tacaaagaatgcttttcaaagaataa 29212
46   Y  K  E  C  F  F  K  E  *
```

Physico-chemical parameters of ORF 77ORF102

1 MSNIYKSYLV AVLCFTVLAI VLMPFLYFTT AWSIAGFASI ATFMYYKECF FKE

Number of amino acids:	53
Average molecular weight (Daltons):	6155.42
Mean amino acid weight (Daltons):	116.14
Monoisotopic molecular weight (Daltons):	6151.07
Mean amino acid monoisotopic weight (Daltons):	116.06

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	6	11.32 %	7.58%	Cys	C	2	3.77 %	1.66%
Asp	D	0	0.00%	5.28%	Glu	E	2	3.77 %	6.37%
Phe	F	7	13.21 %	4.09%	Gly	G	1	1.89 %	6.84%
His	H	0	0.00%	2.24%	Ile	I	4	7.55 %	5.81%
Lys	K	3	5.66%	5.95%	Leu	L	5	9.43 %	9.42%
Met	M	3	5.66%	2.37%	Asn	N	1	1.89 %	4.45%
Pro	P	1	1.89%	4.9%	Gln	Q	0	0.00 %	3.97%
Arg	R	0	0.00%	5.16%	Ser	S	4	7.55 %	7.12%
Thr	T	4	7.55%	5.67%	Val	V	4	7.55 %	6.58%
Trp	W	1	1.89%	1.23%	Tyr	Y	5	9.43 %	3.18%

Number of acidic (negative) amino acids (ED):	2 3.77%
Number of basic (positive) amino acids (KR):	3 5.66%
Total charge (KRED):	5 9.43%
Net charge (KR - ED):	1 1.89%
Theoritical pI:	8.18
Total linear charge density:	0.13
Average hydrophobicity:	10.81
Ratio of hydrophilicity to hydrophobicity:	0.40
Percentage of hydrophilic amino acid:	28.30%
Percentage of hydrophobic amino acid:	71.70%

Ratio of %hydrophilic to %hydrophobic: 0.39

77ORF104 sequence

```
34393     atggtaaccaaagaattttaaaaactaaacttgagtgttcagat
1    M  V  T  K  E  F  L  K  T  K  L  E  C  S  D
34438     atgtacgctcagaaactcatagatgaggcacagggcgatgaaaat
16   M  Y  A  Q  K  L  I  D  E  A  Q  G  D  E  N
34483     aggttgtacgacctatttatccaaaaacttgcagaacgtcataca
31   R  L  Y  D  L  F  I  Q  K  L  A  E  R  H  T
34528     cgccccgctatcgtcgaatattaa 34551
46   R  P  A  I  V  E  Y  *
```

Physico-chemical parameters of ORF 77ORF104

1 MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY

Number of amino acids:	52
Average molecular weight (Daltons):	6193.13
Mean amino acid weight (Daltons):	119.10
Monoisotopic molecular weight (Daltons):	6189.12
Mean amino acid monoisotopic weight (Daltons):	119.02

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	4	7.69 %	7.58%	Cys	C	1	1.92%	1.66%
Asp	D	4	7.69 %	5.28%	Glu	E	6	11.54 %	6.37%
Phe	F	2	3.85 %	4.09%	Gly	G	1	1.92%	6.84%
His	H	1	1.92 %	2.24%	Ile	I	3	5.77%	5.81%
Lys	K	5	9.62 %	5.95%	Leu	L	6	11.54 %	9.42%
Met	M	2	3.85 %	2.37%	Asn	N	1	1.92%	4.45%
Pro	P	1	1.92 %	4.9%	Gln	Q	3	5.77%	3.97%
Arg	R	3	5.77 %	5.16%	Ser	S	1	1.92%	7.12%
Thr	T	3	5.77 %	5.67%	Val	V	2	3.85%	6.58%
Trp	W	0	0.00 %	1.23%	Tyr	Y	3	5.77%	3.18%

Number of acidic (negative) amino acids (ED): 10
19.23%

Number of basic (positive) amino acids (KR): 8
15.38%

Total charge (KRED): 18
34.62%

Net charge (KR - ED): -2
3.85%

Theoritical pI:	5.03
Total linear charge density:	0.38
Average hydrophobicity:	-5.81
Ratio of hydrophilicity to hydrophobicity:	1.47
Percentage of hydrophilic amino acid:	53.85%
Percentage of hydrophobic amino acid:	46.15%

Ratio of %hydrophilic to %hydrophobic: 1.17

77ORF182 sequence

```
29268    atgttcaatataaaacgaaaaacggaggaagtcaagatgtattac
1    M  F  N  I  K  R  K  T  E  E  V  K  M  Y  Y
29313    gaaataggcgaaatcatacgcaaaaatattcatgttaacggattc
16   E  I  G  E  I  I  R  K  N  I  H  V  N  G  F
29358    gattttaagctattcattttaaaggtcatatgggcatatcaata
31   D  F  K  L  F  I  L  K  G  H  M  G  I  S  I
29403    caagttaaagatatgaacaacgtaccaattaaacatgcttatgtc
46   Q  V  K  D  M  N  N  V  P  I  K  H  A  Y  V
29448    gtagatgagaatgacttagatatggcatcagacttatttaaccaa
61   V  D  E  N  D  L  D  M  A  S  D  L  F  N  Q
29493    gcaatagatgaatggattgaagagaacacagacgaacaggacaga
76   A  I  D  E  W  I  E  E  N  T  D  E  Q  D  R
29538    ctaattaacttagtcatgaaatggtag 29564
91   L  I  N  L  V  M  K  W  *
```

Physico-chemical parameters of ORF 77ORF182

```
1       MFNIKRKTEE VKMYYEIGEI IRKNIHVNGF DFKLFILKGH MGISIQVKDM NNVPIKHAYV
61      VDENDLDMAS DLFNQAIDEW IEENTDEQDR LINLVMKW
```

Number of amino acids:	98
Average molecular weight (Daltons):	11691.50
Mean amino acid weight (Daltons):	119.30
Monoisotopic molecular weight (Daltons):	11683.84
Mean amino acid monoisotopic weight (Daltons):	119.22

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	3	3.06 %	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	9.18 %	5.28%	Glu	E	9	9.18%	6.37%
Phe	F	5	5.10 %	4.09%	Gly	G	4	4.08%	6.84%
His	H	3	3.06 %	2.24%	Ile	I	12	12.24 %	5.81%
Lys	K	9	9.18 %	5.95%	Leu	L	6	6.12%	9.42%
Met	M	6	6.12 %	2.37%	Asn	N	9	9.18%	4.45%
Pro	P	1	1.02 %	4.9%	Gln	Q	3	3.06%	3.97%
Arg	R	3	3.06 %	5.16%	Ser	S	2	2.04%	7.12%
Thr	T	2	2.04 %	5.67%	Val	V	7	7.14%	6.58%
Trp	W	2	2.04 %	1.23%	Tyr	Y	3	3.06%	3.18%

Number of acidic (negative) amino acids (ED):	18 18.37%
Number of basic (positive) amino acids (KR):	12 12.24%
Total charge (KRED):	30 30.61%
Net charge (KR - ED): 6.12%	-6
Theoritical pI:	4.76
Total linear charge density:	0.33
Average hydrophobicity:	-3.89
Ratio of hydrophilicity to hydrophobicity:	1.28

Percentage of hydrophilic amino acid:	51.02%
Percentage of hydrophobic amino acid:	48.98%
Ratio of %hydrophilic to %hydrophobic:	1.04

Table 5

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100017|lan|77ORF017 Phage 77 ORF |23269-23982|-3
         (237 letters)

Database: nr
          393,678 sequences; 120,452,765 total letters

                                                                  Score    E
Sequences producing significant alignments:                      (bits)  Value

 gi|4493986|emb|CAB39045.1| (AL034559) predicted using hexExon; ...    41  0.010
 gi|730607|sp|P23250|RPI1_YEAST NEGATIVE RAS PROTEIN REGULATOR P...    38  0.053
 gi|3097044|emb|CAA75299| (Y15035) K1R [Cowpox virus]                  38  0.090
 gi|2146245|pir||S73794 hypothetical protein H91_orf180 - Mycopl...    38  0.090
 gi|83910|pir||S04682 ribosomal protein var1 - yeast (Candida gl...    37  0.15
 gi|133135|sp|P21358|RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN ...    37  0.15
 gi|2128843|pir||H64475 hypothetical protein MJ1409 - Methanococ...    36  0.20
 gi|5107017|gb|AAD39926.1|AF126285_2 (AF126285) RNA polymerase [...    36  0.35
 gi|2146210|pir||S73342 hypothetical protein E07_orf166 - Mycopl...    35  0.60

Database: swissprot
          79,449 sequences; 28,874,452 total letters

                                                                  Score    E
Sequences producing significant alignments:                      (bits)  Value

 sp|P23250 RPI1_YEAST  NEGATIVE RAS PROTEIN REGULATOR PROTEIN.     38  0.014
 sp|P21358 RMAR_CANGA  MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.       37  0.040
 sp|Q21444 LDLC_CAEEL  LDLC PROTEIN HOMOLOG.                        34  0.35
 sp|P27240 RFAY_ECOLI  LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROT.   33  0.46
 sp|P53192 YGC0_YEAST  HYPOTHETICAL 27.1 KD PROTEIN IN ALK1-CKB1.   33  0.60
 sp|P32908 SMC1_YEAST  CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-B.   33  0.60
 sp|P54683 TAGB_DICDI  PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR .   32  0.78
 sp|Q03100 CYAA_DICDI  ADENYLATE CYCLASE, AGGREGATION SPECIFIC (.   32  0.78
```

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100019|lan|77ORF019 Phage 77 ORF|39851-40501|2
        (216 letters)

Database: nr
           373,355 sequences; 114,214,446 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

gi|3341966|dbj|BAA31932| (AB009866) orf 59 [bacteriophage phi PVL] 437 e-122
gi|2689911 (AE000792) B. burgdorferi predicted coding region BB...  38 0.058
gi|1171589|emb|CAA64574| (X95275) frameshift [Plasmodium falcip...  37  0.10
gi|4493986|emb|CAB39045.1| (AL034559) predicted using hexExon; ...  36  0.23
gi|141257|sp|P18019|YPI9_CLOPE HYPOTHETICAL 14.5 KD PROTEIN (OR...  36  0.29
gi|133412|sp|P27059|RPOB_ASTLO DNA-DIRECTED RNA POLYMERASE BETA...  35  0.51
gi|3122231|sp|Q58851|HISX_METJA HISTIDINOL DEHYDROGENASE (HDH) ...  35  0.51
gi|3649757|emb|CAB11106.1| (Z98547) predicted using hexExon; MA...  34  0.66
gi|2688313 (AE001146) sensory transduction histidine kinase, pu...  34  0.87


Database: swissprot
           79,449 sequences; 28,874,452 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

sp|P18019 YPI9_CLOPE  HYPOTHETICAL 14.5 KD PROTEIN (ORF9).          36  0.079
sp|Q58851 HISX_METJA  HISTIDINOL DEHYDROGENASE (EC 1.1.1.23) (H.    35  0.14
sp|P27059 RPOB_ASTLO  DNA-DIRECTED RNA POLYMERASE BETA CHAIN (E.    35  0.14
sp|Q02224 CENE_HUMAN  CENTROMERIC PROTEIN E (CENP-E PROTEIN).       34  0.31
sp|P04931 ARP_PLAFA  ASPARAGINE-RICH PROTEIN (AG319) (ARP) (FRA..   33  0.53
sp|P18011 IPAB_SHIFL  62 KD MEMBRANE ANTIGEN.                       32  0.69
sp|P18709 VTA2_XENLA  VITELLOGENIN A2 PRECURSOR (VTG A2) [CONTA..   32  0.90
sp|Q64409 CP3H_CAVPO  CYTOCHROME P450 3A17 (EC 1.14.14.1) (CYPI..   32  0.90
sp|P21358 RMAR_CANGA  MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.         32  0.90
sp|Q03945 IPAB_SHIDY  62 KD MEMBRANE ANTIGEN.                       32  1.2
```

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100043|lan|77ORF043 Phage 77 ORF|29304-29564|3
         (86 letters)

Database: nr
           373,355 sequences; 114,214,446 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

gi|3341947|dbj|BAA31913| (AB009866) orf 39 [bacteriophage phi PVL] 182  6e-46
gi|744518|prf||2014422A FKBP-rapamycin-associated protein [Homo...  32  0.84
gi|1169736|sp|P42346|FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN...  32  0.84
gi|1169735|sp|P42345|FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTE...  32  0.84
gi|3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa...  32  0.84
gi|3875402|emb|CAA98122| (Z73906) cDNA EST EMBL:D64544 comes fr...  31  2.5
gi|1084792|pir||S54091 hypothetical protein YPR070w - yeast (Sa...  30  4.2

Database: swissprot
           79,449 sequences; 28,874,452 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

sp|P42345 FRAP_HUMAN  FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) .     32  0.24
sp|P42346 FRAP_RAT  FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R.     32  0.24
sp|P34554 YNP1_CAEEL  HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C.     28  3.5
sp|Q24118 LIO_DROME  LINOTTE PROTEIN.                                28  3.5
sp|P80034 ACH2_BOMMO  ANTICHYMOTRYPSIN II (ACHY-II).                 28  3.5
sp|P22922 A1AT_BOMMO  ANTITRYPSIN PRECURSOR (AT).                    28  3.5
sp|Q44363 TRAA_AGRT6  CONJUGAL TRANSFER PROTEIN TRAA.                28  3.5
sp|P38255 YBU5_YEAST  HYPOTHETICAL 51.3 KD PROTEIN IN PHO5-VPS1.     27  6.0
sp|P55822 SH3B_HUMAN  SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PRO.     27  7.9
sp|Q58482 YA82_METJA  HYPOTHETICAL PROTEIN MJ1082.                   27  7.9
sp|P34252 YKK8_YEAST  HYPOTHETICAL 52.3 KD PROTEIN IN HAP4-AAT1.     27  7.9
```

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100102|lan|77ORF102 Phage 77 ORF|29051-29212|2
        (53 letters)

Database: nr
           373,355 sequences; 114,214,446 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

gi|3341946|dbj|BAA31912| (AB009866) orf 38 [bacteriophage phi PVL]   96  3e-20
gi|4325288|gb|AAD17315| (AF123593) voltage-dependent sodium cha...   28  7.1
gi|2649684 (AE001040) A. fulgidus predicted coding region AF092...   28  9.3

Database: swissprot
           79,449 sequences; 28,874,452 total letters

                                                                 Score    E
Sequences producing significant alignments:                      (bits)  Value

sp|P42087 HUTM_BACSU  PUTATIVE HISTIDINE PERMEASE.                   26  7.1
sp|P04775 CIN2_RAT  SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBU...   26  9.2
sp|P42619 YQJF_ECOLI  HYPOTHETICAL 17.2 KD PROTEIN IN EXUR-TDCC...   26  9.2
```

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100104|lan|77ORF104 Phage 77 ORF|34393-34551|1
        (52 letters)

Database: nr
           373,355 sequences; 114,214,446 total letters

                                                                 Score     E
Sequences producing significant alignments:                      (bits)  Value

gi|2315523 (AF016452) similar to the leucine-rich domains found...   29   4.2
gi|4377168|gb|AAD18990| (AE001666) CT711 hypothetical protein [...   29   5.4
gi|3882171|dbj|BAA34445| (AB018268) KIAA0725 protein [Homo sapi...   28   9.3


Database: swissprot
           79,449 sequences; 28,874,452 total letters

                                                                 Score     E
Sequences producing significant alignments:                      (bits)  Value

sp|P04879 RRPP_VSVIG  RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48.    27   5.4
sp|P04880 RRPP_VSVIM  RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48.    27   5.4
sp|Q13946 CN7A_HUMAN  HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC .    26   7.1
sp|P35381 ATPA_DROME  ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL P.    26   9.3
sp|P54659 MVPB_DICDI  MAJOR VAULT PROTEIN BETA (MVP-BETA).          26   9.3
sp|P40397 YHXC_BACSU  HYPOTHETICAL OXIDOREDUCTASE IN APRE-COMK .    26   9.3
```

```
BLASTP 2.0.8 [Jan-05-1999]

Query= sid|122748|lan|77ORF182 Phage 77 ORF|29268-29564|3
        (98 letters)

Database: nr
          393,678 sequences; 120,452,765 total letters

                                                                 Score    E
Sequences producing significant alignments:                     (bits)  Value

gi|3341947|dbj|BAA31913.1| (AB009866) orf 39 [bacteriophage phi..  182  8e-46
gi|1084792|pir||S54091 hypothetical protein YPR070w - yeast (Sa..   35  0.13
gi|1169736|sp|P42346|FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN..   32  1.1
gi|744518|prf||2014422A FKBP-rapamycin-associated protein [Homo..   32  1.1
gi|5051381|emb|CAB44736.1| (AL049653) dJ647M16.2 (FK506 binding..   32  1.1
gi|4826730|ref|NP_004949.1|pFRAP1| FK506 binding protein 12-rap..   32  1.1
gi|3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa..   32  1.1

Database: swissprot
          79,909 sequences; 29,054,478 total letters

                                                                 Score    E
Sequences producing significant alignments:                     (bits)  Value

sp|P42345 FRAP_HUMAN  FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) .    32  0.29
sp|P42346 FRAP_RAT  FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R.   32  0.29
sp|P40557 YIA5_YEAST  PUTATIVE DISULFIDE ISOMERASE YIL005W PREC.   29  3.3
sp|Q24118 LIO_DROME  LINOTTE PROTEIN.                              28  4.4
sp|Q44363 TRAA_AGRT6  CONJUGAL TRANSFER PROTEIN TRAA.              28  4.4
sp|P80034 ACH2_BOMMO  ANTICHYMOTRYPSIN II (ACHY-II).               28  4.4
sp|P34554 YNP1_CAEEL  HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C.   28  4.4
sp|P22922 A1AT_BOMMO  ANTITRYPSIN PRECURSOR (AT).                  28  4.4
```

Table 6

1st position (5' end)	2nd position U	C	A	G	3rd position (3' end)
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Table 7

Bacteriophage 3A, complete genome sequence

1 caaacgctag caacgcggat aaatttttca tgaaaggggg tctttatatg aagttaacaa aaaaacagct
71 aaaagaatat atagaagatt acaaaaaatc tgatgacata ttaattaatt tgtatataga aacatatgaa
141 ttttattgtc ggttaagaga tgaacttaaa aatagtgatt taatgataga gcatacaaac aaggctggtg
211 cgagcaatat tattaagaat ccattaagca tagaactgac aaaaacagtt caaacactaa ataacttact
281 caagtctatg ggtttaactg cagcacaaag aaaaaagata gttcaagaag aaggtggatt cggtgactat
351 taaagtttta aatgaacctt caccaaaact attaacaaca tggtatgcag agcaagtcac tcaagggaaa
421 ataaaaacaa gcaaatatgt tagaaaagaa tgtgagagac atcttagata tctagaaaat ggaggtaaat
491 gggtatttga tgaagaatta gcgcatcgtc ctattcgatt tatagaaaag ttttgtaaac cttccaaagg
561 atctaaacgt caacttgtat tacagccatg gcaacatttt attatcggca gtttgtttgg ttgggttcat
631 aaagaaacaa aactgcgcag gtttaaagaa gctttgatat ttatggggcg aaaaaatggt aaaacaacca
701 ctatttctgg ggttgctaac tatgctgtat cacaagatgg agaaaatggt gcagaaattc atttgttagc
771 aaacgtaatg aaacaagcta ggattctatt tgatgaatct aaggcgatga ttaaagctag cccaaagctt
841 gataaaaatt tcagaacatt aagagatgaa atccattatg acgcaacgat atcaaaaatt atgccccaag
911 catcagatag cgataagtta gatggattga atacacacat ggggattttt gatgaaattc atgaatttaa
981 agactataaa ttgatttcag ttataaaaaa ctcaagagct gcaaggttac aacctcttct catctacatt
1051 acgacagcag ggtatcaatt agatggtcca cttgttgata tggtagaagc gggaagagac accttagatc
1121 aaatcataga agacgaaaga actttttatt atttagcatc tttggatgat gacgatgata ttaatgattc
1191 gtcgaactgg ataaaagcaa atcccaactt aggtgtctct ataaatttag atgagatgaa agaagagtgg
1261 gaaaaagcta agagaacacc agctgaacgt ggagatttta taaccaaaag gtttaatatc tttgctaata
1331 atgacgagat gagttttatt gattacccaa cactccaaaa aaataatgaa attgtttctt tagaagagct
1401 ggaaggcaga ccgtgcacga ttggttatga tttatcagaa acagaggact ttacagccgc gtgtgctact
1471 tttgcgttag ataatggtaa agttgcagtt ttatcgcatt catggattcc taagcacaaa gttgaatatt
1541 ctaacgaaaa aataccctat agagaatggg aagaagatgg cttattaaca gtgcaagata agccttatat
1611 tgactaccaa gatgttttaa attggataat taagatgaat gagcattatg tagtagaaaa aattacttat
1681 gatagagcga acgcattcaa actaaatcaa gagttaaaaa attacgggtt tgaaacggaa gaaacaagac
1751 aaggagcttt gaccttgagc cctgcattga aggatttaaa agaaatgttt ttagatggga aaataatatt
1821 taataataat cctttaatga aatggtatat caataatgtt cagttgaaac tagacagaaa cggaaactgg
1891 ttgccgtcta agcaaagcag atatcgtaaa atagatggct ttgcagcatt tttaaacaca tatacagata
1961 ttatgaataa agttgtttct gatagtggtg aaggaaacat agagtttatt agtattaaag acataatgcg
2031 ttaaggaggt gaatgttatc gcaaaagaga atattgtcac acgcataaag aaaaaattga tagacaattg
2101 gattgatcag tcaacttcta agctttatga ctttagccca tggaaaaata gatctttttg gggtgtaatt
2171 aataatacgc ttgaaactaa tgaaacgata ttttcagcta ttacaaagtt atctaattcg atggctagtt
2241 tgcccttgaa aatgtatgaa gattataaag tagttaatac agaagtatct gatttactta cagtgtcacc
2311 gaataattct ctgagcagtt ttgattttat taatcaaatt gaaacaatca gaaatgaaaa aggtaatgca
2381 tatgtgctaa ttgaacgaga catctatcat caaccatcaa agcttttctt attaaatcca gatgttgttg
2451 aaatgttaat tgaaaaccaa tcacgtgaac tttattattc cattcatgct gcaactggaa ataaattgat
2521 tgttcataat atggacatgt tgcattttaa acacatcgtg gcatctaata tggtgcaagg cattagtccg
2591 attgatgtgt tgaagaatac aactgatttt gataatgcag taagaacctt taatcttaca gaaatgcaaa
2661 aacctgattc tttcatgctt aaatatggtt ccaatgtagg taaagaaaaa aggcagcaag tgttagaaga
2731 tttcaaacag tactatgaag aaaacggtgg aatattattc caagagcctg gtgttgaaat cgaaccgtta
2801 cctaaaaaat atgtctctga agatatagtg gcaagcgaga atttaacaag agaaagagta gctaacgttt
2871 ttcaattgcc ctcagtattc ttaaatgcaa gatcaaatac aaatttcgcg aaaaatgaag agttaaacag
2941 attttacttg cagcatacct tattgccaat cgtcaaacag tatgaagaag aatttaatcg gaaactactt
3011 actaaaacag acagagaaaa aaataggtat tttaaattta acgttaaatc ttatttaagg gctgatagtg
3081 caacacaagc agaagtgtac tttaaagcag ttcgtagtgg ttactacact ataaatgaca ttagagagtg
3151 ggaagattta ccaccagttg aaggtggaga taagccgcta ataagcggtg atttataccc aattgacacg
3221 ccacttgaat taagaaaatc tttgaaaggt ggtgataaaa atgtcaatga aagctaagta ttttcaaatg
3291 aaaagaaaat caaaaagtaa aggtgaaata tttatttatg gtgatattgt aagtgataaa tggtttgaaa
3361 gtgatgtaac tgctacagat ttcaaaaata aactagatga actaggagac atcagtgaaa tagatgttca
3431 tataaattca tctggaggca gtgtatttga agggcatgca atatacaata tgctaaaaat gcatcctgca
3501 aaaattaata tctatgtcga tgccttagcg gcatcaattg ctagtgttat cgctatgagt ggtgacacta
3571 tttttatgca caaaaatagt tttttaatga ttcataattc atgggttatg actgtaggta atgcagaaga
3641 gttaagaaag acagcggatt tacttgaaaa aacagatgct gttagtaatt cagcttattt agataaagca
3711 aaagatttag atcaagaaca cttaaaacag atgttagatg cagaaacttg gcttactgca gaagaagcct
3781 tgtctttcgg cttgatagat gaaattttag gagctaatga aataactgct agtatctcta aagagcaata
3851 taagcgtttc gagaacgtcc cagaagattt aaagaaagat gtagacaaaa tcactaaaat cgatgatgta
3921 gatacgtttg aattggttga aacacctaaa gaaagtatgt cactagaaga aaaagaaaaa agagaaaaaa
3991 ttaaacgcga atgcgaaatt ttaaaaatga caatgagtta ttaggaggaa atgaaatgcc gacattatat
4061 gaattaaaac aatccttagg tatgattgga caacaattaa aaaataaaaa tgatgaattg agtcagaaag
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4201 atttaacatt gttgaaagac aagtaaaaga cattgaagaa aaagaaaaag cgaaagttaa agacacagga
4271 gaagcttatc aatctttaaa tgatcatgag aagatggtta aagctaaggc agagttttat cgtcacgcga
4341 ttttaccaaa tgaatttgaa aaaccttcaa tggaggcaca acgtttatta cacgctttac caacaggtaa
4411 tgattcaggt ggtgataagc tcttaccaaa aacactttct aaagaaattg tttcagaacc atttgctaaa
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4901 atgcgatatg cggattatgt caaaattatt agtgttcttt caaatggaac aacaaatttc tttgacacac
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5181 aagaaaatac aggttcatta cccagctaag ccccaaaagg ttaatgtaac agctaaggct aaatcagctg
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5321 atttcgaaaa tgatttaatt gaaggtctca ttcaatcggc taagtctgaa ttactattaa gtggggttcc
5391 agattatgac aaagatgact tggaataccc gctttttgt acagcgatta gatatatcat tgcaagagat
5461 tatgaaagtc gtgggtactc aaatgaccaa tctagaagca aggtttttaa tgaaaaggga ttgcaaaaaa
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5741 cataattatg aggtcttcta aaattgaata tctaccacaa acaaatcact tagttaaaat tgacagaggc
5811 ttatattccg ataaattatt caacattaaa gaaataagaa ttgatacacc agatattggc tataatacag
5881 tggtttttatc agaaaaatga gtgtagaaat taaagggata cctgaagtgt tgaagaaatt agaatcggta
5951 tacggtaaac aatcaatgca agctaagagt gatagagctt taaatgaagc atctgaattt tttataaagg
6021 ctttaaagaa agaattcgag agttttaaag atacgggtgc tagcatagaa gaaatgacta aatctaagcc
6091 ttatacaaaa gtaggaagtc aagaaagagc tgttttaatt gaatgggtag gccctatgaa tcgcaaaaac
6161 attattcact tgaatgaaca tggttataca agagatggaa aaaaatatac accaagaggt tttggagtta
6231 ttgcaaaaac attagctgct aatgaacgga agtatagaga aattataaaa aaggagttgg ccagataaat
6301 gaatatatta aacaccataa aagaaatttt attatctgat gcagagctcc aaacatatat aaattctaga
6371 atatactatt ataaagtcac tgaaaatgct gaaacttcca aaccttttgt tgttattaca cctatttatg
6441 atttaccttc agacttcatg tctgataaat atcttagtga agaatactta attcaaatag atgtagaatc
6511 ttcaaataat cagaaaacaa ttgatataac aaaacgaata agatatctgt tatatcaaca aaatttaatt
6581 caagcatcta gtcagttaga tgcttatttt gaagaaacta aacgttatgt gatgtcgaga cgttatcaag
6651 gcataccaaa aaatatatat tataaaaatc agcgcatcga ataggtgtgc tttttaattt ttaaggagga
6721 aataagcaat ggcagaagga caaggtcttt ataaagtagg ttttaaaaga ttatacgttg gagtttttaa
6791 cccagaagca acaaaagtag ttaaacgcat gacatgggaa gatgaaaaag gtggtacagt tgatctaaat
6861 atcacaggtt tagcaccaga tttagtagat atgtttgcat ctaacaaacg tgtttggatg aaaaaacaag
6931 gtactaatga agttaagtct gacatgagta tttttaatat tccaagtgaa gatctaaata cagttattgg
7001 tcgttctaaa gataaaaatg gtacatcttg ggtaggagag aatacaagag caccatacgt aacagttatt
7071 ggagaatctg aagatggttt aacaggtcaa ccagtgtacg ttgcgctact taaaggtact tttagcttgg
7141 attcaattga atttaaaaca cgaggagaaa aagcagaagc accagagcca acaaaattaa ctggtgactg
7211 gatgaacaga aaagttgatg ttgatggtac tccacaaggt attgtatacg ggtatcatga aggtaaagaa
7281 ggagaagcag aattcttcaa aaaagtattc gttggataca cggacagtga agatcattca gaggattctg
7351 caagttcgtt acccagctaa cccccaaaat gttgaagtag cagttaattc aaaatctgca acagtttcag
7421 cagaataggg gctttcaaaa taaatcaaag gagaataatt tatgactaaa actttaaagg tttataaagg
7491 agacgacgtc gtagcttctg aacaaggtga aggcaaagtg tcagtaactt tatctaattt agaagcggat
7561 acaacttatc caaaaggtac ttaccaagtg gcatgggaag aaaatggtaa agaatctagt aaagttgatg
7631 tacctcaatt caaaaccaat ccaattctag tctcaggcgt atcatttaca cccgaaacta aatcaatcac
7701 ggtaaatgct gatgacaatg ttgaaccaaa cattgcacca agtacagcaa cgaataaaac gttgaaatat
7771 acaagtgaac atccagagtt tgttactgtt gatgagagaa caggagcaat tcacggtgta gctgagggaa
7841 cttcagttat cactgctacg tctactgacg gaagtgacaa gtctggacaa attacagtaa cagtaacaaa
7911 tggataatta tttgagacgc agaatatctg cgtctttttt atttgaataa aaggagctaa tacaatgatt
7981 aaatttgaaa ttaaagaccg taaaacagga aaaacagaga gctatacaaa agaagatgtg acaatgggcg
8051 aagcagaaaa atgctatgag tatttagaat tagtaaatca agagaataaa aaagaagtac ctaacgcaac
8121 aaaaatgaga caaaaagagc gacagttatt agtagattta tttaaagatg aaggattgac tgaagaagat
8191 gttttgaaca agatgagcac taaaacttat acaaaagcct tgaaagatat atttcgagaa atcaatggtg
8261 aagatgaaga agattcagaa actgaaccag aagagatggg aaagacagaa gaacaatctc aataaaagat
8331 atttatcga acattaagaa aatacaagct ttctgtatgg agcagtatgg gtggacatta actgaagtca
8401 gaaaacagcc gtatgtaaaa cttttagaaa tacttaatga agagaataaa aagagactg aagaaaaaca
8471 aagtgaacaa aaagtcatta caggtacgga tttaagaaaa ctttttggaa gctagaaagg aggttaatat
8541 gaatgaaaaa gtagaaggca tgaccttgga gctgaaatta gaccatttag gtgtccaaga aggcatgaag
8611 ggtttaaagc gacaattagg tgttgttaat agtgaaatga aagctaatct gtcatcattt gataagtctg
8681 aaaaatcaat ggaaaagtat caggcgagaa ttaaggggtt aaatgataag cttaaagttc aaaaaaagat
8751 gtattctcaa gtagaagatg agcttaaaca agttaacgct aattatcaaa aagctaaatc tagtgtaaaa
8821 gatgttgaga aagcatattt aaagctagta gaagctaata aaaaagaaaa attagctctt gataaatcta
8891 aagaagcctt aaaatcttcg aatacagaac ttaaaaaagc tgaaaatcaa tataaacgta caaatcaacg
8961 taaacaagat gcatatcaaa aacttaaaca gttgagagat gcagaacaaa agcttaagaa tagtaaccaa
9031 gctactactg cacaactaaa aagagcaagt gacgcagtac agaagcagtc cgctaagcat aaagcacttg
9101 ttgaacaata taaacaagaa ggcaatcaag ttcaaaaact aaaagtacaa aatgataatc tttcaaaatc
9171 aaacgaaaaa atagaaaatt cttacgctaa aactaatact aaattaaagc aaacagaaaa agaatttaat
9241 gatttaaata atactattaa gaatcatagc gctaatgtcg caaaagctga aacagctgtt aacaaagaaa
9311 aagctgcttt aaataattta gagcgttcaa tagataaagc ttcatccgaa atgaagactt ttaacaaaga
9381 acaaatgata gctcaaagtc atttcggcaa acttgctagt caagcggatg tcatgtcaaa gaaatttagt
9451 tctattggag ataaaatgac ttccctagga cgtacgatga cgatgggcgt atctacaccg attactttag
9521 ggttaggtgc agcattaaaa acaagtgcag acttcgaagg gcaaatgtct cgagttggag cgattgcaca
9591 agcaagcagt aaagacttaa aaagcatgtc taatcaagcg gttgacttag gcgctaaaac aagtaaaagt
9661 gctaacgaag ttgctaaagg tatggaagaa ttggcagctt taggctttaa tgccaaacaa acaatggagg
9731 ctatgccggg tgttatcagt gcagcagaag caagcggtgc agaaatggct acaactgcaa ctgtaatggc
9801 atcagcaatt aattctttcg gtttaaaagc atctgatgca aaccatgttg ctgatttact tgcgagatca
9871 gctaatgata gtgctgcaga tattcaatac atgggagatg cattaaaata tgcaggtact ccagcaaaag
9941 cattaggagt ttcaatagag gacacttctg cagcaattga agttttatct aactcagggt tagaggggtc
10011 tcaagcaggt actgcattaa gagcttcgtt tattaggcta gctaatccaa gtaaaagtac agctaaggaa

10081 atgaaaaaat taggtattca tttgtctgat gctaaaggtc aatttgttgg catgggtgaa ttgattagac
10151 agttccaaga caacatgaaa ggcatgacga gagaacaaaa actagcaaca gtggctacaa tagttggcac
10221 tgaagcagca agtggatttt tagccttgat tgaagcgggt ccagataaaa ttaatagcta tagcaaatca
10291 ttgaagaact ctaatggtga aagtaaaaaa gcagctgatt tgatgaaaga caacctcaaa ggtgctctgg
10361 aacaattagg tggcgctttt gaatcgttag caattgaagt tggtaaagat ttaacgccta tgattagagc
10431 aggtgcggaa ggattaacaa aattagttga tggatttaca catcttcctg gttggtttag aaaggcttcg
10501 gtaggtttag cgatttttgg tgcatctatt ggccctgctg ttcttgctgg tggcttatta atacgtgcag
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38851 attgcgtaat gatccaaatt taaaaggaaa aatagcattt aatgaattta caaaacaaat tgaatgctta
38921 gggaaaatgc catggaataa taattttaaa atacgtcaat ggcaagacgg tgatgatagc agtttaagaa
38991 gttatatcga aaagatttat gacatacacc attcaggcaa aacaaaagat gccattataa gcgtagcaat
39061 gcaaaatgcc tatcatccag taagagatta tctaaataaa atatcgtggg atggacataa acgtcttgaa
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39201 ctgctggaat cgctcgagta atggagccag gatgtaaatt tgactatatg cttacacttt atggtcctca
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42001 gatcaaagag tatataaagc tttacaaaat aaagaactaa cgcaagaaga attgatgaaa gctattaaag
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Table 8

Bacteriophage 3A ORFs list

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100381	3AORF003	1	32188..34149	653	ttaaagaaattgaggtgtcaagaat	ttg	tag
100382	3AORF004	3	17457..19370	637	gctattttattagaaaggaaggtgc	att	taa
100383	3AORF005	1	334..2034	566	agaaaaaagatagttcaagaagaag	gtg	taa
100384	3AORF006	1	15571..17154	527	cttttatttataggtaggtgattta	atg	taa
100385	3AORF007	2	19337..20836	499	atgatagtaaaacaagttcagggcc	atg	taa
100386	3AORF008	3	22176..23630	484	aatgatttagggtaggtgttgacca	atg	tga
100387	3AORF009	1	40726..42093	455	gtaaatacttttataagaatggtag	gtg	taa
100388	3AORF010	3	13491..14738	415	gaggcggactaacgctacagtaaaa	att	taa
100389	3AORF011	2	2039..3277	412	attaaagacataatgcgttaaggag	gtg	taa
100390	3AORF012	2	4001..5209	402	aaaaaagagaaaaaattaaacgcga	atg	taa
100391	3AORF013	1	30379..31545	388	attttatgaatgcgagaataaatgc	atg	taa
100392	3AORF014	2	14738..15562	274	attatatgggaggtttgactaatta	atg	tag
100393	3AORF015	3	3249..4034	261	cttgaattaagaaaatctttgaaag	gtg	tag
100394	3AORF016	-2	25587..26273	228	aagaagctaagaaaaaaataaaaat	atg	tga
100395	3AORF017	3	6729..7370	213	ttaatttttaaggaggaaataagca	atg	taa
100396	3AORF018	3	24540..25154	204	aataaaataaaaagtaggtgataag	atg	taa
100397	3AORF019	2	31565..32128	187	ctataaaaattaaaaaggacggtat	ata	taa
100398	3AORF020	3	36150..36713	187	gcagtaggaattatgacgggtcaag	ttg	taa
100399	3AORF021	2	24011..24535	174	gtaataaaatttataaagaaaggaa	atg	tga
100400	3AORF022	-2	12423..12938	171	taaagtaccagtagacaatgtaggt	att	tga
100401	3AORF023	1	7462..7917	151	aaaataaatcaaaggagaataattt	atg	taa
100402	3AORF024	1	26731..27174	147	actaaataaaaataaggaggacact	atg	tga
100403	3AORF025	1	42106..42543	145	taagcataagtaatggaggtataag	atg	taa
100404	3AORF026	2	35255..35671	138	aagcaactaactttattttaaggag	ata	taa
100405	3AORF027	2	5888..6298	136	atattggctataatacagtggtttt	atc	taa
100406	3AORF028	-3	27845..28255	136	cctttttaagatgtttatgatccttt	ctg	taa
100407	3AORF029	3	34344..34748	134	ttaaggttttagatttagaggtgga	atg	taa
100408	3AORF030	2	6299..6694	131	tataaaaaaggagttggccagataa	atg	tag
100409	3AORF031	1	20833..21225	130	ttaacaaaattataggagtgagaaa	ata	taa
100410	3AORF032	-2	39984..40361	125	aaatagctgttagagggttacccct	ata	tag
100411	3AORF033	1	7957..8325	122	gaatatctgcgtctttttttatttga	ata	taa
100412	3AORF034	-2	28506..28871	121	gttatcaacctaaggaggtgataac	atg	tag
100413	3AORF035	-2	10671..11036	121	tcctagcttcctaacagcaccgcca	ata	tga
100414	3AORF036	2	30020..30382	120	accaattttaaggaggagttaatca	atg	tga
100415	3AORF037	2	21818..22165	115	aagtgtaagtaatagttaagagtca	gtg	tag
100416	3AORF038	-2	42003..42347	114	gtactcactttcaactgcttcaacc	atc	tga
100417	3AORF039	2	21386..21727	113	tccagaaaatctagagtcataggtt	ata	taa
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100419	3AORF041	-1	4333..4671	112	tactaaatctacatctgatccatga	att	tga
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100421	3AORF043	1	25690..26019	109	taccaaattaatatagtcttcgcat	ata	tag
100422	3AORF044	3	29676..30005	109	gtcttaaataattatataaggagtt	att	taa
100423	3AORF045	3	30..353	107	cgctagcaacgcggataaatttttc	atg	taa
100424	3AORF046	3	27894..28214	106	aagatattgaaaagctaatttcccc	ata	tga
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100430	3AORF052	-3	3722..4024	100	gcatttcatttcctcctaataactc	att	tga
100431	3AORF053	3	17145..17444	99	tcgagacaatggatatagggagtgt	att	tag
100432	3AORF054	-1	19915..20211	98	ataatttatagcttgcgaaacataa	ata	tga
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100434	3AORF056	3	40455..40745	96	taaattttgtatacaaggtgaataa	atg	tga
100435	3AORF057	-1	38665..38952	95	atcatcaccgtcttgccattgacgt	att	taa
100436	3AORF058	-1	21265..21549	94	gaaatttctatctaacttgtcataa	att	tga
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100510	3AORF132	-2	1860..2027	55	gcgataacattcacctccttaacgc	att	tga
100511	3AORF133	-3	42317..42484	55	acaaagttctttcgtattgtagtaa	ctg	tag
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100515	3AORF137	1	37186..37347	53	ggcagttgtttgaaaatataaggga	gtg	taa
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100518	3AORF140	3	29442..29603	53	aaaatggtattaggaggattatcaa	atg	taa
100519	3AORF141	-1	39883..40044	53	tacaccataatcttttccaaatcga	att	taa
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Table 9

Bacteriophage 96, complete genome sequence

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41511 taagaggtgt aacacctcgt aatgatttac tgaacgttaa tgtatcagca gaaataaata tcaattatcg
41581 tttatctgaa ttaggtttta ttactaataa aaaagatatg gattggatta agaagaatta tgacttgtat
41651 tctaaattaa tagctggtgc gattcatggt aagcctatag gtggtttggt agctggtaat gttaaaacat
41721 cagctaaaaa ccaaaaaaat ccaccagtgc cagcaggtta tacacttgat aagaataatg tgccttataa
41791 aaaagagact ggtaattaca cagttgccaa tgttaaaggt aataacgtaa gggacggcta ttcaactaat
41861 tcaagaatta caggtgtatt acctaataac gcaacaatca aatatgacgg cgcatattgc atcaatgggt
41931 atagatggat tacttatatt gctaatagtg gacaacgtcg ctatattgcg acaggagagg tagataaagc

42001 aggtaatagg ataagtagtt ttggtaagtt tagcacgatt tagtatttac ttagaataaa aattttgcta
42071 cattaattat agggaatctt acagttatta aataactatt tggatggatg ttaatattcc tatacacttt
42141 ttaacattac tctcaagatt taaatgtaga taacaggcag gtactacggt acttgcctat tttttgtta
42211 taatgtaatt acattaccag taaccaatct ggcttaaaac cacatttccg gtagccaatc cggctatgca
42281 gaggacttac ttgcgtaaag tagtaagaag ctgactgcat atttaaacca cccatactag ttgctgggtg
42351 gttgtttttt atgttatatt ataaatgatc aaaccacacc acctattaat ttaggagtgt ggttattttt
42421 tatgcaaaaa aaacgaaaaa aagttcataa aaagtattgc atatcacgtt taaccgtgtt ataataaggt
42491 ataccagttg agaggaggat aaaaagtgtt agaaaatttt aaaactatag cagaaatcgc cttttataca
42561 atgtcagcaa ttgccatagc gaaaacattg aaaaaagacg ataagtaagt agacaagccc gaaagggctg
42631 tctatatata aattctaaca ctaaaatact atgaaaacaa tttacattat tttaatcatt cttatttgga
42701 taaacgtgtt tttaggcaac gatataagta aaagtgttgt tgcactgctt actactttac tgcttatcaa
42771 tttatggaag agggataaaa atgacagcaa taaaagaaat aattgaatca atagaaaagt tattcgaaaa
42841 agaaacggga tataaaattg ctaaaaattc cggattacca tatcaaactg tgcaagattt aagaaatgga
42911 aaaacatctt tatcagatgc cagatttaga acgataataa agttatacga gtatcaaaga tcgcttgaaa
42981 acgaagaaga taaataaaag gagccaaaaa tatgtttgtt acaaaagaag aatttaaaac tttgaatgta
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43121 atgatagata cgtagtactt gaccataaaa aaggcgattt gtacccgcaa aaagcatacc caaaatatat
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43331 cgcatagtta taggcttttc agctatatac caagataaga tttatcccgc cgtctccata aaaatatgct
43401 tggaaacctt gatttaatgg ggttttaatc tagcaagtgt caaatatgtg tcaagaaaat aattttctga
43471 cacgttgacc ttgctctttt ttatgttcat caagtaagtg agagtaggtg tctaaagtta tagatatatt
43541 ataatggcct aatcttttgc taatatattc aatagg

Table 10

Bacteriophage 96 ORFs list

SID	LAN	FRA	POS	a.a.	RBS sequence	STA	STO
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100734	96ORF002	1	32008..33906	632	ttttacgactaaaggaggcaacca	atg	taa
100735	96ORF003	1	30109..31995	628	ttatatttagataaggagtagcct	atg	taa
100736	96ORF004	1	36760..38634	624	attttgattgaaatgaggtgcatac	atg	taa
100737	96ORF005	3	33903..35729	608	gtttattcgaaggaaaggtggttga	ata	taa
100738	96ORF006	2	40589..42043	484	aatgatttagggtaggtgttgacca	atg	tag
100739	96ORF007	1	18652..20091	479	tatacacacatactaaacctgaacg	att	tga
100740	96ORF008	2	8960..10201	413	tggcagaatttgggggcgataacga	atg	tga
100741	96ORF009	2	17447..18670	407	gacgcaataacggaagtgatcgtca	atg	tga
100742	96ORF010	1	38647..39819	390	taaatataaataaagaggtgtgtaa	atg	tga
100743	96ORF011	-1	119..1195	358	gtagctcgcctacccttattattt	ttg	tga
100744	96ORF012	2	20045..21013	322	tttaatgacaaattacctgacatag	atg	tga
100745	96ORF013	3	29157..30098	313	acttattataagggaggtttgttag	ttg	taa
100746	96ORF014	1	21925..22839	304	agaaaataaagtgaggtaataaaat	atg	tag
100747	96ORF015	1	5812..6591	259	atacacggtaaaggtgggagaatag	atg	taa
100748	96ORF016	1	7852..8607	251	aataaaatgttgaaaggagagaaaa	atg	taa
100749	96ORF017	3	3444..4190	248	aaatttaacattaatatcactttaa	gtg	taa
100750	96ORF018	-3	28281..29000	239	taagctatgttgaacatcgctagtc	atg	tga
100751	96ORF019	3	7188..7859	223	tttaccgttctaggacgtggtttaa	atg	taa
100752	96ORF020	3	21324..21908	194	gaagggcaaaaaggagttttgatat	atg	taa
100753	96ORF021	3	6612..7175	187	attaaaaattaattaaaaggacggt	ata	tag
100754	96ORF022	2	24536..25093	185	aaagaaaaacgaaggagtgtattaa	atg	taa
100755	96ORF023	1	5275..5811	178	catgaaatggtaggaggtatgaaaa	gtg	tag
100756	96ORF024	3	14481..15014	177	taaaacgataggagataacgaataa	atg	taa
100757	96ORF025	2	25157..25666	169	ataaaaaaattgaaaagaggtatat	att	taa
100758	96ORF026	-3	15084..15590	168	tcattcttaacatagcccttaattc	atg	tga
100759	96ORF027	-1	1229..1732	167	aatagcaaataaaggagtgtaaaac	atg	taa
100760	96ORF028	1	16960..17454	164	aaggcgtgtgatacagtgaaaacaa	ttg	taa
100761	96ORF029	-1	1736..2227	163	tatgagaaaaggagtcatataaaag	atg	taa
100762	96ORF030	1	25531..25995	154	ttttcaagagggagagtcgctcgta	ctg	tag
100763	96ORF031	2	23633..24097	154	tttagtattgaaggtgattctgtag	atc	tag
100764	96ORF032	-2	2248..2706	152	ataagacaccaaaggggtttggcgc	atg	tga
100765	96ORF033	-3	39147..39605	152	agcatataaatcgtttagtgtttgt	ttg	taa
100766	96ORF034	2	13181..13615	144	tagaagtcgaaaaagtggaggcaat	ata	taa
100767	96ORF035	2	10628..11053	141	gagctaggattgcaagcaacgatat	ttg	tga
100768	96ORF036	2	24110..24535	141	gtatttttcatagaggtggttaaat	atg	taa
100769	96ORF037	1	12583..12996	137	atgaggaacagaagcaaccaacttt	att	tga
100770	96ORF038	1	15628..16032	134	atgttaagaatgatgcctagtttaa	ttg	taa
100771	96ORF039	3	39816..40220	134	ctaatacactttacttaattaaggg	gtg	taa
100772	96ORF040	-3	27528..27932	134	tttccataaataaacgaggacacca	atg	tga
100773	96ORF041	3	16206..16607	133	gatgagggcggaggtgtcagagtag	atg	tga
100774	96ORF042	2	35720..36106	128	aagttactataactaaaattatggg	gtg	taa
100775	96ORF043	-2	35713..36081	122	ttaaacgtccccctcagtatttgtt	ttg	taa
100776	96ORF044	-2	9460..9828	122	agtatccatcagttgaagataatct	ata	taa
100777	96ORF045	-3	5139..5504	121	ttctttttgtattctgtaatattca	att	tga
100778	96ORF046	2	11513..11872	119	aagtaaatgtatagaggtggaataa	atg	taa
100779	96ORF047	2	22991..23350	119	gtcgtactacgtctgataagagcga	gtg	tag
100780	96ORF048	3	8607..8963	118	tggaaaaagaattgagtgatgacta	atg	tga
100781	96ORF049	1	23353..23697	114	atccgtttaaaccaataaggtagag	gtg	taa
100782	96ORF050	-2	2728..3072	114	tggtaaattagtattacattaagta	ata	taa
100783	96ORF051	3	4692..5021	109	tcaaaatatacggaggtagtcaact	atg	tga
100784	96ORF052	-1	20882..21211	109	gtagcaaagagacaactaaaaaagt	gtg	taa
100785	96ORF053	1	40252..40578	108	acgactaatttttagtcgtttttt	att	tag
100786	96ORF054	1	4942..5262	106	aatataaaactaaaaaacaaaattt	atg	tag
100787	96ORF055	-2	4840..5151	103	ccgtcgcaatatatagttcgcttaa	atc	taa
100788	96ORF056	3	36324..36623	99	aatttaacacaaagtaggtggcgta	atg	taa
100789	96ORF057	2	1394..1690	98	cttcagtggctcttttagcatttaa	ata	taa
100790	96ORF058	-3	26247..26537	96	tacttcttttctcataatctgacca	att	tga
100791	96ORF059	-1	21485..21772	95	agactcaacgccttttgaacatac	ttg	tga
100792	96ORF060	-3	22647..22931	94	cctctttgtaaccgacaagactgta	ata	taa
100793	96ORF061	1	14023..14304	93	ttatctaattaagggggacgagtga	gtg	taa
100794	96ORF062	-2	38281..38559	92	tatataacttagcgattgtacttgc	ttg	taa

100795	96ORF063	-3	30786..31064	92	gtctcctaatactacatcttgctta	gtg	tga
100796	96ORF064	-2	30205..30480	91	atgcatctactttggatgtaatac	ata	tag
100797	96ORF065	1	2617..2886	89	aaggtctaataaaaatttctccttc	ttg	taa
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100799	96ORF067	-3	17142..17411	89	ttccgttattgcgtcgtgaagttgt	ttg	tga
100800	96ORF068	2	12326..12589	87	aatgcatgtcgtttggtctgcctaa	ttg	tag
100801	96ORF069	2	42734..42997	87	ttttaggcaacgatataagtaaaa	gtg	taa
100802	96ORF070	1	11869..12129	86	aaatgttcaagaaatggagtgaagc	ata	taa
100803	96ORF071	3	15396..15656	86	aacaagctatacaaattatcgataa	att	taa
100804	96ORF072	-3	37749..38009	86	agatttttcgggttaccccctagac	att	taa
100805	96ORF073	3	11244..11501	85	acatgcatatatagaggtggaataa	atg	tag
100806	96ORF074	-3	42936..43193	85	aattatttaacttactaattttctt	ttg	taa
100807	96ORF075	-3	26610..26867	85	tactgccaatgttccatcttcaacc	att	taa
100808	96ORF076	-1	11126..11380	84	tttatctaatacatttaagttaacc	atc	taa
100809	96ORF077	-2	16537..16791	84	tacccaccatataggcaggtagtag	gtg	tag
100810	96ORF078	-3	19521..19775	84	aataactttgaattgatacctcaac	ata	tga
100811	96ORF079	3	13608..13859	83	ttagggcaaatggaggcagacacaa	atg	tag
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100813	96ORF081	3	20973..21221	82	aatgaagttatcccattcatgactt	atc	tag
100814	96ORF082	-1	8729..8974	81	cgattattgtgctttcaatttcaaa	ttg	tga
100815	96ORF083	-3	3147..3392	81	tttagcctttatataatcaacttct	gtg	tga
100816	96ORF084	3	1611..1853	80	tgctttatctttagtttctttcttt	ttg	tga
100817	96ORF085	-2	29470..29709	79	ctcttatcaccttcgtttgtaggca	atc	taa
100818	96ORF086	1	35188..35424	78	gcgcaaggcgatttgggatatttaa	ctg	tag
100819	96ORF087	-2	13039..13275	78	ttttgattgagctctaaagtgtctt	att	tag
100820	96ORF088	3	24930..25163	77	gaactatcattaaaagttaaatgga	ata	tga
100821	96ORF089	-3	22329..22562	77	tccagtataagatagtggtaatccc	ata	taa
100822	96ORF090	-3	16803..17036	77	acctttagtcgaatacccctgcgtca	ata	tag
100823	96ORF091	-1	22559..22789	76	aacgcttctggtttaacgttcatgt	atg	taa
100824	96ORF092	3	18360..18587	75	attgcaaaagatattgtaagtagat	atg	taa
100825	96ORF093	-2	25384..25608	74	catgatttccttgtaattctctttc	atc	taa
100826	96ORF094	1	10417..10638	73	aacacacattaaggagtgttaaaaa	atg	tag
100827	96ORF095	3	12963..13184	73	tactaaacgaagataaaactatgac	att	taa
100828	96ORF096	1	42994..43212	72	gatcgcttgaaaacgaagaagataa	ata	taa
100829	96ORF097	-1	36047..36265	72	tcaagcattacacctgtgactttc	atc	taa
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100847	96ORF115	1	13819..14022	67	gcagtaggggttatggcaggtcaag	ttg	tga
100848	96ORF116	-1	41033..41236	67	caacttcatgacctgcatgtcttaa	ata	taa
100849	96ORF117	-3	24711..24914	67	tctgctgtattccatttaactttta	atg	taa
100850	96ORF118	-1	12374..12574	66	tccatctcctctaaaataaagttgg	ttg	taa
100851	96ORF119	-1	3980..4180	66	ctcctatatttcgttttaaaatttc	att	tga
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100866	96ORF134	-2	9250..9435	61	atccatgagcttataacccgtctta	att	tga

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100895	96ORF163	-1	15386..15550	54	agccatcataggactgtaaaattca	ctg	taa
100896	96ORF164	-1	10049..10213	54	tacatcgatttcaataagcttttga	att	tag
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100898	96ORF166	-2	11104..11268	54	ctagccatgattacccttaaattag	ttg	tag
100899	96ORF167	-3	13764..13928	54	agacagtttataatgtgtatctcta	ata	tga
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100908	96ORF176	-3	37170..37328	52	tttatctaaaacattgctgtaagca	gtg	taa
100909	96ORF177	-3	6693..6851	52	ttcctaatctactaagtaactcgat	ata	taa
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101119	96ORF387	2	2207..2308	33	tccaagactctttaactgttaactt	atc	tag
101120	96ORF388	2	2519..2620	33	attgttgaatttcgattgatctaaa	atg	tga
101121	96ORF389	2	22517..22618	33	agaagtaaaatgcgtaatgctttag	atg	tag
101122	96ORF390	2	27302..27403	33	ttccaaaattgggctaatagtgtag	ctg	taa
101123	96ORF391	2	32384..32485	33	actaaaaaggttgagaaagctgtag	atg	taa
101124	96ORF392	2	39287..39388	33	aaaaacggtactgtagtatcaatca	atc	tag
101125	96ORF393	3	18153..18254	33	gtagtatatgccgactttgatttga	atg	taa
101126	96ORF394	3	24189..24290	33	tcagaccctaacattaacaaactag	ttg	tga
101127	96ORF395	-1	15266..15367	33	tcgataatttgtatagcttgtttta	atg	tag
101128	96ORF396	-2	32239..32340	33	ttttagtgaaagcatctagtgttga	ata	tag
101129	96ORF397	-2	16123..16224	33	ttatgtgtgcctatcatattaacaa	ttg	tag
101130	96ORF398	-2	13648..13749	33	tctttaactgaatgttgaatagcat	ttg	tag
101131	96ORF399	-2	10987..11088	33	acttctgtaggtattcttatatcaa	ttg	tga
101132	96ORF400	-2	3382..3483	33	cttactggtaattcttcaaaattaa	atg	taa
101133	96ORF401	-3	40794..40895	33	ccatatgatgtgaaagtgtttaaat	ttg	taa
101134	96ORF402	-3	39978..40079	33	atattcctaaatcacttgaacctaa	att	tga
101135	96ORF403	-3	38607..38708	33	atcttcagtgtaaaatcgacagcca	atg	tag
101136	96ORF404	-3	21288..21389	33	cagacaccgtcttaagtccctttag	ata	taa

Table 11

SEQUENCE INFORMATION FOR PHAGES MATCHING WITH TABLE 1

M32695
Bacteriophage PM2 nuclease cleavage site
gi|166145|gb|M32695|BM2NCS [166145]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M32693
Bacteriophage PM2 Hind III fragment 4
gi|166144|gb|M32693|BM24HIND3 [166144]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M32693
Bacteriophage PM2 Hind III fragment 4
gi|166144|gb|M32693|BM24HIND3 [166144]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M32694
Bacteriophage PM2 Hind III fragment 3
gi|166143|gb|M32694|BM23HIND3 [166143]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M26134
Bacteriophage PM2 structural protein gene containing purine/pyrimidine rich regions and anti-Z-DNA-IgG binding regions, complete cds
gi|289360|gb|M26134|BM2PROTIV [289360]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

J02452
bacteriophage fi 3'-terminal region rna
gi|215409|gb|J02452|PFITR3 [215409]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

AF020798
Bacteriophage Cbp1 genome DNA, complete sequence
gi|217761|dbj|D00624|BCP1 [217761]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 12 protein links, or 1 genome link)

X72793
Clostridium botulinum C phage BONT/C1, ANTP-139, ANTP-33, ANTP-17, ANTP-70 genes and ORF-22
gi|516171|emb|X72793|CBCBONT [516171]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 4 nucleotide neighbors)

X51464
Clostridium botulinum D Phage C3 gene for exoenzyme C3
gi|14907|emb|X51464|CBDPE3 [14907]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

D90210
Bacteriophage c-st (from C. botulinum) C1-tox gene for botulinum C1 neurotoxin
gi|217780|dbj|D90210|CSTC1TOX [217780]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

S49407
type D neurotoxin [bacteriophage d-16 phi, host = C. botulinum, type D, CB16, Genomic, 4087 nt]
gi|260238|gb|S49407|S49407 [260238]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

X53370
Bacteriophage phi29 temperature sensitive mutant TS2(98) DNA polymerase gene
gi|15733|emb|X53370|POTS298 [15733]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 7 nucleotide neighbors)

X53371
Bacteriophage phi29 temperature sensitive mutant TS2(24) DNA polymerase gene
gi|15731|emb|X53371|POTS224 [15731]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 7 nucleotide neighbors)

X05973
Bacteriophage phi29 prohead RNA
gi|15680|emb|X05973|POP29PRO [15680]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 4 nucleotide neighbors)

V01155
Left end of bacteriophage phi-29 coding for 15 potential proteins Among
these are the terminal protein and the proteins encoded by the genes 1, 2 (sus), 3, and (probably) 4
gi|15659|emb|V01155|POP29B [15659]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 16 protein links, or 16 nucleotide neighbors)

X73097
Bacteriophage phi-29 left origin of replication
gi|312194|emb|X73097|BP29ORIL [312194]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors)

M14430
Bacteriophage phi-29 gene-17 gene, complete cds
gi|215321|gb|M14430|P29G17A [215321]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 8 nucleotide neighbors)

M14431
Bacteriophage phi-29 gene-16 gene, complete cds
gi|215319|gb|M14431|P29G16A [215319]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 7 nucleotide neighbors)

M20693
Bacteriophage phi-29 DNA, 3' end
gi|215343|gb|M20693|P29REPINB [215343]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors)

M21016
Bacteriophage phi-29 DNA, 5' end
gi|215342|gb|M21016|P29REPINA [215342]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M12456
Bacteriophage phi-29 genes 9, 10 and 11 encoding p9 tail, incomplete, p10 connector, complete, and p11 lower collar, incomplete, respectively
gi|215338|gb|M12456|P29P9 [215338]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors)

M14782
Bacillus phage phi-29 head morphogenesis, major head protein, head fiber protein, tail protein, upper collar protein, lower collar protein, pre-neck appendage protein, morphogenesis(13), lysis, morphogenesis(15), encapsidation genes, complete cds
gi|215323|gb|M14782|P29LATE2 [215323]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 11 nucleotide neighbors)

M26968
Bacteriophage phi-29 (from Bacillus subtilis) proteins p1 delta-1 genes, complete cds, and the sus1(629) mutation
gi|341558|gb|M26968|P29P1D1A [341558]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

J02448
Bacteriophage f1, complete genome
gi|166201|gb|J02448|F1CCG [166201]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, 205 nucleotide neighbors, or 1 genome link)

M24832
Bacteriophage f2 coat protein gene, partial cds
gi|166228|gb|M24832|F2CRNACA [166228]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

J02451
Bacteriophage fd, strain 478, complete genome
gi|215394|gb|J02451|PFDCG [215394]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 MEDLINE links, 10 protein links, 204 nucleotide neighbors, or 1 genome link)

M34834
Bacteriophage fr replicase gene, 5' end
gi|166139|gb|M34834|BFRREGRA [166139]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors)

M38325
Bacteriophage fr replicase gene, 5' end
gi|166137|gb|M38325|BFRREGR [166137]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors)

M35063
Bacteriophage fr coat protein replicase cistron (R region) RNA
gi|166134|gb|M35063|BFRRCRRA [166134]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 3 nucleotide neighbors)

S66567
alpha-atrial natriuretic factor/coat protein=fusion polypeptide [human, bacteriophage fr, expression vector pFAN15, PlasmidSyntheticRecombinant, 510 nt]
gi|435742|gb|S66567|S66567 [435742]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 15 nucleotide neighbors)

X15031
Bacteriophage fr RNA genome
gi|15071|emb|X15031|LEBFRX [15071]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, 9 nucleotide neighbors, or 1 genome link)

U51233
Mus musculus neutralizing anti-RNA-bacteriophage fr immunoglobulin variable region light chain (IgM) mRNA, partial cds
gi|1277150|gb|U51233|MMU51233 [1277150]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1669 nucleotide neighbors)

U51232
Mus musculus neutralizing anti-RNA-bacteriophage fr immunoglobulin variable region heavy chain (IgM) mRNA, partial cds
gi|1277148|gb|U51232|MMU51232 [1277148]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1073 nucleotide neighbors)

U02303
Bacteriophage If1, complete genome
gi|3676280|gb|U02303|B2U02303 [3676280]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, or 1 genome link)

V00604
Phage M13 genome
gi|14959|emb|V00604|INM13X [14959]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, or 205 nucleotide neighbors)

A32252
Synthetic bacteriophage M13 protein III probe
gi|1567340|emb|A32252|A32252 [1567340]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

A32251
Synthetic bacteriophage M13 protein III probe
gi|1567339|emb|A32251|A32251 [1567339]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M12465
Bacteriophage M13 mp10 mutations in lac operon
gi|215210|gb|M12465|M13LACMUT [215210]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 215 nucleotide neighbors)

M24177
Synthetic Bacteriophage M13 (clone M13.SV.B12) SV40 early promoter region DNA
gi|209416|gb|M24177|SYNSVB12 [209416]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M24176
Synthetic Bacteriophage M13 (clone M13.SV.B11) SV40 early promoter region DNA
gi|209415|gb|M24176|SYNSVB11 [209415]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M24175
Synthetic Bacteriophage M13 (clone M13.SV.8) SV40 early promoter region DNA
gi|208806|gb|M24175|SYNM13SV8 [208806]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 242 nucleotide neighbors)

M19979
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207813|gb|M19979|SYN33M13M [207813]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 617 nucleotide neighbors)

M19565
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207808|gb|M19565|SYN33M13H [207808]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 567 nucleotide neighbors)

M19564
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207807|gb|M19564|SYN33M13G [207807]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 12 nucleotide neighbors)

M19563
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207806|gb|M19563|SYN33M13F [207806]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 262 nucleotide neighbors)

M19561
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207804|gb|M19561|SYN33M13D [207804]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 27 nucleotide neighbors)

M19560
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207803|gb|M19560|SYN33M13C [207803]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M19559
Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33
gi|207802|gb|M19559|SYN33M13B [207802]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 227 nucleotide neighbors)

M10568
Bacteriophage M13 replicative form II, replication origin, specific nick location
gi|215220|gb|M10568|M13ORIB [215220]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 650 nucleotide neighbors)

M10910
Bacteriophage M13 gene II regulatory region and M13sj1 mutant
gi|215209|gb|M10910|M13IIREG [215209]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 72 nucleotide neighbors)

M38295
Bacteriophage M13 HaeIII restriction fragment DNA
gi|215208|gb|M38295|M13HAEIII [215208]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 67 nucleotide neighbors)

E02067
DNA encoding a part of Bacteriophage M13 tg 127
gi|2170311|dbj|E02067|E02067 [2170311]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

J02467
Bacteriophage MS2, complete genome
gi|215232|gb|J02467|MS2CG [215232]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE links, 4 protein links, 20 nucleotide neighbors, or 1 genome link)

AJ004950
Bacteriophage P1 ban gene
gi|3688226|emb|AJ011592|BP1011592 [3688226]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link)

U88974
Bacteriophage P1 structural lytic transglycosylase (orf47), pep44b (orf44b), pep44a (orf44a), and pep43 (orf43) genes, complete cds; and pep42 (orf42) gene, partial cds
gi|2661099|gb|AF035607|AF035607 [2661099]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 1 nucleotide neighbor)

AJ000741
Bacteriophage P1 darA operon
gi|2462938|emb|AJ000741|BPAJ7641 [2462938]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, or 31 nucleotide neighbors

X01828
Bacteriophage P1 recombinase gene cin
gi|15133|emb|X01828|MYP1CIN [15133]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

X98146
Bacteriophage P1 DNA sequence around the Op88 operator
gi|1359513|emb|X98146|BP1OP88OP [1359513]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor)

S61175
immI operon: icd=cell division repressor, ant1=antirepressor {promoters P51a, P51b} [bacteriophage P1, Genomic, 728 nt]
gi|385908|gb|S61175|S61175 [385908]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

X87824
Bacteriophage P1 gene 26
gi|861164|emb|X87824|XXBP1G26 [861164]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link)

X15638
Phage P1 DNA for lytic replicon containing promoter P53 and two open reading frames
gi|15735|emb|X15638|PP1LREP [15735]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 24 nucleotide neighbors

X17512

Bacteriophage P1 DNA for immunity region immI
gi|15479|emb|X17512|P1IMMUNIY [15479]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 4 nucleotide neighbors)

X16005

Bacteriophage P1 c1 gene for P1c1 repressor protein
gi|15477|emb|X16005|P1C1 [15477]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

X03453

Bacteriophage P1 cre gene for recombinase protein
gi|15135|emb|X03453|MYP1CRE [15135]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors)

X06561

Bacteriophage P1 c1 gene 5'-region
gi|15128|emb|X06561|MYP1C1 [15128]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 6 nucleotide neighbors)

V01534

Bacteriophage P1 genome fragment (IS2 insertion spot). This regions contains
four unidentified reading frames and is known as insertion hot spot for IS2 insertion sequences
gi|15118|emb|V01534|MYOVP1 [15118]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 3 nucleotide neighbors)

X56951

Bacteriophage P1 gene10
gi|406728|emb|X56951|BPP1GP10 [406728]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 1 nucleotide neighbor)

K02380

Bacteriophage P1 replication region including repA, parA, and parB genes and
incA, incB, and incC incompatibility determinants
gi|215652|gb|K02380|PP1REP [215652]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 MEDLINE links, 4 protein links, or 8 nucleotide neighbors)

X87674

Bacteriophage P1 lydA & lydB genes
gi|974763|emb|X87674|BACP1LYD [974763]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

X87673

Bacteriophage P1 gene 17
gi|974761|emb|X87673|BACP117 [974761]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

M16618

Bacteriophage P1 ci repressor binding sites
gi|215600|gb|M16618|PP1C1 [215600]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors)

SEG_PP1CIN
Bacteriophage P1 cin gene encoding recombinase, cixL recombination site, and 5' end of C invertible element
gi|215607|gb||SEG_PP1CIN [215607]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

K03173
Bacteriophage P1 C invertible element, right end, and cixR recombination site
gi|215606|gb|K03173|PP1CIN2 [215606]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

215605
Bacteriophage P1 cin gene encoding recombinase, cixL recombination site, and 5' end of C invertible element
gi|215605|lcl|X01828 [215605]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M25470
Bacteriophage P1 tail fiber protein gene, complete cds
gi|341349|gb|M25470|PP1TFPR [341349]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors)

M34382
Bacteriophage P1 sim region proteins, complete cds
gi|215661|gb|M34382|PP1SIM [215661]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

M81956
Bacteriophage P1 R protein (R) gene, complete cds
gi|215658|gb|M81956|PP1RP [215658]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors)

M37080
Bacteriophage P1 mini-P1 plasmid origin of replication
gi|215657|gb|M37080|PP1REPOR [215657]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 46 nucleotide neighbors)

M27041
Bacteriophage P1 ref gene, complete cds
gi|215650|gb|M27041|PP1REF [215650]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

L01408
Bacteriophage P1 partition protein (parB) gene, 3' end
gi|215642|gb|L01408|PP1PARB [215642]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 41 nucleotide neighbors)

SEG_PP1PAR
Bacteriophage miniplasmid P1 parA gene, 5' end
gi|215639|gb||SEG_PP1PAR [215639]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 48 nucleotide neighbors)

M36425
Bacteriophage miniplasmid P1 parB gene, 3' end
gi|215638|gb|M36425|PP1PAR2 [215638]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M36424
Bacteriophage miniplasmid P1 parA gene, 5' end
gi|215637|gb|M36424|PP1PAR1 [215637]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M11129
Bacteriophage P1 miniplasmid origin of replication region
gi|215632|gb|M11129|PP1ORIM [215632]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 43 nucleotide neighbors)

M25414
Bacteriophage P1 c1 repressor binding site, operator 88 (Op88)
gi|215631|gb|M25414|PP1OP88A [215631]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

M25413
Bacteriophage P1 c1 repressor binding site, operator 68 (Op68)
gi|215630|gb|M25413|PP1OP68A [215630]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M25412
Bacteriophage P1 c1 repressor binding site, operator 21 (Op21)
gi|215629|gb|M25412|PP1OP21A [215629]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M10510
Bacteriophage P1 recombination site loxR
gi|215628|gb|M10510|PP1LOXR [215628]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M10287
Bacteriophage P1 loxP X loxP recombination site
gi|215627|gb|M10287|PP1LOXPX [215627]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors)

M10494
Bacteriophage P1 recombination site loxP
gi|215626|gb|M10494|PP1LOXP [215626]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 134 nucleotide neighbors)

M10511
Bacteriophage P1 recombination site loxL
gi|215625|gb|M10511|PP1LOXL [215625]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M10512
Bacteriophage P1 recombination site loxB
gi|215624|gb|M10512|PP1LOXB [215624]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M10145
Bacteriophage P1 genome fragment with recombination site loxP
gi|215623|gb|M10145|PP1CREX [215623]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 21 nucleotide neighbors)

M13327
Bacteriophage P1 Cin recombinase activated cross over site, junction IV, clone pSHI326
gi|215622|gb|M13327|PP1CN26IV [215622]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13325
Bacteriophage P1 Cin recombinase activated cross over site, junction II, clone pSHI326
gi|215621|gb|M13325|PP1CN26II [215621]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1401 nucleotide neighbors)

M13323
Bacteriophage P1 Cin recombinase activated cross over site, junction IV, clone pSHI325
gi|215620|gb|M13323|PP1CN25IV [215620]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13321
Bacteriophage P1 Cin recombinase activated cross over site, junction II, clone pSHI325
gi|215619|gb|M13321|PP1CN25II [215619]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1058 nucleotide neighbors)

M13324
Bacteriophage P1 Cin recombinase activated cross over site, junction I, clone pSHI326
gi|215618|gb|M13324|PP1CIR26I [215618]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13319
Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI327
gi|215617|gb|M13319|PP1CIN27R [215617]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13320
Bacteriophage P1 Cin recombinase activated cross over site, junction I, clone pSHI325
gi|215616|gb|M13320|PP1CIN25I [215616]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13318
Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI324
gi|215615|gb|M13318|PP1CIN24L [215615]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1370 nucleotide neighbors)

M13317
Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI323
gi|215614|gb|M13317|PP1CIN23M [215614]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1055 nucleotide neighbors)

M13316
Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI323
gi|215613|gb|M13316|PP1CIN23L [215613]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13315
Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI322
gi|215612|gb|M13315|PP1CIN22R [215612]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13314
Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI322
gi|215611|gb|M13314|PP1CIN22L [215611]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1401 nucleotide neighbors)

M13313
Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI321
gi|215610|gb|M13313|PP1CIN21R [215610]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M13312
Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI321
gi|215609|gb|M13312|PP1CIN21L [215609]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1058 nucleotide neighbors)

M16568
Bacteriophage P1 c4 repressor gene, complete cds
gi|215603|gb|M16568|PP1C4 [215603]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

M13326
Bacteriophage P1 Cin recombinase activated cross over site, junction III, clone pSHI326
gi|215602|gb|M13326|PP1C26III [215602]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1192 nucleotide neighbors)

M13322
Bacteriophage P1 Cin recombinase activated cross over site, junction III, clone pSHI325
gi|215601|gb|M13322|PP1C25III [215601]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1231 nucleotide neighbors)

J05651
Bacteriophage P1 modulator protein (bof) gene, complete cds
gi|215598|gb|J05651|PP1BOFY1 [215598]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

M33224
Bacteriophage P1 regulatory protein (bof) gene, complete cds
gi|215596|gb|M33224|PP1BOFFO [215596]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

M10288
E.coli/bacteriophage P1 loxR recombination site
gi|146647|gb|M10288|ECOLOXR [146647]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

M10289
E.coli/bacteriophage P1 loxL recombination site
gi|146646|gb|M10289|ECOLOXL [146646]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M10290
E.coli loxB site, which can recombine with bacteriophage P1 loxP site
gi|146645|gb|M10290|ECOLOXB [146645]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M10287
Bacteriophage P1 loxP X loxP recombination site
gi|215627|gb|M10287|PP1LOXPX [215627]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors)

M74046
Bacteriophage P1 pacA and pacB genes, complete cds
gi|215634|gb|M74046|PP1PACAB [215634]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

M95666
Bacteriophage P1 gene 10, doc and phd genes, complete cds
gi|463276|gb|M95666|PP1PHDDOC [463276]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 1 nucleotide neighbor)

M25604
Bacteriophage Q-beta mutated autonomously replicating sequence MDV1 RNA fragment
gi|556359|gb|M25604|PQBARSMUT [556359]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors)

V00643
first half of the phage Q-beta gene for coat protein
gi|15088|emb|V00643|LEQBET [15088]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

M25167
Bacteriophage Q-beta RNA fragment recovered from replicase binding complex
gi|556362|gb|M25167|PQBREPLICB [556362]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M24876
Bacteriophage Q-beta replicase RNA, 5' end
gi|556360|gb|M24876|PQBREPLICA [556360]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

M25444
Synthetic bacteriophage Q-beta DNA
gi|209118|gb|M25444|SYNPQBTERM [209118]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors)

M25463
Bacteriophage Q-beta self-replicating microvariant (+) RNA
gi|532489|gb|M25463|PQBMVSRRNA [532489]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M25014
Bateriophage Q-beta RNA replicase gene, 5'end, and maturation protein gene, 3' end
gi|294316|gb|M25014|PQBREPLC [294316]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

M25065
Bacteriophage Q-beta RNA sequence with putative stem loop
gi|294315|gb|M25065|PQBLOOP [294315]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

M10265
Bacteriophage Q-beta RNA molecule with the ability to replicate extracellularly
gi|215726|gb|M10265|PQBRNA [215726]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors)

M24815
Bacteriophage Q-beta specified replicase subunit RNA,
gi|215725|gb|M24815|PQBREPL [215725]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors)

M25461
Bacteriophage Q-beta plus-strand RNA, 5' terminus
gi|215724|gb|M25461|PQBPS5E [215724]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M25462
Bacteriophage Q-beta plus-strand RNA, 3' terminus
gi|215723|gb|M25462|PQBPS3E [215723]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 8 nucleotide neighbors)

M24871
Bacteriophage Q-beta nanovariant WSIII RNA
gi|215722|gb|M24871|PQBNVWSIC [215722]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M24870
Bacteriophage Q-beta nanovariant WSII RNA
gi|215721|gb|M24870|PQBNVWSIB [215721]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M24869
Bacteriophage Q-beta nanovariant WSI RNA
gi|215720|gb|M24869|PQBNVWSIA [215720]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M10495
Coliphage Q-beta MDV-1(+) RNA
gi|215719|gb|M10495|PQBMDV1A [215719]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors)

J02484
bacteriophage qbeta coat protein cistron first half
gi|215717|gb|J02484|PQBCP5 [215717]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

M57754
Bacteriophage Q-beta minus strand RNA, 5' terminus
gi|215716|gb|M57754|PQBBMS5E [215716]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 8 nucleotide neighbors)

M24297
Bacteriophage Q-beta 5'-terminal region of the minus strand
gi|215715|gb|M24297|PQB5END [215715]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors)

M10695
Bacteriophage Q-beta, MDV-1 RNA
gi|215714|gb|M10695|PQB1IR [215714]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 12 nucleotide neighbors)

M24827
Bacteriophage R17 A protein gene, 5' end
gi|216078|gb|M24827|R17RNACIS [216078]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors)

M24829
Bacteriophage R17 coat protein gene, 5' end
gi|216075|gb|M24829|R17CP5 [216075]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors)

J02488
bacteriophage r17 rna synthetase initiation site
gi|216080|gb|J02488|R17RNASYN [216080]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 6 nucleotide neighbors)

J02487
bacteriophage r17 coat protein initiation site
gi|216073|gb|J02487|R17COATP [216073]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

J02486
bacteriophage r17 a protein initiation site
gi|216071|gb|J02486|R17APROT [216071]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M24826
Bacteriophage R17 coat protein RNA fragment
gi|216077|gb|M24826|R17CPRAA [216077]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors)

M24296
Bacteriophage R17 3'-terminal fragment A RNA
gi|216070|gb|M24296|R173TFA [216070]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 9 nucleotide neighbors)

1TFN
structure refinement for a 24-nucleotide rna hairpin, nmr, minimized average
structure ribonucleic acid, hairpin, bacteriophage r17 mol_id: 1; molecule: r17c; chain: null; engineered: yes
gi|1942336|pdb|1TFN| [1942336]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 structure link)

1RPEA
rna (5'-d(gpgpgpapcpupgpapcpgpapupcpapcpgp cpapgpupcpupapu-3') (24-mer rna
hairpin coat protein binding site for bacteriophage r17) (nmr, minimized average structure)
gi|1421020|pdb|1RHT| [1421020]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 structure link)

M14428

Bacteriophage S13 circular DNA, complete genome
gi|216089|gb|M14428|S13CG [216089]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 12 protein links, 26 nucleotide neighbors, or 1 genome link)

J05393

Bacteriophage T1 DNA N-6-adenine-methyltransferase (M.T1) gene, complete cds
gi|166163|gb|J05393|BT1NAMTA [166163]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

L46845

Bacteriophage T2 frd3, frd2 genes, complete cds
gi|951387|gb|L46845|PT2FRD32G [951387]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 17 nucleotide neighbors)

L43611

Bacteriophage T2 fibritin (wac) gene, complete cds
gi|903869|gb|L43611|PT2WAC [903869]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors)

M24812

Bacteriophage T2 secondary structure RNA sequence
gi|215796|gb|M24812|PT2RNA [215796]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors)

M22342

Bacteriphage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
gi|215792|gb|M22342|PT2DAM [215792]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

S57515

orf 61.2 {intergenic region between 41 and 61} [bacteriophage T2, Genomic, 323 nt]
gi|298524|gb|S57515|S57515 [298524]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

X05312

Bacteriophage T2 gene 38 for receptor recognizing protein
gi|15197|emb|X05312|MYT2G38 [15197]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

X04442

Bacteriophage T2 gene 37 for receptor recognizing protein
gi|15195|emb|X04442|MYT2G37 [15195]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

X12460

Bacteriophage T2 gene 32 mRNA for single-stranded DNA binding protein
gi|15192|emb|X12460|MYT2G32 [15192]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 14 nucleotide neighbors)

X57797

Bacteriophage T2 gene for gp12
gi|14875|emb|X56555|BT2GP12 [14875]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 2 nucleotide neighbors)

X01755
Bacteriophage T2 tail fiber gene 36
gi|15189|emb|X01755|MYT2F36 [15189]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

M14784
Bacteriophage T3 strain amNG220B right end, tail fiber protein, lysis protein and DNA packaging proteins, complete cds
gi|215810|gb|M14784|PT3RE [215810]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 10 nucleotide neighbors)

SEG_PT3RNAPOL
Bacteriophage T3 RNA polymerase III gene, 5' end
gi|710559|gb||SEG_PT3RNAPOL [710559]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

M22610
Bacteriophage T3 RNA polymerase III gene, 3' end
gi|340722|gb|M22610|PT3RNAPOL2 [340722]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M22609
Bacteriophage T3 RNA polymerase III gene, 5' end
gi|340721|gb|M22609|PT3RNAPOL1 [340721]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

X05031
Bacteriophage T3 gene region 1-2.5 with primary origin of replication
gi|15719|emb|X05031|POT3ORI [15719]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 5 nucleotide neighbors)

X03964
Bacteriophage T3 early control region pos. 308-810 from genome left end
gi|15718|emb|X03964|POT3EP [15718]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 20 nucleotide neighbors)

X17255
Bacteriophage T3 gene 1 to gene 11
gi|15682|emb|X17255|POT3111G [15682]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE links, 36 protein links, 17 nucleotide neighbors, or 1 genome link)

X15840
Phage T3 gene 10
gi|15625|emb|X15840|PODT3G10 [15625]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

X02981
Bacteriophage T3 gene 1 for RNA polymerase
gi|15561|emb|X02981|PODOT3P [15561]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

J02503
bacteriophage t3 5' end, terminally redundant sequence (trs)
gi|215816|gb|J02503|PT3TRS1 [215816]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

SEG_PT3TRS
bacteriophage t3 5' end, terminally redundant sequence (trs)
gi|215818|gb||SEG_PT3TRS [215818]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

J02504
bacteriophage t3 3' end, terminally redundant sequence (trs)
gi|215817|gb|J02504|PT3TRS2 [215817]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

H YPERLINK http://www.rs.noda.sut.ac.jp/~kunisawa h t t p://www.rs.noda.sut.ac.jp/~kunisawa
Bacteriophage T4 genomic database compiled by Arisaka et al.

X95646
Bacteriophage T5 DNA for region 60.5%-71% of the T5 genome
gi|2791557|emb|AJ001191|BTJ001191 [2791557]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,7 MEDLINE links, 12 protein links, or 6 nucleotide neighbors)

X56847
Bacteriophage T5 genomic region encoding early genes D10-D15
gi|15407|emb|X12930|MYT5D10 [15407]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 4 nucleotide neighbors)

AF039886
Bacteriophage T5 subclone T5.5.3r5.18r, single pass sequence, genomic survey sequence
gi|2811154|gb|AF039886|AF039886 [2811154]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039885
Bacteriophage T5 subclone T5.40f,41f, single pass sequence, genomic survey sequence
gi|2811153|gb|AF039885|AF039885 [2811153]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039884
Bacteriophage T5 subclone T5.26.fr, single pass sequence, genomic survey sequence
gi|2811152|gb|AF039884|AF039884 [2811152]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039883
Bacteriophage T5 subclone 10-T5.5.7F, single pass sequence, genomic survey sequence
gi|2811151|gb|AF039883|AF039883 [2811151]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039882
Bacteriophage T5 subclone 41-T5.5.4BF, single pass sequence, genomic survey sequence
gi|2811150|gb|AF039882|AF039882 [2811150]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039881
Bacteriophage T5 subclone 39-T5.5.4aF, single pass sequence, genomic survey sequence
gi|2811149|gb|AF039881|AF039881 [2811149]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1
nucleotide neighbor)

AF039880

Bacteriophage T5 subclone 19-T5.7.2r, single pass sequence, genomic survey sequence
gi|2811148|gb|AF039880|AF039880 [2811148]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039879

Bacteriophage T5 subclone 18-T5.7.2F, single pass sequence, genomic survey sequence
gi|2811147|gb|AF039879|AF039879 [2811147]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039878

Bacteriophage T5 subclone 11-T5.5.7R, single pass sequence, genomic survey sequence
gi|2811146|gb|AF039878|AF039878 [2811146]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 nucleotide neighbors)

AF039877

Bacteriophage T5 subclone T5.4FR, single pass sequence, genomic survey sequence
gi|2811145|gb|AF039877|AF039877 [2811145]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039876

Bacteriophage T5 subclone 22-T5.16R, single pass sequence, genomic survey sequence
gi|2811144|gb|AF039876|AF039876 [2811144]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039875

Bacteriophage T5 subclone 21-T5.16R, single pass sequence, genomic survey sequence
gi|2811143|gb|AF039875|AF039875 [2811143]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039874

Bacteriophage T5 subclone 21-T5.16F, single pass sequence, genomic survey sequence
gi|2811142|gb|AF039874|AF039874 [2811142]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039873

Bacteriophage T5 subclone 09-T5.6F, single pass sequence, genomic survey sequence
gi|2811141|gb|AF039873|AF039873 [2811141]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039872

Bacteriophage T5 subclone 09-T5.6R, single pass sequence, genomic survey sequence
gi|2811140|gb|AF039872|AF039872 [2811140]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 nucleotide neighbors)

AF039871

Bacteriophage T5 subclone 04-T5.26.R, single pass sequence, genomic survey sequence
gi|2811139|gb|AF039871|AF039871 [2811139]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF039870

Bacteriophage T5 subclone 13-T5.42F, single pass sequence, genomic survey sequence
gi|2811138|gb|AF039870|AF039870 [2811138]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

X69460
Bacteriophage T5 ltf gene for L-shaped tail fibers
gi|15415|emb|X69460|MYT5LTF [15415]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 1 protein link, or 4 nucleotide neighbors)

X03402
Bacteriophage T5 D15 gene for 5' exonuclease
gi|15413|emb|X03402|MYT5EXOG [15413]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

Z11972
Bacteriophage T5 tRNA-Tyr, tRNA-Glu, tRNA-Trp, tRNA-Phe, tRNA-Cys and tRNA-Asn genes, and ORFs 91aa, 90aa, 42aa and 172aa
gi|15795|emb|Z11972|T56TRNAG [15795]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 3 nucleotide neighbors)

X03898
Bacteriophage T5 genes for tRNA-His, -Ser and -Leu
gi|15786|emb|X03898|STT5RN1 [15786]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 MEDLINE links)

X04177
Bacteriophage T5 gene for transfer RNA-Gln
gi|15421|emb|X04177|MYT5TRNQ [15421]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

X03899
Bacteriophage T5 genes for tRNA-Val, -Lys, -fMet, -Pro and -Ile3
gi|15787|emb|X03899|STT5RN2 [15787]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

X03798
Bacteriophage T5 gene for tRNA-Asp (GUC)
gi|15472|emb|X03798|NCT5TRDG [15472]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

Y00364
Bacteriophage T5 tRNA gene cluster (27.8%-22.4%)
gi|15420|emb|Y00364|MYT5TRN [15420]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors)

X03140
Bacteriophage T5 DNA with rho-dependent transcription terminator (Hind III-P fragment)
gi|15417|emb|X03140|MYT5RHO [15417]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

Z35070
Bacteriophage T6 DNA
gi|535228|emb|Z35074|MYEREGBT6 [535228]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

AF060870
Coliphage T6 small subunit distal tail fiber (gene 36) gene, partial cds; and large subunit distal tail fiber (gene 37) and tail fiber adhesin (gene 38) genes, complete cds
gi|3676458|gb|AF052605|AF052605 [3676458]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 protein links, or 2 nucleotide neighbors)

Z35072
Bacteriophage T6 DNA encoding ORF19.1 gene and g19 gene
gi|535232|emb|Z35072|MYTAILT6 [535232]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

X12488
Bacteriophage T6 gene 32 mRNA for single-stranded DNA binding protein
gi|15843|emb|X12488|MYT6G32 [15843]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 14 nucleotide neighbors)

Z78095
Bacteriophage T6 DNA (1506 bp)
gi|1488562|emb|Z78095|BPHZ78095 [1488562]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors)

Z35079
Bacteriophage T6 DNA for Ip5, Ip6
gi|535215|emb|Z35079|MY57BT6 [535215]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

X68725
E.coli bacteriophage T6 gene for beta-glucosyl-HMC-alpha-glucosyl-transferase
gi|296439|emb|X68725|ECT6 [296439]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

X69894
Bacteriophage T6 alt gene for ADP-Ribosyltransferase
gi|15422|emb|X69894|MYT6ADP [15422]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

L46846
Bacteriophage T6 frd3, frd2 genes, complete cds
gi|951390|gb|L46846|PT6FRD32G [951390]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links)

M27738
Bacteriophage T6 translational repressor protein (regA), complete cds
gi|215993|gb|M27738|PT6REGA [215993]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 5 nucleotide neighbors)

M38465
Bacteriophage T6 DNA ligase gene, complete cds
gi|215991|gb|M38465|PT6LIG55 [215991]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

V01146
Genome of bacteriophage T7
gi|431187|emb|V01146|T7CG [431187]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,13 MEDLINE links, 60 protein links, 105 nucleotide neighbors, or 1 genome link)

X60322
Bacteriophage alpha3 genes A, B, K, C, D, E, J, F, G, H
gi|14775|emb|X60322|BACALPHA [14775]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, 22 nucleotide neighbors, or 1 genome link)

X13332
Bacteriophage alpha3 DNA for origin of replication
gi|15093|emb|X13332|MIA3ORPL [15093]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

X12611
Bacteriophage alpha3 gene for protein A part., finger domain
gi|15092|emb|X12611|MIA3AFIN [15092]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 6 nucleotide neighbors)

X15721
Bacteriophage alpha3 deletion mutation DNA for the origin region (-ori) of replication
gi|14774|emb|X15721|BA3DMOR9 [14774]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors)

X15720
Bacteriophage alpha3 deletion mutant DNA for the origin region (-ori) of replication
gi|14773|emb|X15720|BA3DMOR8 [14773]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

X15719
Bacteriophage alpha3 insertion mutant DNA for the origin region (-ori) of replication
gi|14772|emb|X15719|BA3DMOR7 [14772]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors)

X15718
Bacteriophage alpha3 deletion mutation DNA for origin region (-ori) of replication
gi|14771|emb|X15718|BA3DMOR6 [14771]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors)

X15717
Bacteriophage alpha3 deletion mutatnt DNA for origin region (-ori) of replication
gi|14770|emb|X15717|BA3DMOR5 [14770]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 9 nucleotide neighbors)

X15716
Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication
gi|14769|emb|X15716|BA3DMOR4 [14769]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors)

X15715
Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of of replication
gi|14768|emb|X15715|BA3DMOR3 [14768]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors)

X15714
Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication
gi|14767|emb|X15714|BA3DMOR2 [14767]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors)

X15713
Bacteriophage alpha3 deletion mutant DNA for the origin region (-ori) of replication
gi|14766|emb|X15713|BA3DMOR1 [14766]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors)

X62059
Bacteriophage alpha3 origin of cDNA synthesis (oriGA)
gi|14763|emb|X62059|AL3ORIGA [14763]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors)

X62058
Bacteriophage alpha3 origin of cDNA synthesis (oriAA)
gi|14762|emb|X62058|AL3ORIAA [14762]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors)

J02444
Bacteriophage alpha3 origin of DNA replication
gi|166103|gb|J02444|AL3ORI [166103]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors)

M25640
Bacteriophage alpha-3 H protein gene, complete cds
gi|166101|gb|M25640|AL3HP [166101]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 13 nucleotide neighbors)

M10631
Bacteriophage alpha-3 cleavage site for phage phi-X174 gene A protein
gi|166099|gb|M10631|AL3CSA [166099]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

X00774
Bacteriophage alpha-3 gene J sequence
gi|15431|emb|X00774|NCBA3J [15431]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors)

M25640
Bacteriophage alpha-3 H protein gene, complete cds
gi|166101|gb|M25640|AL3HP [166101]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 13 nucleotide neighbors)

M10631
Bacteriophage alpha-3 cleavage site for phage phi-X174 gene A protein
gi|166099|gb|M10631|AL3CSA [166099]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

J02459
Bacteriophage lambda, complete genome
gi|215104|gb|J02459|LAMCG [215104]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE links, 67 protein links, 190 nucleotide neighbors, or 1 genome link)

J02482
Bacteriophage phi-X174, complete genome
gi|216019|gb|J02482|PX1CG [216019]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,23 MEDLINE links, 11 protein links, 26 nucleotide neighbors, or 1 genome link)

J02454
Bacteriophage G4, complete genome
gi|215415|gb|J02454|PG4CG [215415]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 11 protein links, 20 nucleotide neighbors, or 1 genome link)

X60323
Bacteriophage phiK complete genome
gi|1478118|emb|X60323|BPHIKCG [1478118]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, 18 nucleotide neighbors, or 1 genome link)

L42820
Bacteriophage BF23 tail protein (hrs) gene, complete cds
gi|1048680|gb|L42820|BBFHRS [1048680]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

X54455
Bacteriophage BF23 gene 17 and gene 18
gi|14797|emb|X54455|BF231718G [14797]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors)

M37097
Bacteriophage BF23 DNA, right end of terminal repetition
gi|166115|gb|M37097|BBFRIGH [166115]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M37096
Bacteriophage BF23 DNA, left end of terminal repetition
gi|166114|gb|M37096|BBFLEFT [166114]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M37095
Bacteriophage BF23 A2-A3 gene, complete cds, and A1 gene, 5' end
gi|166110|gb|M37095|BBFA2A3 [166110]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 1 nucleotide neighbor)

AF056281
Bacteriophage BF23 clone bf23.mac5/6.1, genomic survey sequence
gi|3090930|gb|AF056281|AF056281 [3090930]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056280
Bacteriophage BF23 clone bf23.mac3, genomic survey sequence
gi|3090929|gb|AF056280|AF056280 [3090929]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056279
Bacteriophage BF23 clone bf23.mac18/21.34, genomic survey sequence
gi|3090928|gb|AF056279|AF056279 [3090928]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056278
Bacteriophage BF23 clone bf23.mac16/19.33, genomic survey sequence
gi|3090927|gb|AF056278|AF056278 [3090927]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056277
Bacteriophage BF23 clone bf23.mac16/19-33, genomic survey sequence
gi|3090926|gb|AF056277|AF056277 [3090926]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056276
Bacteriophage BF23 clone bf23.mac12/9-9, genomic survey sequence
gi|3090925|gb|AF056276|AF056276 [3090925]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056275
Bacteriophage BF23 clone bf23.mac11/14-24, genomic survey sequence
gi|3090924|gb|AF056275|AF056275 [3090924]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056274
Bacteriophage BF23 clone bf23.57r64r, genomic survey sequence
gi|3090923|gb|AF056274|AF056274 [3090923]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 3 nucleotide neighbors)

AF056273
Bacteriophage BF23 clone bf23.54fr, genomic survey sequence
gi|3090922|gb|AF056273|AF056273 [3090922]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056272
Bacteriophage BF23 clone bf23.47fr.mac10/7, genomic survey sequence
gi|3090921|gb|AF056272|AF056272 [3090921]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056271
Bacteriophage BF23 clone bf23.23.66r, genomic survey sequence
gi|3090920|gb|AF056271|AF056271 [3090920]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056270
Bacteriophage BF23 clone bf23.23.64f, genomic survey sequence
gi|3090919|gb|AF056270|AF056270 [3090919]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056269
Bacteriophage BF23 clone bf23.23.60r, genomic survey sequence
gi|3090918|gb|AF056269|AF056269 [3090918]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056268
Bacteriophage BF23 clone bf23.23.60f, genomic survey sequence
gi|3090917|gb|AF056268|AF056268 [3090917]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor)

AF056267
Bacteriophage BF23 clone bf23.23.59r, genomic survey sequence
gi|3090916|gb|AF056267|AF056267 [3090916]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056266
Bacteriophage BF23 clone bf23.23.59f, genomic survey sequence
gi|3090915|gb|AF056266|AF056266 [3090915]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056265
Bacteriophage BF23 clone bf23.23.56r, genomic survey sequence
gi|3090914|gb|AF056265|AF056265 [3090914]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056264
Bacteriophage BF23 clone bf23.23.56f, genomic survey sequence
gi|3090913|gb|AF056264|AF056264 [3090913]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056263
Bacteriophage BF23 clone bf23.23.68f55r, genomic survey sequence
gi|3090912|gb|AF056263|AF056263 [3090912]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056262
Bacteriophage BF23 clone bf23.23.43fr.66f, genomic survey sequence
gi|3090911|gb|AF056262|AF056262 [3090911]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056261
Bacteriophage BF23 clone bf23.23.2fr, genomic survey sequence
gi|3090910|gb|AF056261|AF056261 [3090910]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056260
Bacteriophage BF23 clone bf23.23.55.f, genomic survey sequence
gi|3090909|gb|AF056260|AF056260 [3090909]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056259
Bacteriophage BF23 clone bf23.23.53.r, genomic survey sequence
gi|3090908|gb|AF056259|AF056259 [3090908]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056258
Bacteriophage BF23 clone bf23.23.53.f, genomic survey sequence
gi|3090907|gb|AF056258|AF056258 [3090907]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056257
Bacteriophage BF23 clone bf23.23.52.r, genomic survey sequence
gi|3090906|gb|AF056257|AF056257 [3090906]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056256
Bacteriophage BF23 clone bf23.23.52.f, genomic survey sequence
gi|3090905|gb|AF056256|AF056256 [3090905]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056255
Bacteriophage BF23 clone bf23.23.49.r, genomic survey sequence
gi|3090904|gb|AF056255|AF056255 [3090904]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056254
Bacteriophage BF23 clone bf23.23.49.f, genomic survey sequence
gi|3090903|gb|AF056254|AF056254 [3090903]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056253
Bacteriophage BF23 clone bf23.23.48.r, genomic survey sequence
gi|3090902|gb|AF056253|AF056253 [3090902]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056252
Bacteriophage BF23 clone bf23.23.48.f, genomic survey sequence
gi|3090901|gb|AF056252|AF056252 [3090901]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056251
Bacteriophage BF23 clone bf23.23.44.r, genomic survey sequence
gi|3090900|gb|AF056251|AF056251 [3090900]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056250
Bacteriophage BF23 clone bf23.23.41.f, genomic survey sequence
gi|3090899|gb|AF056250|AF056250 [3090899]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056249
Bacteriophage BF23 clone bf23.23.22.a.r, genomic survey sequence
gi|3090898|gb|AF056249|AF056249 [3090898]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056248
Bacteriophage BF23 clone bf23.23.22.a.f, genomic survey sequence
gi|3090897|gb|AF056248|AF056248 [3090897]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056247
Bacteriophage BF23 clone bf23.23.68.r, genomic survey sequence
gi|3090896|gb|AF056247|AF056247 [3090896]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

Z50114
Bacteriophage BF23 DNA for putative tail protein gene
gi|2464952|emb|Z50114|BF23LATE [2464952]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link)

D12824
Bacteriophage BF23 genes for minor tail protein gp24 and major tail protein gp25, complete cds
gi|520578|dbj|D12824|BBF2TAIL [520578]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors)

Z34953
Bacteriophage K3 ip9, ip7 and ip8 genes
gi|535261|emb|Z34953|MYK3IP978 [535261]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

Z35075
Bacteriophage K3 DNA for Ip3 and Ip4
gi|535229|emb|Z35075|MYEORF64K [535229]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

X05560
Bacteriophage K3 gene 38 for receptor recognizing protein
gi|15112|emb|X05560|MYK3G38 [15112]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

X04747
Bacteriophage K3 gene 37 for receptor recognizing protein
gi|15110|emb|X04747|MYK3G37 [15110]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

X01754
Bacteriophage K3 tail fiber gene 36
gi|15108|emb|X01754|MYK3F36 [15108]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

M16812
Bacteriophage K3 't' lysis gene, complete cds
gi|215503|gb|M16812|PK3LYST [215503]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

L46833
Bacteriophage K3 frd3, frd2 genes, complete cds
gi|951377|gb|L46833|PK3FRD32G [951377]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors)

L43613
Bacteriophage K3 fibritin (wac) gene, complete cds
gi|903861|gb|L43613|PK3WAC [903861]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors)

X01753

Bacteriophage Ox2 tail fiber gene 36
gi|15122|emb|X01753|MYOX2F36 [15122]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

L43612

Bacteriophage Ox2 fibritin (wac) gene, complete cds
gi|903848|gb|L43612|OX2WAC [903848]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors)

Z46880

Bacteriophage OX2 stp gene
gi|599663|emb|Z46880|BPOX2STP [599663]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

X05675

Bacteriophage Ox2 gene 38 for receptor-recognizing protein and flanking regions
gi|15124|emb|X05675|MYOX2G38 [15124]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

M33533

Bacteriophage RB18 translational repressor protein (regA) and Orf43.1, complete cds
gi|216083|gb|M33533|RB18REGA [216083]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

AF033329

Bacteriophage RB18 single-stranded binding protein (gene 32) gene, partial cds, and 5' region
gi|2645788|gb|AF033329|AF033329 [2645788]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 11 nucleotide neighbors)

M86231

Bacteriophage RB69 gene 62, 3'end; RegA (regA) gene, complete cds
gi|215354|gb|M86231|P6962REGA [215354]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

AF033332

Bacteriophage RB69 single-stranded binding protein (gene 32) gene, partial cds, and 5' region
gi|2645794|gb|AF033332|AF033332 [2645794]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 12 nucleotide neighbors)

U34036

Bacteriophage RB69 DNA polymerase (43) gene, complete cds
gi|1237125|gb|U34036|BRU34036 [1237125]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

V01145

Bacteriophage H1 genome fragment Each Thymine given in this sequence represents a HMU-residue (HMU = 5-hydroxymethyluracil)
gi|15557|emb|V01145|PODOH1 [15557]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

X05676

Bacteriophage M1 gene 38 for receptor recognizing protein and flanking regions
gi|15114|emb|X05676|MYM1G38 [15114]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

AF034575
Bacteriophage M1 putative integrase (int) gene, complete cds, and attP region, complete sequence
gi|2662472|gb|AF034575|AF034575 [2662472]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

AF033321
Bacteriophage M1 single-stranded binding protein (gene 32) gene, partial cds, and 5' region
gi|2645772|gb|AF033321|AF033321 [2645772]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 17 nucleotide neighbors)

X55190
Bacteriophage TuIa 37 and 38 genes for receptor-recognizing proteins 37 and 38 (respectively), partial cds
gi|14860|emb|X55190|BPTUIA [14860]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

AF033334
Bacteriophage TuIb single-stranded binding protein (gene 32) gene, partial cds, and 5' region
gi|2645798|gb|AF033334|AF033334 [2645798]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 5 nucleotide neighbors)

X55191
Bacteriophage TuIb 37 gene for receptor-recognizing protein 37 (partial cds), 38 gene for receptor-recognizing protein 38, and t gene (partial cds)
gi|14863|emb|X55191|BPTUIB [14863]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors)

X13065
Bacteriophage phi80 early region
gi|14800|emb|X13065|BP80ER [14800]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 8 protein links, or 6 nucleotide neighbors)

D00360
Bacteriophage phi80 cor gene
gi|217782|dbj|D00360|P8080COR [217782]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link)

X01639
Bacteriophage phi 80 DNA-fragment with replication origin
gi|15828|emb|X01639|XXPHI80 [15828]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 25 nucleotide neighbors)

X04051
Lambdoid bacteriophage phi 80 int-xis region (integrase-excisionase region)
gi|15770|emb|X04051|STPHI80X [15770]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

X06751
Phage Phi80 DNA for major coat protein
gi|15768|emb|X06751|STPHI80C [15768]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 11 nucleotide neighbors)

X75949
Bacteriophage phi80 DNA for ORF x171.8 and ORF x171.28'
gi|458811|emb|X75949|ECORF171B [458811]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 28 nucleotide neighbors)

L40418
Bacteriophage phi-80 gene, complete cds
gi|1019107|gb|L40418|P80A [1019107]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

M24831
Bacteriophage phi-80 Tyr-tRNA gene, 3' end
gi|215363|gb|M24831|P80TGY [215363]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 43 nucleotide neighbors)

M10670
Bacteriophage phi-80 replication origin
gi|215361|gb|M10670|P80ORI [215361]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

M24825
Bacteriophage phi-80 RNA fragment
gi|215360|gb|M24825|P80M3A [215360]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M11919
Bacteriophage phi-80 cI immunity region encoding the N gene
gi|215358|gb|M11919|P80CI [215358]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

M10891
Bacteriophage phi-80 attP site DNA
gi|215357|gb|M10891|P80ATTP [215357]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor)

M19473
Bacteriophage 933J (from E.coli) proviral Shiga-like toxin type 1 subunits A and B genes, complete cds
gi|215072|gb|M19473|J93SLTI [215072]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 2 protein links, or 20 nucleotide neighbors)

Y10775
Bacteriophage 933W ileX, stx2A and stx2B genes
gi|1938206|emb|Y10775|BP933ILEX [1938206]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 36 nucleotide neighbors)

X83722
Bacteriophage 933W slt-IIB gene
gi|1490229|emb|X83722|B933WSLT [1490229]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 20 nucleotide neighbors)

X07865
Bacteriophage 933W slt-II gene for Shiga-like toxin typeII subunit A and B
gi|14892|emb|X07865|BWSLTII [14892]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 29 nucleotide neighbors)

M16625
Bacteriophage H19B (from E.coli) sltIA and sltIB genes encoding Shiga-like toxin I subunits A and B, complete cds
gi|215043|gb|M16625|H19BSLT [215043]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 24 nucleotide neighbors)

M17358
Bacteriophage H19B shiga-like toxin-1 (SLT-1) A and B subunit DNA, complete cds
gi|215046|gb|M17358|H19BSLTA [215046]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 20 nucleotide neighbors)

U29728
Bacteriophage N4 single-stranded DNA-binding protein (N4SSB) gene, complete cds
gi|939708|gb|U29728|BNU29728 [939708]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 1 protein link)

J02580
Bacteriophage PA-2 (E.coli porcine strain isolate) Rz gene, 5'end; ORF2, outer membrane porin protein (lc) and ORF1 genes. complete cds
gi|215366|gb|J02580|PA2LC [215366]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 4 nucleotide neighbors)

U32222
Bacteriophage 186, complete sequence
gi|3337249|gb|U32222|B1U32222 [3337249]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 46 protein links, or 5 nucleotide neighbors)

X51522
Bacteriophage P4 complete DNA genome
gi|450916|emb|X51522|MYP4CG [450916]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 13 protein links, 6 nucleotide neighbors. or 1 genome link)

X92588
Bacteriophage 82 orf33, orf151, orf56, orf96, rus, orf45, and Q genes
gi|1051111|emb|X92588|BAC82HOLL [1051111]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,7 protein links, or 1 nucleotide neighbor)

J02803
Bacteriophage 82 antitermination protein (Q) gene, complete cds
gi|215364|gb|J02803|P82Q [215364]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, or 1 protein link)

U02466
Bacteriophage HK022 (cro), (cII) and (O) genes, complete cds, (P) gene, partial cds
gi|407285|gb|U02466|BHU02466 [407285]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 1 nucleotide neighbor)

M26291
Bacteriophage D108 regulatory DNA-binding protein (ner) gene, complete cds
gi|166194|gb|M26291|D18NER [166194]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

M11272
Bacteriophage D108 left-end DNA
gi|166193|gb|M11272|D18LEDNA [166193]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors)

M18902
Bacteriophage D108 kil gene encoding a replication protein, 3' end; and containing three ORFs, complete cds
gi|166191|gb|M18902|D18KIL [166191]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

M10191

Bacteriophage D108, left end with Mu A protein binding sites L1 and L2
gi|166190|gb|M10191|D18BSL [166190]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors)

J02447

bacteriophage d108 gene a 5' end
gi|166189|gb|J02447|D18AAA [166189]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

V00865

Bacteriophage D108 fragment from genes A and ner (C-terminus of ner and N-terminus of A)
gi|15437|emb|V00865|NCD108 [15437]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

X01914

Bacteriophage IKe gene for DNA binding protein
gi|14957|emb|X01914|INIKEDBP [14957]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

AF064539

Bacteriophage N15, complete genome
gi|3192683|gb|AF064539|AF064539 [3192683]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 60 protein links, 26 nucleotide neighbors, or 1 genome link)

U02303

Bacteriophage If1, complete genome
gi|3676280|gb|U02303|B2U02303 [3676280]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, or 1 genome link)

AF007792

Bacteriophage Mu late morphogenetic region
gi|3551775|gb|AF007792|AF007792 [3551775]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor)

U24159

Bacteriophage HP1 strain HP1c1, complete genome
gi|1046235|gb|U24159|BHU24159 [1046235]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 41 protein links, 8 nucleotide neighbors, or 1 genome link)

Z71579

Bacteriophage S2 type A 5.6 kb DNA fragment
gi|1679806|emb|Z71579|BPHS1ADNA [1679806]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 9 protein links, or 9 nucleotide neighbors)

X53238

Klebsiella sp. bacteriophage K11 gene 1 for RNA polymerase
gi|14984|emb|X53238|KSK11RPO [14984]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

X85010
Bacteriophage A511 ply511 gene
gi|853748|emb|X85010|BPA511PLY [853748]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

U29728
Bacteriophage N4 single-stranded DNA-binding protein (N4SSB) gene, complete cds
gi|939708|gb|U29728|BNU29728 [939708]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 1 protein link)

J02445
bacteriophage bo1 3'-terminal region rna
gi|166152|gb|J02445|BO1TR3 [166152]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors)

L06183
Bacteriophage L5 (from Leuconostoc oenos) genome
gi|289353|gb|L06183|BL5GENM [289353]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 genome link)

AF074945
Mycoplasma arthritidis bacteriophage MAV1, complete genome
gi|3511243|gb|AF074945|AF074945 [3511243]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,15 protein links, 3 nucleotide neighbors, or 1 genome link)

L13696
Bacteriophage L2 (from Mycoplasma), complete genome
gi|289338|gb|L13696|BL2CG [289338]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 14 protein links, or 1 genome link)

X80191
Bacteriophage PP7 mRNA for maturation, coat, lysis and replicase proteins
gi|517237|emb|X80191|BPP7PR [517237]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 genome link)

M19377
Bacteriophage Pf3 from Pseudomonas aeruginosa (New York strain), complete genome
gi|215380|gb|M19377|PF3COMNY [215380]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 5 nucleotide neighbors)

M11912
Bacteriophage Pf3 from Pseudomonas aeruginosa (Nijmegen strain), complete genome
gi|215371|gb|M11912|PF3COMN [215371]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, 5 nucleotide neighbors, or 1 genome link)

V00605
Bacteriophage Pf1 gene encoding DNA binding protein
gi|14970|emb|V00605|INOPF1 [14970]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 proteine link, or 1 nucleotide neighbor)

L05626
Bacteriophage PR4 capsid protein (P6) gene, complete cds
gi|215735|gb|L05626|PR4P6MAJA [215735]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

D13409

Bacteriophage phiCTX (isolated from Pseudomonas aeruginosa) cosR, attP, int genes
gi|217776|dbj|D13409|BPHCOSR [217776]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors)

D13408

Bacteriophage phiCTX (isolated from Pseudomonas aeruginosa) cosL, ctx genes
gi|217775|dbj|D13408|BPHCOSLCTX [217775]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 3 nucleotide neighbors)

M24832

Bacteriophage f2 coat protein gene, partial cds
gi|166228|gb|M24832|F2CRNACA [166228]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

S72011

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes,partial cds
gi|2618967|gb|AF017629|AF017629 [2618967]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors)

AF017628

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618964|gb|AF017628|AF017628 [2618964]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors)

AF017627

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618961|gb|AF017627|AF017627 [2618961]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors)

AF017626

Bacteriophage 21 isocitrate dehydrogenase (icd) gene, partial cds; and integrase (int) gene, partial cds
gi|2618958|gb|AF017626|AF017626 [2618958]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 49 nucleotide neighbors)

AF017625

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618955|gb|AF017625|AF017625 [2618955]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors)

AF017624

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int)genes, partial cds
gi|2618952|gb|AF017624|AF017624 [2618952]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors)

AF017623

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618949|gb|AF017623|AF017623 [2618949]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017622

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618946|gb|AF017622|AF017622 [2618946]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017621
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618943|gb|AF017621|AF017621 [2618943]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

D26449
Bacteriophage PS17 FI gene for tail sheath protein (gpFI) and FII gene for tail tube protein (gpFII), complete cds
gi|452162|dbj|D26449|BPSFIFII [452162]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links)

X87627
Bacteriophage D3112 A and B genes
gi|974768|emb|X87627|BPD3112AB [974768]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 1 nucleotide neighbor)

U32623
Bacteriophage D3 transcriptional activator CII (cII) gene, complete cds
gi|984852|gb|U32623|BDU32623 [984852]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1 nucleotide neighbor)

L34781
Bacteriophage phi 11 holin homologue (ORF3) gene, complete cds and peptidoglycan hydrolase (lytA) gene, partial cds
gi|511838|gb|L34781|BPHHOLIN [511838]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 2 nucleotide neighbors)

L14810
Bacteriophage P22 (gp10) gene, complete cds, and (gp26) gene, complete cds
gi|294053|gb|L14810|P22GP1026X [294053]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

X87420
Bacteriophage ES18 genes 24, c2, cro, c1, 18, and oL and oR operators
gi|1143407|emb|X87420|BPES18GEN [1143407]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 9 nucleotide neighbors)

L42820
Bacteriophage BF23 tail protein (hrs) gene, complete cds
gi|1048680|gb|L42820|BBFHRS [1048680]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 1 protein link, or 1 nucleotide neighbor)

X14980
Bacteriophage PRD1 XV gene for protein P15 (lytic enzyme)
gi|15802|emb|X14980|TEPRD1XV [15802]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 1 protein link, or 4 nucleotide neighbors)

X06321
Bacteriophage PRD1 gene 8 for DNA terminal protein
gi|15800|emb|X06321|TEPRD18 [15800]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 10 nucleotide neighbors)

X14336
Filamentous Bacteriophage I2-2 genome
gi|14920|emb|X14336|INBI22 [14920]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, 1 nucleotide neighbor, or 1 genome link)

L05001

Bacteriophage X glucosyl transferase gene, complete cds
gi|216044|gb|L05001|PXFCLUSYLT [216044]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

M29479

Bacteriophage p4 sid and psu genes partial cds, and delta gene, complete cds gi|215701|
gb|M29479|PP4SDP [215701]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 protein links, or 4 nucleotide neighbors)

SEG_PP4PSUSID

Bacteriophage P4 capsid size determination protein (sid) gene, 5' end
gi|215698|gb||SEG_PP4PSUSID [215698]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

M29650

Bacteriophage P4 polarity suppression protein (psu) gene, complete cds
gi|215697|gb|M29650|PP4PSUSID2 [215697]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M29651

Bacteriophage P4 capsid size determination protein (sid) gene, 5' end
gi|215696|gb|M29651|PP4PSUSID1 [215696]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M27748

Bacteriophage P4 gop, beta, and cII genes, complete cds and int gene, 3' end
gi|215691|gb|M27748|PP4GOPBC [215691]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 nucleotide neighbor)

K02750

Bacteriophage IKe, complete genome
gi|215061|gb|K02750|IKECG [215061]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 10 protein links, 4 nucleotide neighbors, or 1 genome link)

L40418

Bacteriophage phi-80 gene, complete cds
gi|1019107|gb|L40418|P80A [1019107]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

AF032122

Bacteriophage SfII integrase (int) gene, partial cds; and bactoprenol glucosyl transferase (bgt), and glucosyl tranferase II (gtrII) genes,complete cds
gi|2465412|gb|AF021347|AF021347 [2465412]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 4 protein links, or 2 nucleotide neighbors)

M35825

Bacteriophage SF6 fragment D lysozyme gene, complete cds
gi|216105|gb|M35825|SF6LYZ [216105]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link)

Z35479

Bacteriophage C16 ip1 gene
gi|534936|emb|Z35479|BC16IP1 [534936]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors)

X12638
Bacteriophage 21 DNA for gene 2
gi|296141|emb|X12638|B21GENE2 [296141]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

X02501
Bacteriophage 21 DNA for left end sequence with genes 1 and 2
gi|15825|emb|X02501|XXPHA21 [15825]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors)

M65239
Bacteriophage 21 lysis genes S, R, and Rz, complete cds
gi|215466|gb|M65239|PH2LYSGEN [215466]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

M58702
Bacteriophage 21 late gene regulatory region
gi|215465|gb|M58702|PH2LATEGE [215465]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M81255
Bacteriophage 21 head gene operon
gi|215454|gb|M81255|PH2HEADTL [215454]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 10 protein links, or 4 nucleotide neighbors)

M23775
Bacteriophage 21 glycoprotein 1 gene, complete cds, and glycoprotein gene, 5' end
gi|215451|gb|M23775|PH2GPA [215451]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors)

M61865
Bacteriophage 21 excisionase (xis), integrase (int) and isocitrate dehydrogenase (icd), complete cds
gi|215448|gb|M61865|PH22XISAA [215448]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 9 nucleotide neighbors)

S72011
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618967|gb|AF017629|AF017629 [2618967]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017628
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618964|gb|AF017628|AF017628 [2618964]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017627
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618961|gb|AF017627|AF017627 [2618961]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017626
Bacteriophage 21 isocitrate dehydrogenase (icd) gene, partial cds; and integrase (int) gene, partial cds
gi|2618958|gb|AF017626|AF017626 [2618958]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 49 nucleotide neighbors)

AF017625
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618955|gb|AF017625|AF017625 [2618955]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors

AF017624
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618952|gb|AF017624|AF017624 [2618952]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017623
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618949|gb|AF017623|AF017623 [2618949]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017622
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618946|gb|AF017622|AF017622 [2618946]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

AF017621
Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds
gi|2618943|gb|AF017621|AF017621 [2618943]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors)

M57455
Bacteriophage 42D (clone pDB17) (from Staphylococcus aureus) staphylokinase gene, complete cds
gi|215344|gb|M57455|P42STK [215344]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors)

Y12633
Bacteriophage 85 DNA, promoter sequence of unknown gene
gi|2058285|emb|Y12633|B85PROM [2058285]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

X98146
Bacteriophage P1 DNA sequence around the Op88 operator
gi|1359513|emb|X98146|BP1OP88OP [1359513]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor)

Y07739
Staphylococcus phage Twort holTW, plyTW genes
gi|2764979|emb|Y07739|BPTWGHOLG [2764979]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links)

L07580
Bacteriophage phi-11 rinA and rin B genes, required for the activation of Staphylococcal phage phi-11 int expression
gi|166160|gb|L07580|BPHRINAB [166160]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

M34832
Bacteriophage phi-11 integrase (int) and excisionase (xis) genes, complete cds
gi|166157|gb|M34832|BPHINTXIS [166157]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

M20394
Bacteriophage phi-11 S.aureus attachment site (attP)
gi|166156|gb|M20394|BPHATTP [166156]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors)

X23128
Bacteriophage phi-13 integrase gene
gi|758228|emb|X82312|PHI13INT [758228]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 3 nucleotide neighbors)

X61719
S.aureus phi-13 lysogen right chromosome/bacteriophage DNA junction
gi|46625|emb|X61719|SAP13RJNC [46625]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

X61718
S.aureus phi-13 lysogen left chromosomal/bacteriophage DNA junction
gi|46624|emb|X61718|SAP13LJNC [46624]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

X61717
Bacteriophage phi-13 core sequence for attachment
gi|14799|emb|X61717|BP13ATTP [14799]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 3 nucleotide neighbors)

U01875
Bacteriophage phi-13 putative regulatatory region and integrase (int) gene, partial cds
gi|437118|gb|U01875|U01875 [437118]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, or 4 nucleotide neighbors)

X67739
S.aureus Bacteriophage phi-42 attP gene
gi|14809|emb|X67739|BPATTPA [14809]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

U01872
Bacteriophage phi-42 integrase (int) gene, complete cds
gi|437115|gb|U01872|U01872 [437115]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 3 nucleotide neighbors)

X94423
Staphylococcus aureus bacteriophage phi-42 DNA with ORFs (restriction modification system)
gi|1771597|emb|X94423|SARMS [1771597]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 1 nucleotide neighbor)

M27965
Bacteriophage L54a (from S.aureus) int and xis genes, complete cds
gi|215096|gb|M27965|L54INTXIS [215096]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, MEDLINE 1 link, 2 protein links, or 3 nucleotide neighbors)

U72397
Bacteriophage 80 alpha holin and amidase genes, complete cds
gi|1763241|gb|U72397|B8U72397 [1763241]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors)

AB009866

Bacteriophage phi PVL proviral DNA, complete sequence
gi|3341907|dbj|AB009866|AB009866 [3341907]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,63 protein links, or 1 nucleotide neighbor)

Z47794

Bacteriophage Cp-1 DNA, complete genome
gi|2288892|emb|Z47794|BPCP1XX [2288892]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 28 protein links, 1 nucleotide neighbor, or 1 genome link)

SEG_CP7RSIT

Bacteriophage Cp-7 (S.pneumoniae) 5' inverted terminal repeat
gi|166186|gb||SEG_CP7RSIT [166186]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M11635

Bacteriophage Cp-7 (S.pneumoniae) DNA, 3' inverted terminal repeat
gi|166185|gb|M11635|CP7RSIT2 [166185]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M11636

Bacteriophage Cp-7 (S.pneumoniae) 5' inverted terminal repeat
gi|166184|gb|M11636|CP7RSIT1 [166184]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

SEG_CP5RSIT

Bacteriophage Cp-5 (S.pneumoniae), 5' inverted terminal repeat
gi|166181|gb||SEG_CP5RSIT [166181]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

M11633

Bacteriophage Cp-5 (S.pneumoniae) 3' inverted terminal repeat
gi|166180|gb|M11633|CP5RSIT2 [166180]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M11634

Bacteriophage Cp-5 (S.pneumoniae), 5' inverted terminal repeat
gi|166179|gb|M11634|CP5RSIT1 [166179]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M34780

Bacteriophage Cp-9 muramidase (cpl9) gene
gi|166187|gb|M34780|CP9CPL [166187]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

M34652

Bacteriophage HB-3 amidase (hbl) gene, complete cds
gi|215055|gb|M34652|HB3HBLA [215055]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

U64984

Streptococcus pyogenes phage T12 repressor, excisionase (xis), integrase(int) and erythrogenic toxin A precursor (speA) genes, complete cds gi|1877426|gb|U40453|SPU40453 [1877426]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 22 nucleotide neighbors)

X12375

Phage CP-T1 (Vibrio cholerae) DNA for packaging signal (pac site)
gi|15435|emb|X12375|NCCPPAC [15435]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

AF087814

Vibrio cholerae filamentous bacteriophage fs-2 DNA, complete genome sequence
gi|3702207|dbj|AB002632|AB002632 [3702207]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 1 genome link)

D83518

Bacteriophage KVP40 gene for major capsid protein precursor, complete cds
gi|3046858|dbj|D83518|D83518 [3046858]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

AF033322

Bacteriophage PST single-stranded binding protein (gene 32) gene, partial cds, and 5' region
gi|2645774|gb|AF033322|AF033322 [2645774]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 17 nucleotide neighbors)

X94331

Bacteriophage L cro, 24, c2, and c1 genes
gi|1469213|emb|X94331|BLCRO24C [1469213]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 protein links)

U82619

Shigella flexneri bacteriophage V glucosyl transferase (gtr), integrase (int) and excisionase (xis) genes, complete cds
gi|2465470|gb|U82619|SFU82619 [2465470]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 8 protein links, or 1 nucleotide neighbor)

Table 12

NCBI *Entrez* Nucleotide QUERY

Key words: bacteriophage and lysis

56 citations found (all selected)

AJ011581

Bacteriophage PS119 lysis genes 13, 19, 15, and packaging gene 3, complete cds
gi|3676084|emb|AJ011581|BPS011581 [3676084]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 1 nucleotide neighbor)

AJ011580

Bacteriophage PS34 lysis genes 13, 19, 15, antiterminator gene 23, and packaging gene 3, complete cds
gi|3676078|emb|AJ011580|BPS011580 [3676078]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 2 nucleotide neighbors)

AJ011579

Bacteriophage PS3 lysis genes 13, 19, 15, and packaging gene 3
gi|3676073|emb|AJ011579|BPS011579 [3676073]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 1 nucleotide neighbor)

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds
gi|2668751|gb|AF034975| [2668751]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors)

U37314

Bacateriophage lambda Rz1 protein precursor (Rz1) gene, complete cds
gi|1017780|gb|U37314|BLU37314 [1017780]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 1 protein link, or 9 nucleotide neighbors)

U00005

E. coli hflA locus encoding the hflX, hflK and hflC genes, hfq gene, complete cds; miaA gene, partial cds
gi|436153|gb|U00005|ECOHFLA [436153]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE

links, 5 protein links, or 8 nucleotide neighbors)

U32222

Bacteriophage 186, complete sequence
gi|3337249|gb|U32222|B1U32222 [3337249]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 46 protein links, or 5 nucleotide neighbors)

AF064539

Bacteriophage N15, complete genome
gi|3192683|gb|AF064539|AF064539 [3192683]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 60 protein links, 26 nucleotide neighbors, or 1 genome link)

AF063097

Bacteriophage P2, complete genome
gi|3139086|gb|AF063097|AF063097 [3139086]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,21 MEDLINE links, 42 protein links, 3 nucleotide neighbors, or 1 genome link)

Z97974

Bacteriophage phiadh lys, hol, intG, rad,and tec genes
gi|2707950|emb|Z97974|BPHIADH [2707950]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 9 protein links, or 1 nucleotide neighbor)

AF059243

Bacteriophage NL95, complete genome
gi|3088545|gb|AF059243|AF059243 [3088545]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, 3 nucleotide neighbors, or 1 genome link)

AF052431

Bacteriophage M11 A-protein, coat protein, A1-protein, and replicase genes, complete cds
gi|2981208|gb|AF052431| [2981208]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 8 nucleotide neighbors)

Y07739

Staphylococcus phage Twort holTW, plyTW genes
gi|2764979|emb|Y07739|BPTWGHOLG [2764979]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links)

X94331

Bacteriophage L cro, 24, c2, and c1 genes
gi|1469213|emb|X94331|BLCRO24C [1469213]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 protein links)

X78410

Bacteriophage phiadh holin and lysin genes
gi|793848|emb|X78410|LGHOLLYS [793848]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

X99260

Bacteriophage B103 genomic sequence
gi|1429229|emb|X99260|BB103G [1429229]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 17 protein links, or 12 nucleotide neighbors)

AJ000741

Bacteriophage P1 darA operon
gi|2462938|emb|AJ000741|BPAJ7641 [2462938]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, or 31 nucleotide neighbors)

X87420

Bacteriophage ES18 genes 24, c2, cro, c1, 18, and oL and oR operators
gi|1143407|emb|X87420|BPES18GEN [1143407]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 9 nucleotide neighbors)

L35561

Bacteriophage phi-105 ORFs 1-3
gi|532218|gb|L35561|PH5ORFHTR [532218]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 protein links)

D10027

Group II RNA coliphage GA genome
gi|217784|dbj|D10027|PGAXX [217784]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, 5 nucleotide neighbors, or 1 genome link)

V01128

Bacteriophage phi-X174 (cs70 mutation) complete genome
gi|15535|emb|V01128|PHIX174 [15535]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE links, 11 protein links, or 26 nucleotide neighbors)

S81763

coat gene...replicase gene [bacteriophage KU1, host=Escherichia coli, group II RNA phage, Genomic RNA, 3 genes, 120 nt]
gi|1438766|gb|S81763|S81763 [1438766]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link)

U38906

Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
gi|1353517|gb|U38906|BRU38906 [1353517]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 50 protein links, or 3 nucleotide neighbors)

X91149

Bacteriophage phi-C31 DNA cos region
gi|1107473|emb|X91149|APHIC31C [1107473]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 1 nucleotide neighbor)

V00642

phage MS2 genome
gi|15081|emb|V00642|LEMS2X [15081]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE links, 4 protein links, or 20 nucleotide neighbors)

V01146

Genome of bacteriophage T7
gi|431187|emb|V01146|T7CG [431187]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,13 MEDLINE links, 60 protein links, 105 nucleotide neighbors, or 1 genome link)

X78401

Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13
gi|512343|emb|X78401|POP22NIN [512343]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 13 protein links, or 4 nucleotide neighbors)

Y00408

Bacteriophage T4 gene t for lysis protein
gi|15368|emb|Y00408|MYT4T [15368]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

Z26590

Bacteriophage mv4 lysA and lysB genes
gi|410500|emb|Z26590|MV4LYSAB [410500]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 4 protein links)

X07809

Phage phiX174 lysis (E) gene upstream region
gi|15094|emb|X07809|MIPHIXE [15094]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors)

Z34528

Lactococcal bacteriophage c2 lysin gene
gi|506455|emb|Z34528|LBC2LYSIN [506455]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

X15031

Bacteriophage fr RNA genome
gi|15071|emb|X15031|LEBFRX [15071]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, 9 nucleotide neighbors, or 1 genome link)

X80191

Bacteriophage PP7 mRNA for maturation, coat, lysis and replicase proteins
gi|517237|emb|X80191|BPP7PR [517237]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 genome link)

X85010

Bacteriophage A511 ply511 gene
gi|853748|emb|X85010|BPA511PLY [853748]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

X85009

Bacteriophage A500 hol500 and ply500 genes
gi|853744|emb|X85009|BPA500PLY [853744]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 4 nucleotide neighbors)

X85008

Bacteriophage A118 hol118 and ply118 genes
gi|853740|emb|X85008|BPA118PLY [853740]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

Z35638

Bacteriophage phi-X174 genes for lysis protein and beta-lactamase
gi|520996|emb|Z35638|BPLYSPR [520996]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 516 nucleotide neighbors)

J02459

Bacteriophage lambda, complete genome
gi|215104|gb|J02459|LAMCG [215104]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE links, 67 protein links, 190 nucleotide neighbors, or 1 genome link)

X87674

Bacteriophage P1 lydA & lydB genes
gi|974763|emb|X87674|BACP1LYD [974763]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

X87673

Bacteriophage P1 gene 17
gi|974761|emb|X87673|BACP117 [974761]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor)

M14784

Bacteriophage T3 strain amNG220B right end, tail fiber protein, lysis protein and DNA packaging proteins, complete cds
gi|215810|gb|M14784|PT3RE [215810]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 10 nucleotide neighbors)

M11813

Bacteriophage PZA (from B.subtilis), complete genome
gi|216046|gb|M11813|PZACG [216046]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 27 protein links, 17 nucleotide neighbors, or 1 genome link)

M16812

Bacteriophage K3 't' lysis gene, complete cds
gi|215503|gb|M16812|PK3LYST [215503]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors)

J04356

Bacteriophage P22 proteins 15 (complete cds), and 19 (3' end) genes
gi|215265|gb|J04356|P2215P [215265]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors)

J04343

Bacteriophage JP34 coat and lysis protein genes, complete cds, and replicase protein gene, 5' end
gi|215076|gb|J04343|JP3COLY [215076]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors)

J02482

Bacteriophage phi-X174, complete genome
gi|216019|gb|J02482|PX1CG [216019]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,23 MEDLINE links, 11 protein links, 26 nucleotide neighbors, or 1 genome link)

M99441

Bacteriophage T4 anti-sigma 70 protein (asiA) gene, complete cds and lysis protein, 3' end
gi|215820|gb|M99441|PT4ASIA [215820]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 2 nucleotide neighbors)

M65239

Bacteriophage 21 lysis genes S, R, and Rz, complete cds
gi|215466|gb|M65239|PH2LYSGEN [215466]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

M10637

Phage G4 D/E overlapping gene system, encoding D (morphogenetic) and E (lysis) proteins
gi|215427|gb|M10637|PG4DE [215427]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors)

J02454

Bacteriophage G4, complete genome
gi|215415|gb|J02454|PG4CG [215415]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 11 protein links, 20 nucleotide neighbors, or 1 genome link)

J02580

Bacteriophage PA-2 (E.coli porcine strain isolate) Rz gene, 5'end; ORF2, outer membrane porin protein (lc) and ORF1 genes, complete cds
gi|215366|gb|J02580|PA2LC [215366]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 4 nucleotide neighbors)

M14782

Bacillus phage phi-29 head morphogenesis, major head protein, head fiber protein, tail protein, upper collar protein, lower collar protein, pre-neck appendage protein, morphogenesis(13), lysis, morphogenesis(15), encapsidation genes, complete cds
gi|215323|gb|M14782|P29LATE2 [215323]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 11 nucleotide neighbors)

M10997

Bacteriophage P22 lysis genes 13 and 19, complete cds
gi|215262|gb|M10997|P221319 [215262]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors)

J02467

Bacteriophage MS2, complete genome
gi|215232|gb|J02467|MS2CG [215232]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE links, 4 protein links, 20 nucleotide neighbors, or 1 genome link)

M14035

Bacteriophage lambda lysis S gene with mutations leading to nonlethality of S in the plasmid pRG1
gi|215180|gb|M14035|LAMLYS [215180]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 14 nucleotide neighbors)

U04309

Bacteriophage phi-LC3 putative holin (lysA) gene and putative murein hydrolase (lysB) gene, complete cds
gi|530796|gb|U04309|BPU04309 [530796]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

Table 13

NCBI *Entrez* Nucleotide QUERY

Key word: holin

51 citations found (all selected)

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds
gi|2668751|gb|AF034975| [2668751]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors)

U52961

Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds
gi|1841516|gb|U52961|SAU52961 [1841516]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

U28154

Haemophilus somnus cryptic prophage genes, capsid scaffolding protein gene, partial cds, major capsid protein precursor, endonuclease, capsid completion protein, tail synthesis proteins, holin, and lysozyme genes, complete cds
gi|1765928|gb|U28154|HSU28154 [1765928]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 protein links)

AF032122

Streptococcus thermophilus bacteriophage Sfi19 central region of genome
gi|2935682|gb|AF032122| [2935682]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 14 protein links, or 2 nucleotide neighbors)

AF032121

Streptococcus thermophilus bacteriophage Sfi21 central region of genome
gi|2935667|gb|AF032121|AF032121 [2935667]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 14 protein links, or 2 nucleotide neighbors)

AF021803

Bacillus subtilis 168 prophage SPbeta N-acetylmuramoyl-L-alanine amidase (blyA), holin-like protein (bhlA), holin-like protein (bhlB), and yolK genes, complete cds; and yolJ gene, partial cds
gi|2997594|gb|AF021803|AF021803 [2997594]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 1 nucleotide neighbor)

AF057033

Streptococcus thermophilus bacteriophage sfi11 gp502 (orf502), gp284 (orf284), gp129 (orf129), gp193 (orf193), gp119 (orf119), gp348 (orf348), gp53 (orf53), gp113 (orf113), gp104 (orf104), gp114 (orf114), gp128 (orf128), gp168 (orf168), gp117 (orf117), gp105 (orf105), putative minor tail protein (orf1510), putative minor structural protein (orf512), putative minor structural protein (orf1000), gp373 (orf373), gp57 (orf57), putative anti-receptor (orf695), putative minor structural protein (orf669), gp149 (orf149), putative holin (orf141), putative holin (orf87), and lysin (orf288) genes, complete cds
gi|3320432|gb|AF057033|AF057033 [3320432]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,25 protein links, or 1 nucleotide neighbor)

U32222

Bacteriophage 186, complete sequence
gi|3337249|gb|U32222|B1U32222 [3337249]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 46 protein links, or 5 nucleotide neighbors)

AB009866

Bacteriophage phi PVL proviral DNA, complete sequence
gi|3341907|dbj|AB009866|AB009866 [3341907]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,63 protein links, or 1 nucleotide neighbor)

AF009630

Bacteriophage bIL170, complete genome
gi|3282260|gb|AF009630|AF009630 [3282260]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,63 protein links, 3 nucleotide neighbors, or 1 genome link)

AF064539

Bacteriophage N15, complete genome

gi|3192683|gb|AF064539|AF064539 [3192683]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 60 protein links, 26 nucleotide neighbors, or 1 genome link)

AF063097

Bacteriophage P2, complete genome
gi|3139086|gb|AF063097|AF063097 [3139086]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,21 MEDLINE links, 42 protein links, 3 nucleotide neighbors, or 1 genome link)

Z97974

Bacteriophage phiadh lys, hol, intG, rad,and tec genes
gi|2707950|emb|Z97974|BPHIADH [2707950]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 9 protein links, or 1 nucleotide neighbor)

X95646

Streptococcus thermophilus bacteriophage Sfi21 DNA; lysogeny module, 8141 bp
gi|2292747|emb|X95646|BSFI21LYS [2292747]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 19 protein links, or 3 nucleotide neighbors)

SEG_LLHLYSIN0

Bacteriophage LL-H structural protein gene, partial cds; minor structural protein gp61 (g57), unknown protein, unknown protein, structural protein (g20), unknown protein, unknown protein, major capsid protein (g34), main tail protein gp19 (g17), holin (hol), muramidase (mur), unknown protein, unknown protein, unknown protein, unknown protein, unknown protein, and unknown protein genes, complete cds; unknown protein gene, partial cds; and unknown protein, unknown protein, unknown protein, unknown protein, unknown protein, minor structural protein gp75 (g70), minor structural protein gp89 (g88), minor structural protein gp58 (g71), unknown protein, unknown protein, unknown protein, and unknown protein genes, complete cds
gi|1004337|gb|SEG_LLHLYSIN0 [1004337]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE links, 31 protein links, or 1 nucleotide neighbor)

M96254

Bacteriophage LL-H holin (hol), muramidase (mur), and unknown protein genes, complete cds
gi|1004336|gb|M96254|LLHLYSIN03 [1004336]
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

Y07740

Staphylococcus phage 187 ply187 and hol187 genes
gi|2764982|emb|Y07740|BP187PLYH [2764982]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links)

U88974

Streptococcus thermophilus bacteriophage 01205 DNA sequence
gi|2444080|gb|U88974| [2444080]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 57 protein links, or 6 nucleotide neighbors)

Z99117

Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
gi|2634966|emb|Z99117|BSUB0014 [2634966]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,233 protein links, 51 nucleotide neighbors, or 1 genome link)

Z99115

Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220
gi|2634478|emb|Z99115|BSUB0012 [2634478]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,244 protein links, 64 nucleotide neighbors, or 1 genome link)

Z99110

Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140
gi|2633472|emb|Z99110|BSUB0007 [2633472]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,226 protein links, 31 nucleotide neighbors, or 1 genome link)

X78410

Bacteriophage phiadh holin and lysin genes
gi|793848|emb|X78410|LGHOLLYS [793848]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

Z93946

Bacteriophage Dp-1 dph and pal genes and 5 open reading frames
gi|1934760|emb|Z93946|BPDP1ORFS [1934760]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 6 protein links)

AF011378

Bacteriophage sk1 complete genome
gi|2392824|gb|AF011378|AF011378 [2392824]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,54 protein links, 2 nucleotide neighbors, or 1 genome link)

Z47794

Bacteriophage Cp-1 DNA, complete genome
gi|2288892|emb|Z47794|BPCP1XX [2288892]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 28 protein links, 1 nucleotide neighbor, or 1 genome link)

L35561

Bacteriophage phi-105 ORFs 1-3
gi|532218|gb|L35561|PH5ORFHTR [532218]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 protein links)

D49712

Bacillus licheniformis DNA for ORFs, xpaL2 homologous protein and xpaL1 homologous protein, complete and partial cds
gi|1514423|dbj|D49712|D49712 [1514423]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 4 protein links)

X90511

Lactobacillus bacteriophage phig1e DNA for Rorf162, Holin, Lysin, and Rorf175 genes
gi|1926386|emb|X90511|LBPHIHOL [1926386]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 1 nucleotide neighbor)

X98106

Lactobacillus bacteriophage phig1e complete genomic DNA
gi|1926320|emb|X98106|LBPHIG1E [1926320]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE

link, 50 protein links, or 4 nucleotide neighbors)

U72397

Bacteriophage 80 alpha holin and amidase genes, complete cds
gi|1763241|gb|U72397|B8U72397 [1763241]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors)

U38906

Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
gi|1353517|gb|U38906|BRU38906 [1353517]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 50 protein links, or 3 nucleotide neighbors)

X91149

Bacteriophage phi-C31 DNA cos region
gi|1107473|emb|X91149|APHIC31C [1107473]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 1 nucleotide neighbor)

U24159

Bacteriophage HP1 strain HP1c1, complete genome
gi|1046235|gb|U24159|BHU24159 [1046235]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 41 protein links, 8 nucleotide neighbors, or 1 genome link)

Z26590

Bacteriophage mv4 lysA and lysB genes
gi|410500|emb|Z26590|MV4LYSAB [410500]
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 4 protein links)

Z70177

B.subtilis DNA (28 kb PBSX/skin element region)
gi|1225934|emb|Z70177|BSPBSXSE [1225934]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,32 protein links, or 4 nucleotide neighbors)

Z36941

B.subtilis defective prophage PBSX xhlA, xhlB, and xylA genes
gi|535793|emb|Z36941|BSPBSXXHL [535793]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 5 nucleotide neighbors)

X89234

L.innocua DNA for phagelysin and holin gene
gi|1134844|emb|X89234|LICPLYHOL [1134844]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors)

X85010

Bacteriophage A511 ply511 gene
gi|853748|emb|X85010|BPA511PLY [853748]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

X85009

Bacteriophage A500 hol500 and ply500 genes
gi|853744|emb|X85009|BPA500PLY [853744]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 4 nucleotide neighbors)

X85008

Bacteriophage A118 hol118 and ply118 genes
gi|853740|emb|X85008|BPA118PLY [853740]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

L34781

Bacteriophage phi 11 holin homologue (ORF3) gene, complete cds and peptidoglycan hydrolase (lytA) gene, partial cds
gi|511838|gb|L34781|BPHHOLIN [511838]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 2 nucleotide neighbors)

U11698

Serratia marcescens SM6 extracellular secretory protein (nucE), putative phage lysozyme (nucD), and transcriptional activator (nucC) genes, complete cds
gi|509550|gb|U11698|SMU11698 [509550]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE

link, 3 protein links, or 1 nucleotide neighbor)

U31763

Serratia marcescens phage-holin analog protein (regA), putative phage lysozyme (regB), and transcriptional activator (regC) genes, complete cds
gi|965068|gb|U31763|SMU31763 [965068]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor)

X87674

Bacteriophage P1 lydA & lydB genes
gi|974763|emb|X87674|BACP1LYD [974763]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors)

L48605

Bacteriophage c2 complete genome
gi|1146276|gb|L48605|C2PVCG [1146276]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 39 protein links, 3 nucleotide neighbors, or 1 genome link)

L33769

Bacteriophage bIL67 DNA polymerase subunit (ORF3-5), essential recombination protein (ORF13), lysin (ORF24), minor tail protein (ORF31), terminase subunit (ORF32), holin (ORF37), unknown protein (ORF 1-2,6-12,14-23,25-30,33-36), complete genome
gi|522252|gb|L33769|L67CG [522252]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 37 protein links, 2 nucleotide neighbors, or 1 genome link)

L31348

Bacteriophage Tuc2009 integrase (int) gene, complete cds; lysin (lys) gene, 3' end
gi|508612|gb|L31348|TU2INT [508612]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 3 nucleotide neighbors)

L31364

Bacteriophage Tuc2009 holin (S) gene, complete cds; lysin (lys) gene, complete cds
gi|496281|gb|L31364|TU2SLYS [496281]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

L31366

Bacteriophage Tuc2009 structural protein (mp2) gene, complete cds
gi|496278|gb|L31366|TU2MP2A [496278]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

L31365

Bacteriophage Tuc2009 structural protein (mp1) gene, complete cds
gi|496276|gb|L31365|TU2MP1A [496276]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link)

U04309

Bacteriophage phi-LC3 putative holin (lysA) gene and putative murein hydrolase (lysB) gene, complete cds
gi|530796|gb|U04309|BPU04309 [530796]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor)

Table 14

NCBI *Entrez* Nucleotide QUERY

Key word: bacteriophage and kil

5 citations found (all selected)

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds
gi|2668751|gb|AF034975| [2668751]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors)

X15637

Bacteriophage P22 P(L) operon encompassing ral, 17, kil and arf genes
gi|15646|emb|X15637|POP22PL [15646]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 7 protein links, or 2 nucleotide neighbors)

J02459

Bacteriophage lambda, complete genome
gi|215104|gb|J02459|LAMCG [215104]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE links, 67 protein links, 190 nucleotide neighbors, or 1 genome link)

M64097

Bacteriophage Mu left end
gi|215543|gb|M64097|PMULEFTEN [215543]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 39 protein links, or 15 nucleotide neighbors)

M18902

Bacteriophage D108 kil gene encoding a replication protein, 3' end; and containing three ORFs, complete cds
gi|166191|gb|M18902|D18KIL [166191]
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors)

Table 15

U77328	V01282	U11787	U93688	A47599	D21131	U76864	U38428
AF151117	AF121672	U11786	U93687	A47598	D30690	U76863	U66665
AF151218	AF072726	U11785	AJ224764	A47597	D14711	U76862	U66664
AF146368	AF115379	U11784	AF064774	A47596	D90119	U76861	U66663
AF144661	AF034153	U11783	AF064773	A47595	D00730	U76860	X87104
AF132117	AF029244	U11782	Y14370	A47594	D83357	U76859	X87105
Y15477	U67965	U11781	AF065394	A44534	D83356	U76858	X89233
Y09928	U96610	U11780	AF062376	A44533	D83355	U76857	M28521
Y09594	U96609	U11779	AF062375	A44529	D83354	U76855	U54636
AF134905	U73027	U11778	AF062374	A44528	D83353	U76854	U46541
AB019536	U73026	U11777	AF062373	A44527	D12572	U76853	L14017
AJ237696	U73025	U11776	AB007500	A44526	D86727	U76852	U60589
AF106851	AF068904	U11775	Y09924	A44525	D86240	U76851	X48003
AF106850	U60050	U11774	U63529	A39696	D67075	U76850	M37889
AF106849	D10907	U11773	AF033191	AF001783	D67074	U76849	V01281
M26321	D10906	AF053772	Y15856	AF001782	U97062	U76848	X97985
AF060191	AF053140	AF053771	AB000439	L77194	U96620	U76847	X00127
AF060190	AB013298	AF029731	AF041467	AF003593	U96619	Y09929	X03286
AF060189	Y16431	AF027155	Y14051	AF003592	Z84573	Y09570	X62282
AF060188	AF076684	AF024571	U82085	X73889	AB001896	X95848	X01645
AF060187	AF076683	U87144	AF026122	X74219	Y07645	Y09428	X16471
AF060186	Y13225	AF086644	AF026121	Y10419	U92441	S76611	X52734
AF060185	AF094826	AJ223781	AF026120	M63177	U91741	S76213	X13290
AF060184	AJ223480	AF076030	AB009635	E08773	U29454	S75707	X66088
AF036324	AF093548	AF044951	AB006796	E07163	U29478	S75706	Z30588
AF036323	AJ005352	AF044906	U39769	E07162	U77374	S75705	X16457
AF053568	AF051916	AF044905	D00184	E07161	L42945	S76270	X00342
AJ132841	Y09927	AF044904	X56628	E07160	U38429	S72497	V01287
Y13766	AF051917	AF044903	AF033018	E07159	U81980	S72488	X61307
AF101234	S77058	AF044902	AF034076	E07158	X55185	S74031	Y00356
AJ133520	S65052	AF044901	D82063	E07157	V01278	S67449	X06603
AJ133495	AF009671	AF044900	D76414	E07156	U31979	U75367	Z93205
AJ132803	U81973	AF044899	U57060	E07155	X91786	U75368	X64172
AB016487	U77308	AF044898	D89066	E03836	U36912	U31175	X72700
AB016431	U20869	AF044897	U85095	E03835	U36911	X53096	X60827
AB015981	U89396	AF044075	U85097	E03526	U36910	X53951	X64389
AB015195	U94706	AF044074	U85096	E02873	U64885	X53952	X62288
AF107307	U41072	AF044073	D42078	E01690	U76872	X03408	X55798
AF079518	U52961	AF044072	AF015929	E00876	U76871	U50629	X58434
AJ223806	U21636	AF044071	D10369	E00203	U76870	U38656	X06627
Y18018	U65000	AF044070	A48955	D83951	U76869	U58139	X12831
Y17795	U48826	AF044069	A48501	D17366	U76868	A31894	X07371
AJ005647	U20503	AF044068	A48500	D42144	U76867	L42943	X02529
AJ005646	U11789	AF044067	A48499	D42143	U76866	U51474	Y00688
AJ005645	U11788	AF044066	A47600	D10489	U76865	U50077	X04121
X59477	X54338	A12915	U51133	M63176	M10500	L01055	M63917
X59478	X51661	A12913	U51132	L11998	M10499	M83994	M58515
X63598	X05815	A12906	X02588	L05004	AH000934	J03947	L10909
X52593	X15574	A12905	X61716	L42764	M10498	J03479	M15067

X76490	Y07536	A12904	X61719	M32103	M10497	M64724	M92376
X81586	X02166	A12903	X61718	U10927	M18264	M14372	M62650
X72014	Z49245	A12902	X67743	AH003057	J01786	M14371	M32312
X72013	X16298	A12901	X67742	M73535	M33833	M14374	M20393
X71437	Z18852	A12900	X67741	M73536	M32470	M15215	M90536
X62992	X68417	A12899	X67740	U20782	M20270	M36694	M21854
X52594	X68425	A12898	X67738	L37598	J03323	M37915	M36771
X14827	X17679	A12897	U02910	L37597	M33479	M12715	L14020
X13404	X63072	A12896	AH003349	L36472	M94061	J04151	M81736
X17301	X02872	A09523	M11118	L25288	M37888	L22566	U11702
X17688	V01277	A04518	M18086	L25893	M76714	L13379	L19300
X03097	X52543	A04517	U19459	K02687	M17123	L13378	L25372
Z16422	A19943	A04512	U35773	L23109	M97169	L13377	L22565
Z33409	A19942	L41499	U26702	L07778	M81346	L13376	M58516
Z33408	A19941	U19770	U21221	M90056	M90693	L13375	U06462
Z33407	A19940	X53818	U36379	J02615	M25257	L13374	L19298
Z33406	A19939	M20129	U06451	M18970	M25256	M17348	M80252
Z33405	A19938	L43098	U35036	K02985	M25255	M17357	L11530
Z33404	A19937	L43082	U20794	M21136	M25254	M17347	
X75439	A19936	X03216	L25426	M10501	M25253	M28364	
X62587	A17958	X70648	M86227	AH000935	M25252	M21319	

Table 16

Phage 44AHJD complete genome sequence. 16668 nucleotides.

1 tccatttctt tactaaactt aaaaatgctg tgcaacaact taaccaactt atctaaccta ttacatattc
71 atcaaataca aaatttatgt atctattgac ttttattcaa aattatgatt tcaacatata ataaaattaa
141 tttacttatt taaatattct atgatataat tagttataaa atatttggag gtgtataaat gacagaattt
211 gatgaaatcg taaaaccaga cgacaaagaa gaaacttcag aatcaactga agaaaattta gaatcaactg
281 aagaaacttc agaatcaact gaagaatcaa ctgaagaatc aactgaagaa tcaactgaag ataaaacagt
351 agaaacaatc gaagaagaaa atgaaaacaa attagaacct actacaacag atgaagatag ttcgaaattt
421 gaccctgttg tattagaaca acgtattgct tcattagaac aacaagtgac tacttttta tcttcacaaa
491 tgcaacaacc acaacaagta caacaaacac aatcagatgt aacagaatca aacaaagaag ataacgacta
561 ttcagatgaa gaactagttg ataagttaga tttagattag gaggaattta aacatgtatg agggaaacaa
631 catgcgttct atgatgggta catcatatga agattcaaga ttaaataaac gaacagaatt aaatgaaaac
701 atgtcaattg atacaaataa aagtgaagat agttatggtg tacaaattca ttcactttca aaacaatcat
771 ttacaggtga cgttgaggag gaataataaa ttatggcaca acaatctaca aaaaatgaaa ctgcactttt
841 agtagcaaag tcagctaaat cagcgttaca agattttaat catgattatt caaaatcttg gacatttggc
911 gacaaatggg ataattcaaa tacaatgttc gaaacatttg taaataaata tttattccct aagattaatg
981 agactttatt aatcgatatt gcattaggta atcgttttaa ttggttagct aaagagcaag attttattgg
1051 acaatatagt gaagaatacg tgattatgga cacagtacca attaacatgg acttatctaa aaatgaggaa
1121 ttaatgttga aacgtaatta tccacgtatg gcaactaagt tatatggtaa cggaattgtg aagaaacaaa
1191 aattcacatt aaacaacaat gatacacgtt tcaatttcca aacattagca gacgcaacta attacgcttt
1261 aggtgtatac aaaaagaaaa tttctgatat taatgtatta gaagaaaaag aaatgcgtgc aatgttagtt
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15541 aatctcgcta atgtgttttg gtgtcttgat aaaatatctt ttacgtttgt cattttattt ctcctcttat
15611 ttaaattatt tgctttctgc aattgcgatt tgtagtaaat cattgtaata aacttgaatt gttttcgttg
15681 tgcgtgtagt ggacaatagt ttacatgtgt ctggtaataa ttcttttgct tgtgttttgg ttaaatgata
15751 ctcgtgaagt ggtaaaaatt cctcaatgta ttcattatca tcatctaagt aatgaagtat ataacctttg
15821 acacgtaagg taacaatgtc gtcaactttc attattatat cactcctttc taaaaaacgt aaacgttata
15891 cgtttcataa aatcctttat gcatattcca ttgttctatt gggtcatcac cagcaatata agacaatatt
15961 gattctggtt tagtttcgtt gtttagttca tcatttaaga attgaacaac agaactatta tagtttaata
16031 atagttgttg gcaagccgat aataagttaa ttgcattgtc aaatgtataa gctggattcc attgaatcag
16101 tttattgaat agttgcaaca tttcagtata ggcttgtcct ttttcttctg gtgcattatc aacattaacc
16171 attattatca cttcctaata aagttgaaat tacgcgtaaa acagaattat gatttaaatc ttcaatttca
16241 tcaatgtcaa catcataaaa tgaaatttca ttttctgttc tatcaaataa cgctatacat aaacttccat
16311 tcttaaaacg aaaaacatgc ttcaactcaa tgtttttgt ttcattttcc atttttgtta ctccttgttt
16381 tgattacata cttagtatag caaacgttta aaagttttgt caatagtttt tcttaaaaaa gtttaaataa
16451 ttttaaaact actatttaat agaagaaata agattttaag ttcaaatcat aattttgaat aaaagtcaat
16521 agatacataa attttgtatt tgatgaatat gtaataggtt agataagttg gttaagttgt tgcacagtat
16591 ttttaagttt agtaaagaaa tgataagtaa atttataagt tttgatttgt ataatcgttt attttaaacc
16661 ggtggggt

Table 17

Phage 44AHJD ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	44AHJDORF001	-1	10342..12627	761	DNA polymerase;
2	44AHJDORF002	3	3789..5732	647	Techoic acid; Staph;
3	44AHJDORF003	2	6626..8389	587	Tail;
4	44AHJDORF004	1	8764..10227	487	Serine protease motif;
5	44AHJDORF005	-1	12643..13890	415	
6	44AHJDORF006	2	803..2029	408	
7	44AHJDORF007	1	2044..3027	327	Upper collar;
8	44AHJDORF008	2	3020..3775	251	Lower collar;
9	44AHJDORF009	2	5744..6496	250	Amidase; Staph;
10	44AHJDORF010	-2	13938..14420	160	
11	44AHJDORF012	3	8391..8813	140	Holin;
12	44AHJDORF013	-2	14586..14996	136	
13	44AHJDORF113	1	199..600	133	
14	44AHJDORF011	-2	15225..15593	122	
15	44AHJDORF114	-2	15870..16172	100	
16	44AHJDORF014	3	6243..6521	92	
17	44AHJDORF015	1	15403..15645	80	
18	44AHJDORF016	-1	15616..15852	78	
19	44AHJDORF017	-2	10536..10757	73	
20	44AHJDORF018	-1	886..1098	70	
21	44AHJDORF019	-2	9630..9836	68	
22	44AHJDORF121	-1	16165..16362	65	
23	44AHJDORF020	2	13865..14053	62	
24	44AHJDORF123	2	614..796	60	
25	44AHJDORF021	-2	5634..5816	60	
26	44AHJDORF023	-2	6315..6494	59	
27	44AHJDORF024	1	14275..14451	58	
28	44AHJDORF025	-3	14999..15175	58	
29	44AHJDORF026	-3	14426..14593	55	
30	44AHJDORF027	1	12916..13080	54	
31	44AHJDORF029	-1	15019..15183	54	
32	44AHJDORF028	-3	9071..9235	54	
33	44AHJDORF030	3	14487..14648	53	
34	44AHJDORF031	2	11039..11191	50	
35	44AHJDORF135	3	693..842	49	
36	44AHJDORF033	-1	3646..3795	49	
37	44AHJDORF032	-2	9306..9455	49	
38	44AHJDORF034	-3	14000..14146	48	
39	44AHJDORF035	-3	13811..13957	48	
40	44AHJDORF036	-3	10019..10165	48	
41	44AHJDORF022	-3	8468..8611	47	
42	44AHJDORF037	1	14788..14931	47	
43	44AHJDORF038	-2	3528..3671	47	
44	44AHJDORF039	3	1743..1883	46	
45	44AHJDORF040	2	9740..9877	45	
46	44AHJDORF041	2	15836..15973	45	
47	44AHJDORF042	-1	5014..5151	45	
48	44AHJDORF043	-1	4402..4539	45	
49	44AHJDORF044	-2	12783..12917	44	
50	44AHJDORF149	-2	639..770	43	
51	44AHJDORF046	1	4891..5019	42	
52	44AHJDORF047	1	11911..12039	42	
53	44AHJDORF045	2	10655..10783	42	
54	44AHJDORF048	-3	15212..15340	42	
55	44AHJDORF049	3	5784..5909	41	
56	44AHJDORF050	3	13158..13283	41	
57	44AHJDORF051	-2	10944..11066	40	
58	44AHJDORF052	-3	14216..14338	40	
59	44AHJDORF053	3	3348..3467	39	
60	44AHJDORF054	3	7551..7670	39	
61	44AHJDORF055	3	15705..15821	38	
62	44AHJDORF056	1	5512..5625	37	
63	44AHJDORF057	2	10121..10231	36	
64	44AHJDORF058	3	10767..10877	36	

65	44AHJDORF164	-1	592..702	36	
66	44AHJDORF059	-2	8250..8360	36	
67	44AHJDORF060	-2	6147..6257	36	
68	44AHJDORF061	2	15551..15658	35	
69	44AHJDORF062	1	4285..4389	34	
70	44AHJDORF063	-3	9383..9487	34	
71	44AHJDORF065	1	5029..5130	33	
72	44AHJDORF064	2	2609..2710	33	
73	44AHJDORF066	-2	10380..10481	33	

Table 18

Predicted amino acid sequences

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44AHJDORF001
12627  atgggattactagaatgcatgcaatatcataaacatgaacgtcgaatgatttatactgggatatagaaacattagcgtacaat
1      M G L L E C M Q Y H K H E R R M I L Y W D I E T L A Y N
12543  aaagttaacggacgaaaaaaaccaaccaaatataaaaacgttacttattctgtagcaattggttggtttaatggttatgaaatt
29     K V N G R K K P T K Y K N V T Y S V A I G W F N G Y E I
12459  gatgttgaagtatttccgagtttcgaatcttttatgacgcattttatacgtatgtgaaaagacgtgatacaatcacaaaatca
57     D V E V F P S F E S F Y D A F Y T Y V K R R D T I T K S
12375  aaaacagatattatcatgattgcacataactgtaataaatacgataatcatttttacttaaagacaccatgcgttattttgat
85     K T D I I M I A H N C N K Y D N H F L L K D T M R Y F D
12291  aatattacacgcgaaaatatatatttaaaatctgcagaagaaaatgaacacacattaaaaatgaaagaggctactattttagcc
113    N I T R E N I Y L K S A E E N E H T L K M K E A T I L A
12207  aaaaatcaaaatgtaattttagaaaaacgtgttaaatcttcaatcaatttagatttaacaatgtttttaaatggtttaaattt
141    K N Q N V I L E K R V K S S I N L D L T M F L N G F K F
12123  aatattattgataactttatgaaaaccaatacatcaattgcaacattaggtaagaaattacttgatggtggttatttaacagaa
169    N I I D N F M K T N T S I A T L G K K L L D G G Y L T E
12039  tcacaacttaaaacagatttaattatacgattttgataaagataatgatatgaatgatagtgaagcctatgactatgctgtg
197    S Q L K T D F N Y T I F D K D N D M N D S E A Y D Y A V
11955  aaatgttttgcaaaactcacacctgaacaacttacatacattcataatgacgtgattatattaggtatgtgccatattcattat
225    K C F A K L T P E Q L T Y I H N D V I I L G M C H I H Y
11871  agtgatatatttccaaatttgactataacaaattaacattttcattgaatattatggaatcttacttgaataatgaaatgaca
253    S D I F P N F D Y N K L T F S L N I M E S Y L N N E M T
11787  cgttttcagttactcaaccaatatcaagatattaaaatatcttatacacattatcatttccatgatatgaatttttatgactat
281    R F Q L L N Q Y Q D I K I S Y T H Y H F H D M N F Y D Y
11703  attaaatcattctatcgtggtggtttaaatatgtataacaccaaatacataaacaaactaattgatgagccttgtttttctatt
309    I K S F Y R G G L N M Y N T K Y I N K L I D E P C F S I
11619  gacatcaattcgagttatccttatgtgatgtatcatgaaaaaattccaacatggttatactttacgaacactattcagaacca
337    D I N S S Y P Y V M Y H E K I P T W L Y F Y E H Y S E P
11535  acgttaatccctactttttagatgatgacaattatttttcattatataagattgataaagatgtatttaacgatgatttatta
365    T L I P T F L D D D N Y F S L Y K I D K D V F N D D L L
11451  attaaaattaaatcacgtgtattacgtcaaatgattgtaaaatactataataatgataatgattacgttaatatcaatacaaat
393    I K I K S R V L R Q M I V K Y Y N N D N D Y V N I N T N
11367  acattaagaatgattcaagacattacgggtattgattgcatgcatatacgtgttaattcgtttgttatatatgaatgtgaatac
421    T L R M I Q D I T G I D C M H I R V N S F V I Y E C E Y
11283  tttcatgcacgtgatattatttttcaaaactattttattaaaacacaaggtaagttaaaaaacaaaatcaatatgacatcacct
449    F H A R D I I F Q N Y F I K T Q G K L K N K I N M T S P
11199  tacgactatcacattactgatgatatcaacgaacacccatactcaaatgaggaggttatgttatctaaagtcgttttaaatgga
477    Y D Y H I T D D I N E H P Y S N E E V M L S K V V L N G
11115  ttatatggcatacctgcattacgttcacatttaacttattccgtttagatgataacaatgaactatacaatatcattaacggt
505    L Y G I P A L R S H F N L F R L D D N N E L Y N I I N G
11031  tacaaaaacactgaacgtaatatattattctctacatttgtcacatcacgttcattgtataacttattggttcctttccaatac
533    Y K N T E R N I L F S T F V T S R S L Y N L L V P F Q Y
10947  ttaacggaaagtgaaattgacgacaatttttatttattgcgatactgatagtttgtatatgaaatccgttgttaaacccttattg
561    L T E S E I D D N F I Y C D T D S L Y M K S V V K P L L
10863  aaccccagtttattcgacccgatagccttaggtaaatgggatattgaaaacgaacagatagataagatgtttgtactgaatcat
589    N P S L F D P I A L G K W D I E N E Q I D K M F V L N H
10779  aagaaatatgcatatgaagtgaatggaaagattaaaattgcttctgctggtataccgaaaaacgcctttgatacaagcgtcgat
617    K K Y A Y E V N G K I K I A S A G I P K N A F D T S V D
10695  tttgaaacctttgtacgtgaacaattctttgacggtgccattattgaaaacaataaaagtatctataatgagcaaggtacaata
645    F E T F V R E Q F F D G A I I E N N K S I Y N E Q G T I
10611  tcgatatatccgtctaaaactgaaattgtatgtggtaatgtatatgatgaatatttactgatgaacttaatatgaaacgtgaa
673    S I Y P S K T E I V C G N V Y D E Y F T D E L N M K R E
10527  tttatattaaaagacgctagagaaaatttcgaccatagtcaatttgatgatattctttatattgaaagtgacatcggttcattt
701    F I L K D A R E N F D H S Q F D D I L Y I E S D I G S F
10443  tcacttaacgacttatttccagttgaacgttcagtacataacaaatctgatttgcatatattaaaacgtgaacatgatgaaata
729    S L N D L F P V E R S V H N K S D L H I L K R E H D E I
10359  aaaaaaggcaactgttaa 10342
757    K K G N C *
44AHJDORF002
3789   atggcatataatgaaaacgatttaaatatttgatgacattcgtccattttagacgaaatttataaaacgagagaacgttat
1      M A Y N E N D F K Y F D D I R P F L D E I Y K T R E R Y
3873   acaccgttttacgatgatagagcagattataatactaattcaaaatcatattatgattatatttcaagattatcaaaactaatt
29     T P F Y D D R A D Y N T N S K S Y Y D Y I S R L S K D I
3957   gaagtattagcacgtcgtatttgggactatgacaatgaattaaaaaaacgtttcaaaaattgggacgacttaatgaaagcattt
57     E V L A R R I W D Y D N E L K K R F K N W D D L M K A F
4041   ccagagcaagcgaaagacttatttagaggttggttaaacgacggtacgattgacagtattattcatgacgagtttaaaaaatat
85     P E Q A K D L F R G W L N D G T I D S I I H D E F K K Y
4125   agcgcaggattaacatcggcatttgctttatttaaagttactgaaatgaaacaaatgaatgactttaaatcagaagttaaagac
113    S A G L T S A F A L F K V T E M K Q M N D F K S E V K D
4209   ttaattaaagatattgaccgtttcgttaatgggtttgaattaaatgagcttgaaccaaagtttgtgatgggctttggtggtatt
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141    L I K D I D R F V N G F E L N E L E P K F V M G F G G I
4293   cgcaacgcagttaaccaatctattaatattgataaagaaacaaatcacatgtactctacacaatccgattctcaaaaacctgaa
169    R N A V N Q S I N I D K E T N H M Y S T Q S D S Q K P E
4377   ggtttttggataaataaattaacacctagtggtgacttaatttcaagcatgcgtattgtacagggtggtcatggtacaacaatc
197    G F W I N K L T P S G D L I S S M R I V Q G G H G T T I
4461   ggattagaacgtcaatccaatggtgaaatgaaaatctggttacatcacgatggtgttgcaaaactgttacaagtcgcatataaa
225    G L E R Q S N G E M K I W L H H D G V A K L L Q V A Y K
4545   gataattatgtattagatttagaagaggctaaaggtttaacagattatacaccacagtcactttttaaacaaacacacatttaca
253    D N Y V L D L E E A K G L T D Y T P Q S L L N K H T F T
4629   ccgttaattgatgaagcaaatgacaaactcatttttaagattcggtgacggaacaatacaggttcgttcaagagcagacgtaaaa
281    P L I D E A N D K L I L R F G D G T I Q V R S R A D V K
4713   aatcacattgataatgtagaaaaagaaatgacaattgataattcagaaaacaatgataatcgttggatgcaaggcattgctgtt
309    N H I D N V E K E M T I D N S E N N D N R W M Q G I A V
4797   gatggtgatgatttatactggttaagtggtaacagttcagttaattcacatgttcaaatcggtaaatattcattaacaacaggt
337    D G D D L Y W L S G N S S V N S H V Q I G K Y S L T T G
4881   caaaagatttatgattatccatttaagttatcatatcaagacggtattaatttcccacgtgataactttaaagagcctgagggt
365    Q K I Y D Y P F K L S Y Q D G I N F P R D N F K E P E G
4965   atttgcatttatacaaatccaaaaacaaaacgtaaatcgttattacttgctatgacaaacggcggtggtggaaaacgtttccat
393    I C I Y T N P K T K R K S L L L A M T N G G G G K R F H
5049   aatttatatggtttcttccaacttggtgagtatgaacactttgaagcattacgcgcaagaggttcacaaaactataaattaaca
421    N L Y G F F Q L G E Y E H F E A L R A R G S Q N Y K L T
5133   aaagacgacggtcgtgcattatctattccagaccatatcgacgatttaaatgacttaacgcaagctggtttttattatattgac
449    K D D G R A L S I P D H I D D L N D L T Q A G F Y Y I D
5217   gggggtactgcagaaaaacttaagaatatgccaatgaatggtagcaagcgtataattgacgctggttgtttcattaatgtatac
477    G G T A E K L K N M P M N G S K R I I D A G C F I N V Y
5301   cctacaacacaaacattaggtacggttcaagaattaacacgtttctcaacaggtcgtaaaatggttaaaatggtgcgtggtatg
505    P T T Q T L G T V Q E L T R F S T G R K M V K M V R G M
5385   actttagacgtatttacgttaaaatgggattatggattatggacaacaatcaaaactgacgcaccatatcaagaatatttggaa
533    T L D V F T L K W D Y G L W T T I K T D A P Y Q E Y L E
5469   gcaagtcaatacaataactggattgcttatgtaacaacagctggtgagtattacattacaggtaaccaaatggaattatttaga
561    A S Q Y N N W I A Y V T T A G E Y Y I T G N Q M E L F R
5553   gacgcgccagaagaaattaaaaaagtgggtgcatggttacgtgtgtcaagtggtaacgcagtcggtgaagtaagacaaacatta
589    D A P E E I K K V G A W L R V S S G N A V G E V R Q T L
5637   gaggctaatatatcggaatataaagaattcttcagtaatgttaatgcggaaacaaaacatcgtgaatatggttgggtagcaaaa
617    E A N I S E Y K E F F S N V N A E T K H R E Y G W V A K
5721   catcaaaaatag 5732
645    H Q K *
44AHJDORF003
6626   atgagaaagttaacgaatttttaagtttttctataacacaccgtttacagactatcaaaacacgattcatttttaatagtaataaa
1      M R K L T N F K F F Y N T P F T D Y Q N T I H F N S N K
6710   gaacgtgatgattatttttttaaatggtcgtcattttaaatcgttagactattcaaaacaaccgtataatttttatacgtgataga
29     E R D D Y F L N G R H F K S L D Y S K Q P Y N F I R D R
6794   atggaaatcaatgttgatatgcagtggcatgacgcacaaggtattaactacatgacgtttttatcagatttttgaggatagaaga
57     M E I N V D M Q W H D A Q G I N Y M T F L S D F E D R R
6878   tattacgcttttgtaaaccaaatcgaatacgtgaatgacgttgtggttaaaatatattttgtcattgataccattatgacgtat
85     Y Y A F V N Q I E Y V N D V V V K I Y F V I D T I M T Y
6962   acacaagggaatgtattagagcaactctcaaacgtcaatattgaacgtcaacatttatcaaaacgcacgtataactatatgtta
113    T Q G N V L E Q L S N V N I E R Q H L S K R T Y N Y M L
7046   ccaatgttacgtaataatgatgatgtgttaaaagtatcaaataaaaactatgtttataaccaaatgcaacaatatttggaaaat
141    P M L R N N D D V L K V S N K N Y V Y N Q M Q Q Y L E N
7130   ttagtattattccagtcaagcgctgatttatcaaagaaatttggtactaaaaaagagccaaacttagatacgtcaaaaggtacg
169    L V L F Q S S A D L S K K F G T K K E P N L D T S K G T
7214   atttatgacaatatcacatcaccagtcaacttatacgttatggaatatggtgactttattaactttatggataaaatgagtgcc
197    I Y D N I T S P V N L Y V M E Y G D F I N F M D K M S A
7298   tatccatggattacgcaaaactttcaaaaggttcaaatgttacctaaagactttattaatacaaaagacttagaggacgttaaa
225    Y P W I T Q N F Q K V Q M L P K D F I N T K D L E D V K
7382   accagtgaaaaaattacaggattaaaaacattaaaacagggtggtaaatcaaaagaatggagtctaaaagatttatcattaagt
253    T S E K I T G L K T L K Q G G K S K E W S L K D L S L S
7466   ttctcaaatcttcaagagatgatgttatctaaaaaagatgaatttaaacatatgatacgtaatgagtatatgacaattgaattt
281    F S N L Q E M M L S K K D E F K H M I R N E Y M T I E F
7550   tatgactggaatggaaatacgatgttactcgacgctggtaagatttcacaaaaaactggtgttaagttacgtacaaaatcaatt
309    Y D W N G N T M L L D A G K I S Q K T G V K L R T K S I
7634   attggttatcataatgaagttcgagtatatccagtagattataacagtgctgaaaacgacagaccaatactcgctaaaaataaa
337    I G Y H N E V R V Y P V D Y N S A E N D R P I L A K N K
7718   gaaatattgattgatacgggttcattcttaaatacaaatataacatttaatagttttgcacaagtaccaatattaatcaataat
365    E I L I D T G S F L N T N I T F N S F A Q V P I L I N N
7802   ggtatcttaggacaatcacaacaagccaaccgacaaaaaaatgcagaaagtcaattaattacaaatcgtattgataatgtatta
393    G I L G Q S Q Q A N R Q K N A E S Q L I T N R I D N V L
7886   aatggtagcgacccgaaatcacgcttttatgacgctgtgagtgtagcaagtaatttaagtccaactgctttatttggtaagttt
421    N G S D P K S R F Y D A V S V A S N L S P T A L F G K F
7970   aatgaagaatataatttctacaaacaacaacaagctgaatataaagatttagccttacaaccaccttctgtaactgaatcagaa
449    N E E Y N F Y K Q Q Q A E Y K D L A L Q P P S V T E S E
8054   atgggcaacgcattccaaattgcgaatagcattaacggtttaacgatgaaaattagtgtaccgtcacctaaagaaattacattt
477    M G N A F Q I A N S I N G L T M K I S V P S P K E I T F
8138   ttacaaaaatattatatgttgtttggttttgaagtgaatgactataattcatttattgaaccaattaacagtatgactgtttgc
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505 L Q K Y Y M L F G F E V N D Y N S F I E P I N S M T V C
8222 aattatttaaaatgtacaggtacgtatactatacgtgacatcgaccccatgttaatggaacaattaaaagcaatttagaatct
533 N Y L K C T G T Y T I R D I D P M L M E Q L K A I L E S
8306 ggtgtaagatttggcataatgacggttcaggtaatccaatgttacaaaatccattaaataacaaatttagagaggggtataa
8389
561 G V R F W H N D G S G N P M L Q N P L N N K F R E G V *
44AHJDORF004
8764 atgatactgaaaagagtgataacaatgaacgatcaagagaagatagataaatttacgcattcctatattaatgatgatttggt
1 M I L K R V I T M N D Q E K I D K F T H S Y I N D D F G
8848 ttaacgatagaccagttagtccctaaagtaaaaggatatgggcgctttaatgtatggcttggtggtaatgaaagtaaaatcaga
29 L T I D Q L V P K V K G Y G R F N V W L G G N E S K I R
8932 caagtattaaaagcagtaaaagagataggtgtttcacctactctttttgccgtatatgaaaaaaatgagggttttagttctgga
57 Q V L K A V K E I G V S P T L F A V Y E K N E G F S S G
9016 cttggttggttaaaccatacgtctgcacgtggtgattatttaacagatgctaaattcatagcaagaaagttagtatcacaatca
85 L G W L N H T S A R G D Y L T D A K F I A R K L V S Q S
9100 aaacaagctggacaaccgtcttggtatgacgcaggtaacatcgtccactttgtaccacaagacgtacaaagaaaaggtaatgca
113 K Q A G Q P S W Y D A G N I V H F V P Q D V Q R K G N A
9184 gatttgcaaaaaatatgaaagcaggtacaattggacgtgcatatattccattaacagcagctgctacttgggcggcatattat
141 D F A K N M K A G T I G R A Y I P L T A A A T W A A Y Y
9268 cctttaggtttgaaagcatcatataacaaagtacaaaactatggtaatccatttttagacggtgcgaatactattctagcttgg
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9352 ggtggtaaattagacggtaaaggtggatcacctagtgattcgtctgacagtggtagtagtggtgacagtggtagttcactactc
197 G G K L D G K G G S P S D S S D S G S S G D S G S S L L
9436 gctttagcaaaacaagccatgcaagaattattaaaaaaaatacaagacgcattacaatgggacgttcatagtattggtagtgat
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9520 aaatttttagtaatgattatttacattagaaaaacatttaacaacacatatcatattaaaatgacgattggtttacttgat
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9604 tcattaaaaaaactgattgatagcgttcaagtagatagtgggagtagtagttctaatcctactgatgatgacggagaccataaa
281 S L K K L I D S V Q V D S G S S S S N P T D D D G D H K
9688 ccaattagtggtaaatcagtcaagccaaatggaaaaagtggtcgtgtgattggtggtaactggacatatgcacagttaccagaa
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9772 aaatataaaaaagcaattggtgtacctttattcaaaaaagaatacttatacaaaccaggtaacatatttcctcaaacgggtaat
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9856 gcaggacaatgtacagaattaacatgggcgtatatgtcacaactacatggtaaaagacaacctaccgacgacggtcaaataaca
365 A G Q C T E L T W A Y M S Q L H G K R Q P T D D G Q I T
9940 aacggtcagcgtgtatggtacgtctataaaaagttaggtgcaaaaacaacacataatccaacagtaggttatggtttctctagt
393 N G Q R V W Y V Y K K L G A K T T H N P T V G Y G F S S
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421 K P P Y L Q A T A Y G I G H T G V V V A V F E D G S F L
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10192 ggtgataatattgtattctttagtggtattgcttaa 10227
477 G D N I V F F S G I A *
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29 N Q I E L V D E L M N D D I D Y Y I S I S N R S D G K S
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13638 gacgcttaccgtgatttattgaagaaatcatagatgaaaatccactatttaaatcaaaacgtgtcacgttcagaagtgctagg
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113 D Y L A I I Y Q D K E I G V I T D L N S A T D L K Y H S
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13386 ttaaaaacaatatatgaatcaatcgaccgtaaccatggtaacgttgattatattggattccctaaaatgtttttactaggtaat
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13302 gcagtcaacttttcaagtcctatattatccaatttaaatatatacaatttattacaaaagcataaaatgaatacatcaagactt
197 A V N F S S P I L S N L N I Y N L L Q K H K M N T S R L
13218 tacaaaaacatttttttagaaatgcgacgaaacgattacgtgaatgaaaaacgtaacacacgtgcgtttaattcaaatgacgac
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253 A M T T G E F E F N E Y N L A D D N L R N H I N Q N G D
13050 ttcttctatatcaaaactgatgataaatatattaaagtcatgtataatgtaactactttatgacaaatattatcgttgtacca
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12966 tatacaaaacaatatgaattttgtactaaaattagggatatagacaatcatgttacctatttacgtgatgatatgttttataaa
309 Y T K Q Y E F C T K I R D I D N H V T Y L R D D M F Y K

12882 gaaaacatggaacgttattactacaatccaagcaatttacatttgacaatgcttactctaaaaattacgtggttgataatgat
337 E N M E R Y Y Y N P S N L H F D N A Y S K N Y V V D N D
12798 agatatttatatttagatatgaataaaattataaaatttcatataaaaaatgaaatgaagaaaaatatgagtgagtttgaaaga
365 R Y L Y L D M N K I I K F H I K N E M K K N M S E F E R
12714 aaagaaaaaatatacgaagataactatatagagaatacgaaaaagtatctaatgaaacaatatggcttataa 12643
393 K E K I Y E D N Y I E N T K K Y L M K Q Y G L *
44AHJDORF006

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29 Y S K S W T F G D K W D N S N T M F E T F V N K Y L F P
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57 K I N E T L L I D I A L G N R F N W L A K E Q D F I G Q
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113 Y P R M A T K L Y G N G I V K K Q K F T L N N N D T R F
1223 aatttccaaacattagcagacgcaactaattacgctttaggtgtatacaaaaagaaaatttctgatattaatgtattagaagaa
141 N F Q T L A D A T N Y A L G V Y K K K I S D I N V L E E
1307 aaagaaatgcgtgcaatgttagttgattactcattgaatcaattatccgaaacaaatgtacgtaaagcaacatcaaaagaagat
169 K E M R A M L V D Y S L N Q L S E T N V R K A T S K E D
1391 ttagcaagcaaagtttttgaagcaatcctaaacttacaaaacaacagtgctaaatataatgaagtacatcgtgcatcaggtggt
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1643 aaagtaacaaaagaatttaagttacaaaaccaagattcaattgactttttacgtgcgtatggagattatcaatcacaattagga
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309 D T I P V G A V F T Y D V S K L K E F T G N V E E I K P
1811 aaatcagatttatatgcgtttattttggatattaattcaattaaatataaacgttacacaaaaggtatgttaaaaccaccattc
337 K S D L Y A F I L D I N S I K Y K R Y T K G M L K P P F
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1979 attactgaccaagatgtaaatccaaaaccagaggaagaattacaagaataa 2029
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1 M N N D K R G L N V E L S K E I S K R V V E H R N R F K
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29 R L M F N R Y L E F L P L L I N Y T N R D T V G I D F I
2212 cagttagaatcagctttaagacaaaacattaatgtagttgttggtgaagctagaaataagcaaattatgattcttggttatgta
57 Q L E S A L R Q N I N V V V G E A R N K Q I M I L G Y V
2296 aataacacttacttcaatcaagcaccaaatttttcatcaaactttaatttccaattccaaaaacgattaactaaagaagatata
85 N N T Y F N Q A P N F S S N F N F Q F Q K R L T K E D I
2380 tattttattgtacctgactatttaatacctgatgattgtctacaaattcataagctatatgataactgtatgagtggtaacttt
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2464 gttgtcatgcaaaataaaccaattcaatataatagtgatatagaaattatagaacattatactgatgaattagcagaagttgct
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2548 ttatctcgcttttctttaatcatgcaagcaaaatttagcaagatatttaaatcagaaattaatgacgagtcaatcaatcaactt
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2632 gtgtccgaaatatataacggtgcaccatttgttaaaatgtcacctatgtttaatgcagatgacgatatcattgatttaacaagt
197 V S E I Y N G A P F V K M S P M F N A D D D I I D L T S
2716 aatagcgtaatcccagcattaactgaaatgaaacgggaatatcaaaacaaaattagtgaattaagtaactatttaggcattaat
225 N S V I P A L T E M K R E Y Q N K I S E L S N Y L G I N
2800 tcattagccgttgataaagaaagcggtgtttcagacgaagaggcaaaaagtaatcgtggatttaccacatcaaacagtaatatc
253 S L A V D K E S G V S D E E A K S N R G F T T S N S N I
2884 tatttaaaaggtcgtgaaccaattacgtttttatcaaagcgttatggtttagatattaaaccgtattacgatgatgaaacaacg
281 Y L K G R E P I T F L S K R Y G L D I K P Y Y D D E T T
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309 S K I S M V D T L F K D E S S D I N G *
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29 K L T F Y D D E F Q F M Q K M L K F D K D V L A I V N E
3188 aaagtatttaaaggtttttcattgaaagatgaattatcagatttactttttaaaaaatcatttacgattcattttttagataga
57 K V F K G F S L K D E L S D L L F K K S F T I H F L D R
3272 gaaatcaacagacaaacagttgaagcatttggcatgcaagtgattactgtatgtattacacatgaggattatttaaatgtggtt
85 E I N R Q T V E A F G M Q V I T V C I T H E D Y L N V V
3356 tattcatcaagtgaagttgaaaaatacttacaatcacaaggcttcacagaacacaatgaagatacaacaagtaacactgatgaa
113 Y S S S E V E K Y L Q S Q G F T E H N E D T T S N T D E
3440 acatcgaatcaaaatgctacatctttagacaattcaactggcatgactgcaaacagaaacgcttatgtgtcattaccacaaagt
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3524 gaggttaacattgatgttgataatacaacgttacgattcgctgataataatacgattgataacggtaaaactgtgaataaatcg
169 E V N I D V D N T T L R F A D N N T I D N G K T V N K S
3608 agtaacgaaagtaatcaaaacgcaaaacgtaatcaaaatcaaaaaggtaatgcaaaaggtacacaattcactaagcagtattta
197 S N E S N Q N A K R N Q N Q K G N A K G T Q F T K Q Y L
3692 attgataatattgataaagcgtacgatttaagaaagaaaattttaaatgaatttgataaaaaatgttttttacaaatttggtag
3775
225 I D N I D K A Y D L R K K I L N E F D K K C F L Q I W *
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29 C M D L S V A Y V Y Y I T D G K V R M W G N A K D A I N
5912 aatgactttaaaggtttagcgacggtgtataaaaatacaccgagctttaaacctcaattaggggacgttgctgtatatacaaat
57 N D F K G L A T V Y K N T P S F K P Q L G D V A V Y T N
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6080 tttgacggttgggaaaaagcaaccattagaacacattattatgacggtgtaactcactttattagacctaaatttcaggtagt
113 F D G W E K A T I R T H Y Y D G V T H F I R P K F S G S
6164 aatagcaaagcattagaaacatcaaaagtaaatacatttggaaaatggaaacgaaaccaatacggcacatattatagaaatgaa
141 N S K A L E T S K V N T F G K W K R N Q Y G T Y Y R N E
6248 aatggtacatttacatgtggtttttaccaatatttgcacgtgtcggtagtccaaaattatcagaacctaatggctattggttc
169 N G T F T C G F L P I F A R V G S P K L S E P N G Y W F
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6416 tattatttaccagtgcgccaatggaatggaaaaacaggtaatagttacagtgttggtattccttggggggtgttctcataa 6496
225 Y Y L P V R Q W N G K T G N S Y S V G I P W G V F S *
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57 P Y F P K E R N V S Y V N A V S L V R G S R H K K L N Y
14168 attcttgaaatatataaccgtaatgatgattctaataataaaaacgctaaaaagcataaatacgctttatataatttacaagct
85 I L E I Y N R N D D S N N K N A K K H K Y A L Y N L Q A
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113 K N N N S S M Y K Y I K E I D T L Y K E I G K S D R P V
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141 T N I D D E D V R Y N F L Y Y A T F D E *
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15257 tactcaatcaatttggtcaagtatcattttaa 15225
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8643 ctactcatgattacaatattttattatattgcaaatgagggactttctattgtagaaaattgtgcagaaatggacgtattagta
85 L L M I T I F Y Y I A N E G L S I V E N C A E M D V L V
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8811 taa 8813
141 *
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1 M K I K T T F R L N N L I Y Y L L T N R D Y Y N D K F E
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14828 tttgaaattgaaaaagagttatttacgttagatatcgacattgatattaaaaaacatgtttttaatatacttgtattttattat
57 F E I E K E L F T L D I D I D I K K H V F N I L V F Y Y
14744 agaaattatttaagtaatgaattaataagagaaattttattaaacgttacaattgacgacgtattatcaaattttgataaacct
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113 L E S E L M I I Y Q N K V I Y D N G K V I D H E *
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199 atgacagaatttgatgaaatcgtaaaaccagacgacaaagaagaaacttcagaatcaactgaagaaaatttagaatcaactgaa
1 M T E F D E I V K P D D K E E T S E S T E E N L E S T E
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29 E T S E S T E E S T E E S T E E S T E D K T V E T I E E
367 gaaaatgaaaacaaattagaacctactacaacagatgaagatagttcgaaatttgaccctgttgtattagaacaacgtattgct
57 E N E N K L E P T T T D E D S S K F D P V V L E Q R I A
451 tcattagaacaacaagtgactactttttttatcttcacaaatgcaacaaccacaacaagtacaacaaacacaatcagatgtaaca
85 S L E Q Q V T T F L S S Q M Q Q P Q Q V Q Q T Q S D V T
535 gaatcaaacaaagaagataacgactattcagatgaagaactagttgataagttagatttagattag 600

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113     E S N K E D N D Y S D E E L V D K L D L D *
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16172   atggttaatgttgataatgcaccagaagaaaaaggacaagcctatactgaaatgttgcaactattcaataaactgattcaatgg
1       M V N V D N A P E E K G Q A Y T E M L Q L F N K L I Q W
16088   aatccagcttatacatttgacaatgcaattaacttattatcggcttgccaacaactattattaaactataatagttctgttgtt
29      N P A Y T F D N A I N L L S A C Q Q L L L N Y N S S V V
16004   caattcttaaatgatgaactaaacaacgaaactaaaccagaatcaatattgtcttatattgctggtgatgacccaatagaacaa
57      Q F L N D E L N N E T K P E S I L S Y I A G D D P I E Q
15920   tggaatatgcataaaggattttatgaaacgtataacgtttacgtttttag 15870
85      W N M H K G F Y E T Y N V Y V F *
44AHJDORF014
6243    atgaaaatggtacatttacatgtggtttttaccaatatttgcacgtgtcggtagtccaaaattatcagaacctaatggctatt
1       M K M V H L H V V F Y Q Y L H V S V V Q N Y Q N L M A I
6327    ggttccaaccaaacggttatacaccatataacgaagtttgtttatcagatggttacgtatggattggttataactggcaaggca
29      G S N Q T V I H H I T K F V Y Q M V T Y G L V I T G K A
6411    cacgttattatttaccagtgcgccaatggaatggaaaaacaggtaatagttacagtgttggtattccttgggggtgttctcat
57      H V I I Y Q C A N G M E K Q V I V T V L V F L G G C S H
6495    aatgggtattttagcctttttctttga 6521
85      N G Y F S L F L *
44AHJDORF015
15403   gtgacgataacaccttgttcaccgaattttgattctttgtttgtgaataatgctctaacgatatactctttttcataccgtat
1       V T I T P C S P N F D S L F V N N A L T I Y S F F I P Y
15487   ttttctactaattctgatagtttgataaattctctttctttttcctcaaattcaaatctcgctaatgtgttttggtgtcttgat
29      F S T N S D S L I N S L S F S S N S N L A N V F W C L D
15571   aaaatatcttttacgtttgtcattttatttctcctcttatttaaattatttgctttctgcaattgcgatttgtag 15645
57      K I S F T F V I L F L L L F K L F A F C N C D L *
44AHJDORF016
15852   atgaaagttgacgacattgttaccttacgtgtcaaaggttatatacttcattacttagatgatgataatgaatacattgaggaa
1       M K V D D I V T L R V K G Y I L H Y L D D D N E Y I E E
15768   tttttaccacttcacgagtatcatttaaccaaaacacaagcaaaagaattattaccagacacatgtaaactattgtccactaca
29      F L P L H E Y H L T K T Q A K E L L P D T C K L L S T T
15684   cgcacaacgaaaacaattcaagtttattacaatgatttactacaaatcgcaattgcagaaagcaaataa 15616
57      R T T K T I Q V Y Y N D L L Q I A I A E S K *
44AHJDORF017
10757   atggaaagattaaaattgcttctgctggtataccgaaaaacgcctttgatacaagcgtcgatttgaaacctttgtacgtgaac
1       M E R L K L L L L V Y R K T P L I Q A S I L K P L Y V N
10673   aattctttgacggtgccattattgaaaacaataaaagtatctataatgagcaaggtacaatatcgatatatccgtctaaaactg
29      N S L T V P L L K T I K V S I M S K V Q Y R Y I R L K L
10589   aaattgtatgtggtaatgtatatgatgaatatttactgatgaacttaatatga 10536
57      K L Y V V M Y M M N I L L M N L I *
44AHJDORF018
1098    atgttaattggtactgtgtccataatcacgtattcttcactatattgtccaataaaatcttgctctttagctaaccaattaaaa
1       M L I G T V S I I T Y S S L Y C P I K S C S L A N Q L K
1014    cgattacctaatgcaatatcgattaataaagtctcattaatcttagggaataaatatttatttacaaatgtttcgaacattgta
29      R L P N A I S I N K V S L I L G N K Y L F T N V S N I V
930     tttgaattatcccatttgtcgccaaatgtccaagattttgaataa 886
57      F E L S H L S P N V Q D F E *
44AHJDORF019
9836    atgttacctggtttgtataagtattctttttgaataaaggtacaccaattgctttttttatatttttctggtaactgtgcatat
1       M L P G L Y K Y S F L N K G T P I A F L Y F S G N C A Y
9752    gtccagttaccaccaatcacacgaccacttttccatttggcttgactgatttaccactaattggtttatggtctccgtcatca
29      V Q L P P I T R P L F P F G L T D L P L I G L W S P S S
9668    tcagtaggattagaactactactcccactatctacttga 9630
57      S V G L E L L L P L S T *

44AHJDORF121
16362   atggaaaatgaaacaaaaaacattgagttgaagcatgtttttcgttttaagaatggaagtttatgtatagcgttatttgataga
1       M E N E T K N I E L K H V F R F K N G S L C I A L F D R
16278   acagaaaatgaaatttcattttatgatgttgacattgatgaaattgaagatttaaatcataattctgttttacgcgtaatttca
29      T E N E I S F Y D V D I D E I E D L N H N S V L R V I S
16194   actttattaggaagtgataataatggttaa 16165
57      T L L G S D N N G *
44AHJDORF020
13865   atgtctaaacgatttgttttaccatgtttttgctccttgtaatagtttatgatgtcgtttacagtgttaaatttattcgtcaa
1       M S K R F C F T M F L L L V I V Y D V V Y S V K F I R Q
13949   atgttgcataatataaaaagttatacctcacatcttcatcatcaatatttgtcactggtctatctgatttaccaatttctttat
29      M L H N I K S Y T S H L H H Q Y L S L V Y L I Y Q F L Y
14033   ataaagtatcgatttctttaa 14053
57      I K Y R F L *
44AHJDORF123
614     atgtatgagggaaacaacatgcgttctatgatgggtacatcatatgaagattcaagattaaataaacgaacagaattaaatgaa
1       M Y E G N N M R S M M G T S Y E D S R L N K R T E L N E
698     aacatgtcaattgatacaaataaaagtgaagatagttatggtgtacaaattcattcactttcaaaacaatcatttacaggtgac
29      N M S I D T N K S E D S Y G V Q I H S L S K Q S F T G D
782     gttgaggaggaataa 796
57      V E E E *
```

44AHJDORF021
5816 atgcaccatcaaagtcaacacctgccccctcatgcttatatatccattcttttgcttgttgttgtgatttcatttatatcactc
1 M H H Q S Q H L P P H A Y I S I L L L V V V I S F I S L
5732 ctattttgatgtttgctacccaaccatattcacgatgttttgtttccgcattaacattactgaagaattctttatattccga
29 L F L M F C Y P T I F T M F C F R I N I T E E F F I F R
5648 tatattagcctctaa 5634
57 Y I S L *
44AHJDORF022
8611 atgtttgctaaaatgataatacagaatatcaataatttttagaaaatcctctcattgatttttttgaccataagttattatt
1 M F A K M I I Q N I N N F L E N P L I D F F D H K L L F
8527 ttaattgcttttgaaatacctgtaataatatcaacgaacattaatacaaataaaaagtag 8468
29 L I A F E I P V I I S T N I N T N K K *
44AHJDORF023
6494 atgagaacacccccccaaggaataccaacactgtaactattacctgtttttccattccattggcgcactggtaaataataacgtg
1 M R T P P K E Y Q H C N Y Y L F F H S I G A L V N N N V
6410 tgccttgccagttataaccaatccatacgtaaccatctgataaacaaacttcgttatatggtgtataaccgtttggttggaacc
29 C L A S Y N Q S I R N H L I N K L R Y M V Y N R L V G T
6326 aatagccattag 6315
57 N S H *
44AHJDORF024
14275 gtgtcaatgtacgcctcttgtaaatctttatcatcaaatttaaaattaacattactaaaatcatttaaaaataaatctttttct
1 V S M Y A S C K S L S S N L K L T L L K S F K N K S F S
14359 tgctcttttctagcttctctttctttttccatctatccatttcagacgtatgtctaaccaatgttatcaacctccatataaag
29 C S F L A S L S F F H L S I S D V C L T N V I N L H I K
14443 cataaataa 14451
57 H K *
44AHJDORF025
15175 atggaacgtaaatacaaaacggtattattatattgcgatgagattaaaggacattttccacatcaaatctcaatgtttgaagat
1 M E R K Y K T V L L Y C D E I K G H F P H Q I S M F E D
15091 ttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaaatacgcgtatatcatagaatacattaag
29 L Y D A K V V Y S Y Y E Y N L F T K K Y A Y I I E Y I K
15007 gagatataa 14999
57 E I *
44AHJDORF026
14593 atgaataacctattaaacatagccattgttttccttttagcattttttaattacacttatcatacttatgacactgcatatacgc
1 M N N L L N I A I V F L L A F L I T L I I L M T L H I R
14509 gtgtcatttggtgttttattcactacattgattatattctatattatctttttaatggttatttatgctttatatggaggttga
14426
29 V S F G V L F T T L I I F Y I I F L M V I Y A L Y G G *
44AHJDORF027
12916 atgattgtctatatccctaattttagtacaaaattcatattgttttgtatatggtacaacgataatatttgtcataaaagtagt
1 M I V Y I P N F S T K F I L F C I W Y N D N I C H K S S
13000 tacattatacatgactttaatatatttatcatcagttttgatatagaagaaatcaccgttttgattgatgtgatttcttaa
13080
29 Y I I H D F N I F I I S F D I E E I T V L I D V I S *
44AHJDORF029
15183 gtgtttaaatggaacgtaaatacaaaacggtattattatattgcgatgagattaaaggacattttccacatcaaatctcaatgt
1 V F K W N V N T K R Y Y Y I A M R L K D I F H I K S Q C
15099 ttgaagatttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaaatacgcgtatatcatag
15019
29 L K I Y M T L K L Y I H I M N I T C S L K N T R I S *

44AHJDORF028
9235 atggaatatatgcacgtccaattgtacctgctttcatatttttgcaaaatctgcattacctttttctttgtacgtcttgtggta
1 M E Y M H V Q L Y L L S Y F L Q N L H Y L F F V R L V V
9151 caaagtggacgatgttacctgcgtcataccaagacggttgtccagcttgtttgattgtgatactaactttcttgctatga 9071
29 Q S G R C Y L R H T K T V V Q L V L I V I L T F L L *
44AHJDORF030
14487 gtgaataaaacaccaaatgacacgcgtatatgcagtgtcataagtatgataagtgtaattaaaaatgctaaaaggaaaacaatg
1 V N K T P N D T R I C S V I S M I S V I K N A K R K T M
14571 gctatgtttaataggttattcatggtcaatcactttcccattatcgtatatgactttgttttgataaataatcattaa 14648
29 A M F N R L F M V N H F P I I V Y D F V L I N N H *
44AHJDORF031
11039 atgatattgtatagttcattgttatcatctaaacggaataagttaaaatgtgaacgtaatgcaggtatgccatataatccattt
1 M I L Y S S L L S S K R N K L K C E R N A G M P Y N P F
11123 aaaacgactttagataacataacctcctcatttgagtatgggtgttcgttgatatcatcagtaatgtga 11191
29 K T T L D N I T S S F E Y G C S L I S S V M *
44AHJDORF135
693 atgaaaacatgtcaattgatacaaataaaagtgaagatagttatggtgtacaaattcattcactttcaaaacaatcatttacag
1 M K T C Q L I Q I K V K I V M V Y K F I H F Q N N H L Q
777 gtgacgttgaggaggaataataaattatggcacaacaatctacaaaaaatgaaactgcacttttag 842
29 V T L R R N N K L W H N N L Q K M K L H F *
44AHJDORF033
3795 atgccattatttaaccacctctaccaaatttgtaaaaaacatttttttatcaaattcatttaaaatttttcttttcttaaatcgtac
1 M P L F N H L Y Q I C K K H F L S N S F K I F F L K S Y

3711 gctttatcaatattatcaattaaatactgcttagtgaattgtgtaccttttgcattaccttttga 3646
29 A L S I L S I K Y C L V N C V P F A L P F *

44AHJDORF032
9455 atggcttgttttgctaaagcgagtagtgaactaccactgtcaccactactaccactgtcagacgaatcactaggtgatccacct
1 M A C F A K A S S E L P L S P L L P L S D E S L G D P P
9371 ttaccgtctaatttaccaccccaagctagaatagtattcgcaccgtctaaaaatggattaccatag 9306
29 L P S N L P P Q A R I V F A P S K N G L P *

44AHJDORF034
14146 atgatgattctaataataaaaacgctaaaaagcataaatacgctttatataatttacaagctaaaaataataattcttcaatgt
1 M M I L I I K T L K S I N T L Y I I Y K L K I I I L Q C
14062 ataaatatattaaagaaatcgatactttatataaagaaattggtaaatcagatagaccagtga 14000
29 I N I L K K S I L Y I K K L V N Q I D Q *

44AHJDORF035
13957 atgcaacatttgacgaataaatttaacactgtaaacgacatcataaactattacaaggagcaaaaacatggtaaaacaaaatcg
1 M Q H L T N K F N T V N D I I N Y Y K E Q K H G K T K S
13873 tttagacatggtaagagattatcaaaatgctgtcaatcatgtcagaaaaaaaatcccagataa 13811
29 F R H G K R L S K C C Q S C Q K K N P R *

44AHJDORF036
10165 gtgtatacaataccacacgtgatggtgcaacatatggtggtacattatagtttgcaactaaaaacgaaccatcttcaaaaactg
1 V Y T I P H V M V Q H M V V H Y S L Q L K T N H L Q K L
10081 ctacaacaacacctgtgtgaccaataccatatgcagttgcttgtaagtatggtggtttactag 10019
29 L Q Q H L C D Q Y H M Q L L V S M V V Y *

44AHJDORF037
14788 atgtcgatatctaacgtaaataactcttttcaatttcaaaatcatcatattgtttgtcaaactcaatatacacatcacccata
1 M S I S N V N N S F S I S K S S Y C L S N S I Y T S P I
14872 tttattttactatacatttttattagatgaagtaaatttttcaaatttatcattataa 14931
29 F I F T I H F L L D E V N F S N L S L *

44AHJDORF038
3671 gtgtaccttttgcattaccttttgatttgattacgttttgcgttttgattactttcgttactcgatttattcacagttttac
1 V Y L L H Y L F D F D Y V L R F D Y F R Y S I Y S Q F Y
3587 cgttatcaatcgtattattatcagcgaatcgtaacgttgtattatcaacatcaatgttaa 3528
29 R Y Q S Y Y Y Q R I V T L Y Y Q H Q C *

44AHJDORF039
1743 gtgctgtatttacttatgatgtatctaaacttaaagagtttactggcaacgttgaagaaattaaaccaaaatcagatttatatg
1 V L Y L L M M Y L N L K S L L A T L K K L N Q N Q I Y M
1827 cgtttatttggatattaattcaattaaatataaacgttacacaaaaggtatgttaa 1883
29 R L F W I L I Q L N I N V T Q K V C *

44AHJDORF040
9740 gtggtaactggacatatgcacagttaccagaaaaatataaaaaagcaattggtgtacctttattcaaaaaagaatacttataca
1 V V T G H M H S Y Q K N I K K Q L V Y L Y S K K N T Y T
9824 aaccaggtaacatatttcctcaaacgggtaatgcaggacaatgtacagaattaa 9877
29 N Q V T Y F L K R V M Q D N V Q N *

44AHJDORF041
15836 atgtcgtcaactttcattattatatcactccctttctaaaaaacgtaaacgttatacgtttcataaaatcctttatgcatattcc
1 M S S T F I I I S L L S K K R K R Y T F H K I L Y A Y S
15920 attgttctattgggtcatcaccagcaatataagacaatattgattctggtttag 15973
29 I V L L G H H Q Q Y K T I L I L V *

44AHJDORF042
5151 atgcacgaccgtcgtcttttgttaatttatagttttgtgaacctcttgcgcgtaatgcttcaaagtgttcatactcaccaagtt
1 M H D R R L L L I Y S F V N L L R V M L Q S V H T H Q V
5067 ggaagaaaccatataaattatggaaacgttttccaccaccgccgtttgtcatag 5014
29 G R N H I N Y G N V F H H R R L S *

44AHJDORF043
4539 atgcgacttgtaacagttttgcaacaccatcgtgatgtaaccagattttcatttcaccattggattgacgttctaatccgattg
1 M R L V T V L Q H H R D V T R F S F H H W I D V L I R L
4455 ttgtaccatgaccaccctgtacaatacgcatgcttgaaattaagtcaccactag 4402
29 L Y H D H P V Q Y A C L K L S H H *

44AHJDORF044
12917 atgttacctatttacgtgatgatatgttttataaagaaaacatggaacgttattactacaatccaagcaatttacattttgaca
1 M L P I Y V M I C F I K K T W N V I T T I Q A I Y I L T
12833 atgcttactctaaaaattacgtggttgataatgatagatatttatatttag 12783
29 M L T L K I T W L I M I D I Y I *

44AHJDORF149
770 atgattgttttgaaagtgaatgaatttgtacaccataactatcttcacttttatttgtatcaattgacatgttttcatttaatt
1 M I V L K V N E F V H H N Y L H F Y L Y Q L T C F H L I
686 ctgttcgtttatttaatcttgaatcttcatatgatgtacccatcatag 639
29 L F V Y L I L N L H M M Y P S *

44AHJDORF046
4891 atgattatccatttaagttatcatatcaagacggtattaatttcccacgtgataactttaaagagcctgagggtatttgcattt
1 M I I H L S Y H I K T V L I S H V I T L K S L R V→F A F
4975 atacaaatccaaaaacaaaacgtaaatcgttattacttgctatga 5019
29 I Q I Q K Q N V N R Y Y L L *

44AHJDORF047
11911 atgaatgtatgtaagttgttcaggtgtgagttttgcaaaacatttcacagcatagtcataggcttcactatcattcatatcatt
1 M N V C K L F R C E F C K T F H S I V I G F T I I H I I

11995 atctttatcaaaaatcgtataattaaaatctgtttaagttgtga 12039
29 I F I K N R I I K I C F K L *

44AHJDORF045
10655 atggcaccgtcaaagaattgttcacgtacaaaggtttcaaaatcgacgcttgtatcaaaggcgtttttcggtataccagcagaa
1 M A P S K N C S R T K V S K S T L V S K A F F G I P A E
10739 gcaattttaatctttccattcacttcatatgcatatttcttatga 10783
29 A I L I F P P T S Y A Y F L *

44AHJDORF048
15340 atgaggacgttgttgacattatcaatgctggagaagttcaattcacaatttatgaatatgaaaacaaaaaaggtcaaaaaggtt
1 M R T L L T L S M L E K F N S Q F M N M K T K K V K K V
15256 actcaatcaatttggtcaagtatcattttaatacaattcatag 15212
29 T Q S I L V K Y H F N T I S *

44AHJDORF049
5784 atgagggggcaggtgttgactttgatggtgcatatggatttcaatgtatggacttatcagttgcttatgtgtattacattactg
1 M R G Q V L T L M V H M D F N V W T Y Q L L M C I T L L
5868 acggtaaagttcgcatgtggggtaatgctaaagacgcgataa 5909
29 T V K F A C G V M L K T R *

44AHJDORF050
13158 gtgtgttacgttttttcattcacgtaatcgtttcgtcgcatttctaaaaaaatgtttttgtaaagtcttgatgtattcattttat
1 V C Y V F H S R N R F V A F L K K C F C K V L M Y S F Y
13242 gcttttgtaataaattgtatatatttaaattggataatatag 13283
29 A F V I N C I Y L N W I I *

44AHJDORF051
11066 atgataacaatgaactatacaatatcattaacggttacaaaaacactgaacgtaatatattattctctacatttgtcacatcac
1 M I T M N Y T I S L T V T K T L N V I Y Y S L H L S H H
10982 gttcattgtataacttattggttcctttccaatacttaa 10944
29 V H C I T Y W F L S N T *

44AHJDORF052
14338 atgatttttagtaatgttaattttaaatttgatgataaagatttacaagaggcgtacattgacacatggaaacattttgcacatc
1 M I L V M L I L N L M I K I Y K R R T L T H G N I L H I
14254 tgccctatttttcctaaagaaagaaacgtatcatatgtaa 14216
29 C P I F L K K E T Y H M *

44AHJDORF053
3348 atgtggtttattcatcaagtgaagttgaaaaatacttacaatcacaaggcttcacagaacacaatgaagatacaacaagtaaca
1 M W F I H Q V K L K N T Y N H K A S Q N T M K I Q Q V T
3432 ctgatgaaacatcgaatcaaaatgctacatctttag 3467
29 L M K H R I K M L H L *

44AHJDORF054
7551 atgactggaatggaaatacgatgttactcgacgctggtaagatttcacaaaaaactggtgttaagttacgtacaaaatcaatta
1 M T G M E I R C Y S T L V R F H K K L V L S Y V Q N Q L
7635 ttggttatcataatgaagttcgagtatatccagtag 7670
29 L V I I M K F E Y I Q *

44AHJDORF055
15705 atgtgtctggtaataattctttttgcttgtgttttggttaaatgatactcgtgaagtggtaaaaattcctcaatgtattcattat
1 M C L V I I L L L V F W L N D T R E V V K I P Q C I H Y
15789 catcatctaagtaatgaagtatataacctttga 15821
29 H H L S N E V Y N L *

44AHJDORF056
5512 gtgagtattacattacaggtaaccaaatggaattatttagagacgcgccagaagaaattaaaaaagtgggtgcatggttacgtg
1 V S I T L Q V T K W N Y L E T R Q K K L K K W V H G Y V
5596 tgtcaagtggtaacgcagtcggtgaagtaa 5625
29 C Q V V T Q S V K *

44AHJDORF057
10121 atgtaccaccatatgttgcaccatcacgtgtggtattgtatacactcattaatggcgtaccaaataatgctggtgataatattg
1 M Y H H M L H H H V W Y C I H S L M A Y Q I M L V I I L
10205 tattctttagtggtattgcttaattaa 10231
29 Y S L V V L L N *

44AHJDORF058
10767 atgcatatttcttatgattcagtacaaacatcttatctatctgttcgttttcaatatcccatttacctaaggctatcgggtcga
1 M H I S Y D S V Q T S Y L S V R F Q Y P I Y L R L S G R
10851 ataaactggggttcaataagggtttaa 10877
29 I N W G S I R V *

44AHJDORF164
702 atgttttcatttaattctgttcgtttatttaatcttgaatcttcatatgatgtacccatcatagaacgcatgttgtttccctca
1 M F S F N S V R L F N L E S S Y D V P I I E R M L F P S
618 tacatgtttaaattcctcctaatctaa 592
29 Y M F K F L L I *

44AHJDORF059
8360 atggatttttgtaacattggattacctgaaccgtcattatgccaaaatcttacaccagattctaaaattgcttttaattgttcca
1 M D F V T L D Y L N R H Y A K I L H Q I L K L L L I V P
8276 ttaacatggggtcgatgtcacgtatag 8250
29 L T W G R C H V *

44AHJDORF060
6257 atgtaccattttcatttctataatatgtgccgtattggtttcgtttccatttccaaatgtatttactttgatgtttctaatg
1 M Y H F H F Y N M C R I G F V S I F Q M Y L L L M F L M

6173 ctttgctattactacctgaaaatttag 6147
29 L C Y Y Y L K I *
44AHJDORF061
15551 atgtgttttggtgtcttgataaaatatcttttacgtttgtcattttatttctcctcttatttaaattatttgctttctgcaatt
1 M C F G V L I K Y L L R L S F Y F S S Y L N Y L L S A I
15635 gcgatttgtagtaaatcattgtaa 15658
29 A I C S K S L *
44AHJDORF062
4285 gtggtattcgcaacgcagttaaccaatctattaatattgataaagaaacaaatcacatgtactctacacaatccgattctcaaa
1 V V F A T Q L T N L L I L I K K Q I T C T L H N P I L K
4369 aacctgaaggtttttggataa 4389
29 N L K V F G *
44AHJDORF063
9487 atgcgtcttgtatttttttaataattcttgcatggcttgttttgctaaagcgagtagtgaactaccactgtcaccactactac
1 M R L V F F L I I L A W L V L L K R V V N Y H C H H Y Y
9403 cactgtcagacgaatcactag 9383
29 H C Q T N H *
44AHJDORF065
5029 gtggtggaaaacgtttccataatttatatggtttcttccaacttggtgagtatgaacactttgaagcattacgcgcaagaggtt
1 V V E N V S I I Y M V S S N L V S M N T L K H Y A Q E V
5113 cacaaaactataaattaa 5130
29 H K T I N *
44AHJDORF064
2609 atgacgagtcaatcaatcaacttgtgtccgaaatatataacggtgcaccatttgttaaaatgtcacctatgtttaatgcagatg
1 M T S Q S I N L C P K Y I T V H H L L K C H L C L M Q M
2693 acgatatcattgatttaa 2710
29 T I S L I *
44AHJDORF066
10481 atgatattctttatattgaaagtgacatcggttcattttcacttaacgacttatttccagttgaacgttcagtacataacaaat
1 M I F F I L K V T S V H F H L T T Y F Q L N V Q Y I T N
10397 ctgatttgcatatattaa 10380
29 L I C I Y *

Table 19

Sequence similarities between ORFs 44AHJD and public databases

```
Phage: 44AHJD

Database: nr

Query= sid|110871|lan|44AHJDORF001 Phage 44AHJD ORF|10342-12627|-1
         (761 letters)

gi|118848|sp|P19894|DPOL_BPM2 DNA POLYMERASE >gi|76896|pir||JQ0...    55   1e-06
gi|1072656|pir||S51275 DNA polymerase - phage CP-1 >gi|836593|e...    53   6e-06
gi|1429230|emb|CAA67649| (X99260) DNA polymerase [Bacteriophage...    49   1e-04
gi|1572479|emb|CAA65712| (X96987) DNA polymerase [Bacteriophage...    46   0.001
gi|118851|sp|P06950|DPOL_BPPZA DNA POLYMERASE (EARLY PROTEIN GP...    45   0.002
gi|2435429 (AF012250) unassigned reading frame (possible DNA po...    45   0.002
gi|1084487|pir||S41618 DNA polymerase - slime mold (Physarum po...    45   0.002
gi|4877819|gb|AAD31446.1| (AF133505) DNA polymerase [Neurospora...    44   0.004
gi|461962|sp|P33537|DPOM_NEUCR PROBABLE DNA POLYMERASE >gi|2833...    44   0.004
gi|2499511|sp|Q12471|6P22_YEAST 6-PHOSPHOFRUCTO-2-KINASE 2 (PHO...    41   0.041
gi|2258375|gb|AAD11909.1| (AF007261) transcription initiation f...    40   0.070
gi|15734|emb|CAA37450| (X53370) DNA polymerase (AA 1-575) [Bact...    39   0.092

Query= sid|110872|lan|44AHJDORF002 Phage 44AHJD ORF|3789-5732|3
         (647 letters)

gi|135273|sp|P27622|TAGC_BACSU TEICHOIC ACID BIOSYNTHESIS PROTE...   112   7e-24
gi|142847 (M64050) DNase inhibitor [Bacillus subtilis]                52   1e-05
gi|4038407 (AF103943) factor C protein precursor [Streptomyces ...    39   0.10

Query= sid|110873|lan|44AHJDORF003 Phage 44AHJD ORF|6626-8389|2
         (587 letters)

gi|138123|sp|P04331|VG9_BPPH2 TAIL PROTEIN (LATE PROTEIN GP9) >...    92   8e-18
gi|138124|sp|P07534|VG9_BPPZA TAIL PROTEIN (LATE PROTEIN GP9) >...    82   1e-14
gi|1429238|emb|CAA67657| (X99260) tail protein [Bacteriophage B...    78   2e-13
gi|215339 (M12456) p9 tail protein [Bacteriophage phi-29] >gi|2...    71   2e-11
gi|1181968|emb|CAA87738.1| (Z47794) tail protein [Bacteriophage...    54   3e-06
gi|1181970|emb|CAA87740.1| (Z47794) tail protein [Bacteriophage...    42   0.010

Query= sid|110875|lan|44AHJDORF005 Phage 44AHJD ORF|12643-13890|-1
         (415 letters)

gi|3845203 (AE001399) GAF domain protein (cyclic nt signal tran...    52   6e-06
gi|3758843|emb|CAB11128.1| (Z98551) predicted using hexExon; MA...    49   5e-05
gi|3845297 (AE001421) hypothetical protein [Plasmodium falciparum]    48   1e-04
gi|4493936|emb|CAB38972.1| (AL034556) predicted using hexExon; ...    47   2e-04
gi|3845165 (AE001390) hypothetical protein [Plasmodium falciparum]    46   6e-04

Query= sid|110877|lan|44AHJDORF007 Phage 44AHJD ORF|2044-3027|1
         (327 letters)

gi|1181960|emb|CAA87731.1| (Z47794) connector protein [Bacterio...    46   5e-04
gi|1429239|emb|CAA67658| (X99260) upper collar protein [Bacteri...    45   8e-04
gi|137915|sp|P07535|VG10_BPPZA UPPER COLLAR PROTEIN (CONNECTOR ...    44   0.002
gi|137914|sp|P04332|VG10_BPPH2 UPPER COLLAR PROTEIN (CONNECTOR ...    41   0.009

Query= sid|110878|lan|44AHJDORF008 Phage 44AHJD ORF|3020-3775|2
         (251 letters)

gi|4982468|gb|AAD30963.2| (AF118151) SNF1/AMP-activated kinase ...    52   3e-06
gi|1730077|sp|P18160|KYK1_DICDI NON-RECEPTOR TYROSINE KINASE SP...    46   2e-04
gi|3758855|emb|CAB11140.1| (Z98551) predicted using hexExon; MA...    46   2e-04
gi|585795|sp|P21538|REB1_YEAST DNA-BINDING PROTEIN REB1 (QBP) >...    46   3e-04
gi|172372 (M58728) DNA-binding protein [Saccharomyces cerevisiae]     46   3e-04
gi|2952545 (AF051898) coronin binding protein [Dictyostelium di...    45   6e-04
gi|535260|emb|CAA82996| (Z30339) STARP antigen [Plasmodium reic...    45   7e-04
gi|1429240|emb|CAA67659| (X99260) lower collar protein [Bacteri...    44   0.001
```

```
Query= sid|110879|lan|44AHJDORF009 Phage 44AHJD ORF|5744-6496|2
         (250 letters)

gi|2764981|emb|CAA69021.1| (Y07739) N-acetylmuramoyl-L-alanine ...   180  1e-44
gi|113675|sp|P24556|ALYS_STAAU AUTOLYSIN (N-ACETYLMURAMOYL-L-AL...   118  6e-26
gi|1763243 (U72397) amidase [bacteriophage 80 alpha]                 118  6e-26
gi|4574237|gb|AAD23962.1|AF106851_1 (AF106851) LytN [Staphyloco...    84  9e-16
gi|3767593|dbj|BAA33856.1| (AB015195) LytN [Staphylococcus aureus]    84  9e-16
gi|2764983|emb|CAA69022.1| (Y07740) cell wall hydrolase Ply187 ...    77  2e-13
gi|3287732|sp|O05156|ALE1_STACP GLYCYL-GLYCINE ENDOPEPTIDASE AL...    73  2e-12
gi|79926|pir||A25881 lysostaphin precursor - Staphylococcus sim...    69  3e-11
gi|126496|sp|P10548|LSTP_STAST LYSOSTAPHIN PRECURSOR (GLYCYL-GL...    69  3e-11
gi|3287967|sp|P10547|LSTP_STASI LYSOSTAPHIN PRECURSOR (GLYCYL-G...    69  3e-11
gi|3341932|dbj|BAA31898.1| (AB009866) amidase (peptidoglycan hy...    68  6e-11

Query= sid|110882|lan|44AHJDORF012 Phage 44AHJD ORF|8391-8813|3
         (140 letters)

gi|140528|sp|P24811|YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN ...    80  6e-15
gi|4126631|dbj|BAA36651.1| (AB016282) ORF45 [bacteriophage phi-...    76  1e-13
gi|141088|sp|P26835|YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN ...    61  4e-09
gi|2293160 (AF008220) YtkC [Bacillus subtilis] >gi|2635548|emb|...    36  0.099
gi|1181973|emb|CAA87743.1| (Z47794) holin protein [Bacteriophag...    31  3.3
```

Table 20

Homolgies between phage 44 AHJD ORFs and proteins in public databases

```
Query= pt|110871 44AHJDORF001 Phage 44AHJD ORF |10342-12627|-1 1
        (761 letters)

>gi|118848|sp|P19894|DPOL_BPM2 DNA POLYMERASE >gi|76896|pir||JQ0161
          DNA-directed DNA polymerase (EC 2.7.7.7) - phage M2
          >gi|215509 (M33144) DNA polymerase [Bacteriophage M2]
          Length = 572

 Score = 55.4 bits (131), Expect = 1e-06
 Identities = 96/426 (22%), Positives = 159/426 (36%), Gaps = 88/426 (20%)

Query: 229 KLTPEQLTYIHNDVIILGMCHIHYSDIFPNFDYNKLTFSLNIMESYLNNEMTR-----FQ 283
           ++TPE+  YI ND+ I+        DI       +++T   + ++ + +    T+      F
Sbjct: 154 EITPEEYEYIKNDIEIIARA----LDIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVFP 209

Query: 284 LLNQYQDIKISYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYP 343
             L+   D +I                 +  YRGG    N KY  K I E     D+NS YP
Sbjct: 210 KLSLPMDKEI----------------RKAYRGGFTWLNDKYKEKEIGEGMV-FDVNSLYP 252

Query: 344 YVMYHEKIPTWLYFYEHYSEPTLIPTFLDDDNYFSLYKIDKDVFNDDLLIKIKSRVLRQM 403
            MY   +P          Y  P +      + D  + LY I  +  F  +L     K  +  +
Sbjct: 253 SQMYSRPLP--------YGAPIVFQGKYEKDEQYPLY-IQRIRFEFEL----KEGYIPTI 299

Query: 404 XXXXXXXXXXXXXXXXXXLRMIQ-DITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIK 462
                             +  ++  +T +D    I+ + + +Y  EY            F +
Sbjct: 300 QIKKNPFFKGNEYLKNSGVEPVELYLTNVDLELIQEH-YELYNVEYIDGFK------FRE 352

Query: 463 TQGKLKNKINMTSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYG-----------IPAL 511
            G  K+ I+  +      H                +  L+K++LN LYG           +P L
Sbjct: 353 KTGLFKDFIDKWTYVKTH---------EEGAKKQLAKLMLNSLYGKFASNPDVTGKVPYL 403

Query: 512 RSHFNL-FRLDDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNF 570
           +    +L FR+ D          YK+     +    F+T+ +  +  +  Q            D
Sbjct: 404 KDDGSLGFRVGDEE--------YKDPVYTPM-GVFITAWARFTTITAAQACY-----DRI 449

Query: 571 IYCDTDSLYMKSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKK-----YAYEVNG 625
           IYCDTDS+++     P +   + DP   LG W  E+     +  L  K        Y  EV+G
Sbjct: 450 IYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWAHES-TFKRAKYLRQKTYIQDIYVKEVDG 508

Query: 626 KIKIAS 631
           K+K  S
Sbjct: 509 KLKECS 514


>gi|1072656|pir||S51275 DNA polymerase - phage CP-1
          >gi|836593|emb|CAA87725.1| (Z47794) DNA polymerase
          [Bacteriophage CP-1]
          Length = 568

 Score = 53.5 bits (126), Expect = 6e-06
 Identities = 104/464 (22%), Positives = 169/464 (36%), Gaps = 66/464 (14%)

Query: 230 LTPEQLTYIHNDVIIL--GMCHIHYSDIFPNFDYNKLTFSLNIMESYLNNEMTRFQLLNQ 287
           + PE + YIH DV IL  G+   ++Y + F      Y   + +L    +            +F+
Sbjct: 152 IKPEWIDYIHVDVAILARGIFAMYYEENFTK--YTSASEALTEFKRIFRKSKRKFRDFFP 209

Query: 288 YQDIKISYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYPYVMY 347
             D K+                D+ +      G    +  K+  + +++       DINS YP   M
Sbjct: 210 ILDEKVD------------DFCRKHIVGAGRLPTLKHRGRTLNQLIDIYDINSMYPATML 257

Query: 348 HEKIPTWLYFYEHYSEPTLIPTFLDDDNYFSLY-KIDKDVFNDDL-LIKIKSRVLRQMXX 405
              +P   +   + Y         P  + +D+Y+  + K D D+      L   I+IK ++
Sbjct: 258 QNALPIGIP--KRYKGK---PKEIKEDHYYIYHIKADFDLKRGYLPTIQIKKKLDALRIG 312

Query: 406 XXXXXXXXXXXXXXXXLRMIQDITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIKTQG 465
                           L +     +      H        +   E F        +F +Y
Sbjct: 313 VRTSDYVTTSKNEVIDLYLTNFDLDLFLKHYDATIMYVETLE-FQTESDLFDDYI----- 366
```

```
Query: 466 KLKNKINMTSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYGIPALR--SHFNLFRLDDN 523
                    + Y Y       E+  S  E   +K++LN LYG    +  S   L  LDD
Sbjct: 367 ---------TTYRYK-----KENAQSPAEKQKAKIMLNSLYGKFGAKIISVKKLAYLDDK 412

Query: 524 NELYNIINGYKNTERNIL------FSTFVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDS 577
             L      +KN +   +       + FVTS + + ++   Q     E  DNF+Y DTDS
Sbjct: 413 GILR-----FKNDDEEEVQPVYAPVALFVTSIARHFIISNAQ-----ENYDNFLYADTDS 462

Query: 578 LYMKSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKKYAYEVNGKIKIASAGIPKN 637
           L++      +L+    DP   GKW  E   + K   L  K Y  E+  +       + K
Sbjct: 463 LHLFHSDSLVLD---IDPSEFGKWAHEGRAV-KAKYLRSKLYIEELIQEDGTTHLDV-KG 517

Query: 638 AFDTSVDFETFVREQFFDGAIIENNKSIYNEQGTISIYPSKTEI 681
           A  T    E    E F  GA  E  ++    +G   IY + +I
Sbjct: 518 AGMTPEIKEKITFENFVIGATFEGKRASKQIKGGTLIYETTFKI 561
```

>gi|1429230|emb|CAA67649| (X99260) DNA polymerase [Bacteriophage B103]
Length = 572

Score = 49.2 bits (115), Expect = 1e-04
Identities = 93/422 (22%), Positives = 155/422 (36%), Gaps = 88/422 (20%)

```
Query: 229 KLTPEQLTYIHNDVIILGMCHIHYSDIFPNFDYNKLTFSLNIMESYLNNEMTR-----FQ 283
           ++TPE+  YI ND+ I+        DI      +++T   + ++ + +   T+     F
Sbjct: 154 EITPEEYEYIKNDIEIIARA----LDIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVFP 209

Query: 284 LLNQYQDIKISYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYP 343
            L+   D +I                +  YRGG    N KY  K I E     D+NS YP
Sbjct: 210 KLSLPMDKEI----------------RRAYRGGFTWLNDKYKEKEIGEGMV-FDVNSLYP 252

Query: 344 YVMYHEKIPTWLYFYEHYSEPTLIPTFLDDDNYFSLYKIDKDVFNDDLLIKIKSRVLRQM 403
             MY   +P        Y  P +     + D  + LY I +  F  +L    K   +  +
Sbjct: 253 SQMYSRPLP--------YGAPIVFQGKYEKDEQYPLY-IQRIRFEFEL----KEGYIPTI 299

Query: 404 XXXXXXXXXXXXXXXXXXLRMIQ-DITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIK 462
                                ++  +T +D   I+ + + +Y  EY           F +
Sbjct: 300 QIKKNPFFKGNEYLKNSGAEPVELYLTNVDLELIQEH-YEMYNVEYIDGFK------FRE 352

Query: 463 TQGKLKNKINMTSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYG-----------IPAL 511
             G  K  I+  +    H             +  L+K++ + LYG           +P L
Sbjct: 353 KTGLFKEFIDKWTYVKTH---------EKGAKKQLAKLMFDSLYGKFASNPDVTGKVPYL 403

Query: 512 RSHFNL-FRLDDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNF 570
           +   +L FR+ D          YK+     +   F+T+ + +  +   Q        D
Sbjct: 404 KEDGSLGFRVGDEE--------YKDPVYTPM-GVFITAWARFTTITAAQACY-----DRI 449

Query: 571 IYCDTDSLYMKSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKK-----YAYEVNG 625
           IYCDTDS+++     P +   + DP  LG W  E+    +   L  K      YA EV+G
Sbjct: 450 IYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWAHES-TFKRAKYLRQKTYIQDIYAKEVDG 508

Query: 626 KI 627
           K+
Sbjct: 509 KL 510
```

>gi|1572479|emb|CAA65712| (X96987) DNA polymerase [Bacteriophage GA-1]
Length = 578

Score = 46.1 bits (107), Expect = 0.001
Identities = 80/376 (21%), Positives = 146/376 (38%), Gaps = 54/376 (14%)

```
Query: 234 QLTYIHNDVIILGMCHIHYSDIFPNFDYNKLTFSLNIMESYLNNEMTRFQLLNQYQDIKI 293
           ++ Y+ +D++I+ +       +F N D+  +T   + + +Y   EM   +   +Y  +
Sbjct: 162 EIEYLKHDLLIVALA---LRSMFDN-DFTSMTVGSDALNTY--KEMLGVKQWEKYFPVL- 214

Query: 294 SYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYPYVMYHEKIPT 353
                    +     I+  Y+GG    N KY  + +       D+NS YP +M ++ +P
Sbjct: 215 --------SLKVNSEIRKAYKGGFTWVNPKYQGETVYGGMV-FDVNSMYPAMMKNKLLP- 264

Query: 354 WLYFYEHYSEPTLIPTFLDDDNYFSLYKIDKDVFNDDLLIKIKSRVLRQMXXXXXXXXXX 413
                  Y EP +       +  + LY      F +    KI    ++
```

```
Sbjct: 265 -------YGEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIKGNARFGQNEYLS 317

Query: 414 XXXXXXXXLRMIQDITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIKTQGKLKNKINM 473
                    L      +T +D    I+ + + I+E E+       +F+ +            I
Sbjct: 318 TSGDEYVDLY----VTNVDWELIKKH-YDIFEEEFIGG--FMFKGF-----------IGF 359

Query: 474 TSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYGIPALRSHFN--LFRLDDNNELYNIIN 531
              Y       +  N     S E+ + +K++LN LYG  A         +  LD+N  L
Sbjct: 360 FDEYIDRFMEIKNSPDSSAEQSLQAKLMLNSLYGKFATNPDITGKVPYLDENGVLKFRKG 419

Query: 532 GYKNTERNILFST---FVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDSLYMKSVVKPLL 588
       K  ER+ +++      F+T+ +  N+L   Q L            FIY DTDS++++ + +
Sbjct: 420 ELK--ERDPVYTPMGCFITAYARENILSNAQKLYP-----RFIYADTDSIHVEGLGEVDA 472

Query: 589 NPSLFDPIALGKWDIE 604
          + DP  LG WD E
Sbjct: 473 IKDVIDPKKLGYWDHE 488
```

>gi|118851|sp|P06950|DPOL_BPPZA DNA POLYMERASE (EARLY PROTEIN GP2)
>gi|75812|pir||ERBP2Z DNA-directed DNA polymerase (EC 2.7.7.7) - phage PZA >gi|216051 (M11813) gene 2 product [Bacteriophage PZA] >gi|224741|prf||1112171E ORF 2 [Bacteriophage PZA]
Length = 572

Score = 45.3 bits (105), Expect = 0.002
Identities = 98/461 (21%), Positives = 166/461 (35%), Gaps = 110/461 (23%)

```
Query: 198 QLKTDFNYTIFDKDNDMNDSEAYDYAVKCFAKLTPEQLTYIHNDVIILGMCHIHYSDIFP 257
            ++  DF  T+    D D +         Y       ++TP++   YI ND+ I+      +      I
Sbjct: 129 KIAKDFKLTVLKGDIDYHKERPVGY------EITPDEYAYIKNDIQIIAEALL----IQF 178

Query: 258 NFDYNKLTFSLNIMESYLNNEMTR-----FQLLNQYQDIKISYTHYHFHDMNFYDYIKSF 312
              +++T    + ++ + +     T+       F  L+    D ++ Y
Sbjct: 179 KQGLDRMTAGSDDLKGFKDIITTKKFKKVFPTLSLGLDKEVRYA---------------- 222

Query: 313 YRGGLNMYNTKYINKLIDEPCFSIDINSSYPYVMYHEKIPTWLYFYEHYSEPTLIPT--F 370
            YRGG      N ++   K I  E         D+NS YP  MY      +P              Y EP +
Sbjct: 223 YRGGFTWLNDRFKEKEIGEGMV-FDVNSLYPAQMYSRLLP--------YGEPIVFEGKYV 273

Query: 371 LDDDNYFSLYKID-----KDVFNDDLLIKIKSRVLRQMXXXXXXXXXXXXXXXXXXXLRMI 425
             D+D      +    I           K+  +      +   IK  +SR     +
Sbjct: 274 WDEDYPLHIQHIRCEFELKEGYIPTIQIK-RSRFYKGNEYLKSSGGEIADLW-------- 324

Query: 426 QDITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIKTQGKLKNKINMTSPYDYHITDDI 485
              ++ +D + +      + +Y   EY                  F   T   G    K+ I+     +                I
Sbjct: 325 --VSNVD-LELMKEHYDLYNVEYISGLK------FKATTGLFKDFIDKWTHIKTTSEGAI 375

Query: 486 NEHPYSNEEVMLSKVVLNGLYG-----------IPALRSHFNL-FRLDDNNELYNIINGY 533
             +            L+K++LN LYG                     +P L+ +  L FRL                G
Sbjct: 376 KQ---------LAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRL-----------GE 415

Query: 534 KNTERNIL--FSTFVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDSLYMKSVVKPLLNPS 591
            + T+   +        F+T+ + Y    +    Q         D  IYCDTDS+++       P +
Sbjct: 416 EETKDPVYTPMGVFITAWARYTTITAAQACF-----DRIIYCDTDSIHLTGTEIPDVIKD 470

Query: 592 LFDPIALGKWDIENEQIDKMFVLNHKKYAY-----EVNGKI 627
            + DP  LG W  E+        +      L  K Y                EV+GK+
Sbjct: 471 IVDPKKLGYWAHES-TFKRAKYLRQKTYIQDIYMKEVDGKL 510
```

>gi|2435429 (AF012250) unassigned reading frame (possible DNA polymerase) [Physarum polycephalum]
Length = 544

Score = 44.9 bits (104), Expect = 0.002
Identities = 118/545 (21%), Positives = 206/545 (37%), Gaps = 104/545 (19%)

```
Query: 179 TSIATLGKKLLDGGYLTESQLKTDFNYTIFDKDNDMNDSEAYDYAVKCFAKLTPEQLTYI 238
            T + L K L D  + T  Q              F  N M       Y  + CF  L P++  I
Sbjct: 62  TQLFNLLKSLQDSSFYTFKQ---------FTYQNIM-----YSLEISCF--LYPKKKILI 105

Query: 239 HNDVIILGMCHIHYSDIFPNFD-----YNKL--TFSLNIMESY-LNNEMTRFQLLNQYQD 290
              D+        +I Y+D+  ++          YN++  +++NI   Y L+          ++ +
Sbjct: 106 -KDLYNFFSENIIYNDVVKDYKLLAILYNEIQTAYNINRKYILSTASLSLRIFKKSFP 164
```

```
Query: 291 IKISYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYPYVMYHEK 350
           K      +   D +  +YI+  Y GG N        I + + +   +   D+NS YPY+M   EK
Sbjct: 165 EKYRLIPHLTRDED--NYIRKSYIGGRNE-----IFEHVAQRNYFYDVNSLYPYIMKKEK 217

Query: 351 IPTWLYFYEHYSEPTLIPTFLDD-DNYFS----LYKIDKDVFNDDLL---IKIKSRVLRQ 402
           +P  +      Y +    +  F   + +N+F        L  I+K    N  +L    + IK+ V
Sbjct: 218 MPIGI---PEYRDKEYMKKFEKNIENFFGFIDVLITIEKTNNNIPVLPYRMGIKNNV-EV 273

Query: 403 MXXXXXXXXXXXXXXXXXXXLRMIQDITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIK 462
                                  L + Q      I+                IY     +  ++++F+  Y   +
Sbjct: 274 GIIYAKGTLRGIYFSEEIKLALKQGYKIIE----------IYSAYEYKEKEVVFEEYVEQ 323

Query: 463 TQGK-LKNKINMTSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYG--------IPALRS 513
              + LK K          D   + D                      L K +LN LYG             I   +
Sbjct: 324 MYNRRLKAK-------DPALKD-------------LYKKLLNTLYGRFGLVYEQIDIISP 363

Query: 514 HFNLFRLDDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNFIYC 573
              L   + DN  + +       + +       N   ++         + ++ +         F Y T       + + IY
Sbjct: 364 EKEL--ITDNTYISHDTTEFIDITANTCYNNIAITSAITSYARIFMYNTILNYNLHVIYI 421

Query: 574 DTDSLYMKSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKKYAY-EVNGKIKIASA 632
           DTD L++K+     P+ + +L          +GK+ +E+         +  F+ N K Y Y  +N  I
Sbjct: 422 DTDGLFLKN---PIPDIALTTSKEMGKFRLESINAEAHFIAN-KFYIYAPINSPIIYKFK 477

Query: 633 GIPK-----NAFDTSVDFETFVR----EQFFDGAIIENNKSIYNEQGT-----ISIYPSK 678
           GIP        N   D           +  +        +F  +I   NN      Y+ Q +         I   Y +
Sbjct: 478 GIPLQKPIFNIHDIITQHKKILNITLGHHYFTFSIRLNNNQTYSFQASRKRKLIPNYKTT 537

Query: 679 TEIVC 683
             I+C
Sbjct: 538 PWIIC 542
```

>gi|1084487|pir||S41618 DNA polymerase - slime mold (Physarum polycephalum) >gi|509721|dbj|BAA06121.1| (D29637) DNA polymerase [Physarum polycephalum]
Length = 547

Score = 44.9 bits (104), Expect = 0.002
Identities = 118/545 (21%), Positives = 206/545 (37%), Gaps = 104/545 (19%)

```
Query: 179 TSIATLGKKLLDGGYLTESQLKTDFNYTIFDKDNDMNDSEAYDYAVKCFAKLTPEQLTYI 238
           T +  L K L D   + T  Q              F    N M      Y     + CF   L P++      I
Sbjct: 65  TQLFNLLKSLQDSSFYTFKQ---------FTYQNIM-----YSLEISCF--LYPKKKILI 108

Query: 239 HNDVIILGMCHIHYSDIFPNFD-----YNKL--TFSLNIMESY-LNNEMTRFQLLNQYQD 290
             D+      +I Y+D+  ++          YN++ +   +++NI      Y L++               ++   +
Sbjct: 109 -KDLYNFFSENIIYNDVVKDYKLLAILYNEIQTAYNININRKYILSTASLSLRIFKKSFP 167

Query: 291 IKISYTHYHFHDMNFYDYIKSFYRGGLNMYNTKYINKLIDEPCFSIDINSSYPYVMYHEK 350
           K      +   D +  +YI+  Y GG N        I + + +   +   D+NS YPY+M   EK
Sbjct: 168 EKYRLIPHLTRDED--NYIRKSYIGGRNE-----IFEHVAQRNYFYDVNSLYPYIMKKEK 220

Query: 351 IPTWLYFYEHYSEPTLIPTFLDD-DNYFS----LYKIDKDVFNDDLL---IKIKSRVLRQ 402
           +P  +      Y +    +  F   + +N+F        L  I+K    N  +L    + IK+ V
Sbjct: 221 MPIGI---PEYRDKEYMKKFEKNIENFFGFIDVLITIEKTNNNIPVLPYRMGIKNNV-EV 276

Query: 403 MXXXXXXXXXXXXXXXXXXXLRMIQDITGIDCMHIRVNSFVIYECEYFHARDIIFQNYFIK 462
                                  L + Q      I+                IY     +  ++++F+  Y   +
Sbjct: 277 GIIYAKGTLRGIYFSEEIKLALKQGYKIIE----------IYSAYEYKEKEVVFEEYVEQ 326

Query: 463 TQGK-LKNKINMTSPYDYHITDDINEHPYSNEEVMLSKVVLNGLYG--------IPALRS 513
              + LK K          D   + D                      L K +LN LYG             I   +
Sbjct: 327 MYNRRLKAK-------DPALKD-------------LYKKLLNTLYGRFGLVYEQIDIISP 366

Query: 514 HFNLFRLDDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNFIYC 573
              L   + DN  + +       + +       N   ++         + ++ +         F Y T       + + IY
Sbjct: 367 EKEL--ITDNTYISHDTTEFIDITANTCYNNIAITSAITSYARIFMYNTILNYNLHVIYI 424

Query: 574 DTDSLYMKSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKKYAY-EVNGKIKIASA 632
           DTD L++K+     P+ + +L          +GK+ +E+         +  F+ N K Y Y  +N  I
Sbjct: 425 DTDGLFLKN---PIPDIALTTSKEMGKFRLESINAEAHFIAN-KFYIYAPINSPIIYKFK 480

Query: 633 GIPK-----NAFDTSVDFETFVR----EQFFDGAIIENNKSIYNEQGT-----ISIYPSK 678
```

```
          GIP     N  D     +  +       +F  +I  NN  Y+ Q +     I  Y +
Sbjct: 481 GIPLQKPIFNIHDIITQHKKILNITLGHHYFTFSIRLNNNQTYSFQASRKRKLIPNYKTT 540

Query: 679 TEIVC 683
            I+C
Sbjct: 541 PWIIC 545
```

>gi|4877819|gb|AAD31446.1| (AF133505) DNA polymerase [Neurospora crassa]
Length = 1035

Score = 44.1 bits (102), Expect = 0.004
Identities = 36/172 (20%), Positives = 82/172 (46%), Gaps = 14/172 (8%)

```
Query: 521 DDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDSLYM 580
           + N EL + ++G K+    I  ++    + + ++ ++ ++++  S      Y DTDS+++
Sbjct: 817 EKNYELLSYLDGEKDDGFIINSTSIAAATASWSRILMYKHIINSA------YTDTDSIFV 870

Query: 581 KSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKKYAYEVNGKIKIASAGIPKNAFD 640
           +    KPL +  + +       K +    + I +    ++ K Y  +  GK++I   GI KN  +
Sbjct: 871 E---KPLDSAFIGEGCGKFKAEYNGQLIKRAIFISGKLYLLDFGGKLEIKCKGITKNKDN 927

Query: 641 TSVDFETFVREQFFDG---AIIENNKSIYNEQGTISIYPSKTEIVCGNVYDE 689
           T+ + +    E  ++G     + +           E GT+++    K  ++ G  YD+
Sbjct: 928 TTHNLDINDFEALYNGESRVLFQERWGRSLELGTVTVKYQKYNLISG--YDK 977
```

>gi|461962|sp|P33537|DPOM_NEUCR PROBABLE DNA POLYMERASE
>gi|283351|pir||S26985 probable DNA-directed DNA polymerase (EC 2.7.7.7) - Neurospora crassa mitochondrion plasmid maranhar (SGC3)
>gi|578156|emb|CAA39046| (X55361) putative DNA polymerase [Neurospora crassa]
Length = 1021

Score = 44.1 bits (102), Expect = 0.004
Identities = 36/172 (20%), Positives = 82/172 (46%), Gaps = 14/172 (8%)

```
Query: 521 DDNNELYNIINGYKNTERNILFSTFVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDSLYM 580
           + N EL + ++G K+    I  ++    + + ++ ++ ++++  S      Y DTDS+++
Sbjct: 815 EKNYELLSYLDGEKDDGFIINSTSIAAATASWSRILMYKHIINSA------YTDTDSIFV 868

Query: 581 KSVVKPLLNPSLFDPIALGKWDIENEQIDKMFVLNHKKYAYEVNGKIKIASAGIPKNAFD 640
           +    KPL +  + +       K +    + I +    ++ K Y  +  GK++I   GI KN  +
Sbjct: 869 E---KPLDSAFIGEGCGKFKAEYNGQLIKRAIFISGKLYLLDFGGKLEIKCKGITKNKDN 925

Query: 641 TSVDFETFVREQFFDG---AIIENNKSIYNEQGTISIYPSKTEIVCGNVYDE 689
           T+ + +    E  ++G     + +           E GT+++    K  ++ G  YD+
Sbjct: 926 TTHNLDINDFEALYNGESRVLFQERWGRSLELGTVTVKYQKYNLISG--YDK 975
```

>gi|2499511|sp|Q12471|6P22_YEAST 6-PHOSPHOFRUCTO-2-KINASE 2 (PHOSPHOFRUCTOKINASE 2 II) (6PF-2-K 2)
>gi|2131162|pir||S61066 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae)
>gi|2131163|pir||S71026 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae)
>gi|1085116|emb|CAA62371| (X90861) 6-phosphofructo-2-kinase [Saccharomyces cerevisiae]
>gi|1420028|emb|CAA99157| (Z74878) ORF YOL136c [Saccharomyces cerevisiae] >gi|1628439|emb|CAA64733| (X95465) 6-phosphofructo-2-kinase [Saccharomyces cerevisiae]
Length = 397

Score = 40.6 bits (93), Expect = 0.041
Identities = 48/208 (23%), Positives = 92/208 (44%), Gaps = 29/208 (13%)

```
Query: 175 MKTNTSIATLGKKLLDGGYLTESQLKTDFNYTIFDKDNDMNDSEAYDYAVKCFAKLTPEQ 234
           ++    S AT+ K LL     L+ +  +  +  FN      K+ND  ++           +A++T ++
Sbjct: 139 IRRQISCATISKPLL----LSNTSSEDLFN----PKNNDKKET---------YARITLQK 181

Query: 235 LTY-IHNDVIILGMCHIHYSDIFPNFDYNKLTFSLNIMESYLNNEMTRFQLLN---QYQD 290
           L + I+ND    +G+      S I           +  F      + S+  +E++ F L++      Q
Sbjct: 182 LFHEINNDECDVGIFDATNSTI------ERRRFIFEEVCSFNTDELSSFNLVPIILQVSC 235
```

```
Query: 291 IKISYTHYHFHDMNFY-DYIKSFYRGGLNMYNTKYINKLIDEPCFSID-INSSYPYVMYH 348
               S+  Y+ H+ +F  DY+   Y    +  +  +  +        FS+D  N  + Y+  H
Sbjct: 236 FNRSFIKYNIHNKSFNEDYLDKPYELAIKDFAKRLKHYYSQFTPFSLDEFNQIHRYISQH 295

Query: 349 EKIPTWLYFYEHYSEPTLIPTFLDDDNY 376
            E+I T L+F+    +    + P  L+  +Y
Sbjct: 296 EEIDTSLFFFNVINAGVVEPHSLNQSHY 323
```

>gi|2258375|gb|AAD11909.1| (AF007261) transcription initiation
factor sigma [Reclinomonas americana]
Length = 532

Score = 39.9 bits (91), Expect = 0.070
Identities = 49/205 (23%), Positives = 84/205 (40%), Gaps = 14/205 (6%)

```
Query: 100 NHFLLKDTMRYFDNITRENIYLKSAEENEHTLKMKEATILAKNQNVIL---EKRVKSSIN 156
            N+ +      +  F  +  ++IY+  +          +KE   L K  NVI+      K +K   N
Sbjct: 177 NYLVKNSYLNLFKTVPHDSIYMNYSYIQTPLNILKEYLQLIKIINVIILQINKNIKKKNN 236

Query: 157 LDLTMFLNGFKFNIIDNFM---KTNTSIATLGKKLLDGGYLTESQLKTDFNYTIFDKDND 213
            L++++FL  F   + N++    K + +   +  K L   Y+T   L T   Y   K
Sbjct: 237 LNISLFLYKFYQELKWNYIFINKISRNTQKINIKTLKNSYITFYNLITFIQYYTTKKQRL 296

Query: 214 MNDSEAYDYAVKCFAK--LTPEQLTYIHNDVIILGMCHIHYSDIFPNFDYN-KLTFSLNI 270
               D          +K F K     P+      +N +I  G+ HI+    +         N K+T       I
Sbjct: 297 KKDIFYKQIFIKTFLKQHKIPKINKIKNNSLIKYGLTHIYDMILISILRENIKVTLKNRI 356

Query: 271 MESYLNNEMTRFQLLNQYQDIKISY 295
            + +Y+      T    +  QY  +KI Y
Sbjct: 357 IFNYMPYITT---ISKQY--VKIGY 376
```

>gi|15734|emb|CAA37450| (X53370) DNA polymerase (AA 1-575)
[Bacteriophage phi-29]
Length = 575

Score = 39.5 bits (90), Expect = 0.092
Identities = 41/150 (27%), Positives = 64/150 (42%), Gaps = 36/150 (24%)

```
Query: 497 LSKVVLNGLYG-----------IPALRSHFNL-FRLDDNNELYNIINGYKNTERNIL--F 542
            L+K++LN LYG            +P L+ +  L FRL         G + T+ +
Sbjct: 381 LAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRL-----------GEEETKDPVYTPM 429

Query: 543 STFVTSRSLYNLLVPFQYLTESEIDDNFIYCDTDSLYMKSVVKPLLNPSLFDPIALGKWD 602
             F+T+ + Y  +  Q        D  IYCDTDS+++      P +   + DP  LG W
Sbjct: 430 GVFITAWARYTTITAAQACY-----DRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWA 484

Query: 603 IENEQIDKMFVLNHKKYAY-----EVNGKI 627
             E+    ++  L  K Y        EV+GK+
Sbjct: 485 HES-TFKRVKYLRQKTYIQDIYMKEVDGKL 513
```

Query= pt|110872 44AHJDORF002 Phage 44AHJD ORF |3789-5732|3 1
(647 letters)

>gi|135273|sp|P27622|TAGC_BACSU TEICHOIC ACID BIOSYNTHESIS PROTEIN C
>gi|478126|pir||D49757 techoic acid biosynthesis protein
tagC - Bacillus subtilis (strain 168) >gi|143727
(M57497) putative [Bacillus subtilis]
>gi|2636103|emb|CAB15594.1| (Z99122) alternate gene
name: dinC [Bacillus subtilis]
Length = 442

Score = 112 bits (278), Expect = 7e-24
Identities = 91/314 (28%), Positives = 147/314 (45%), Gaps = 58/314 (18%)

```
Query: 152 FELNELEPKFVMGFGGIRNAVNQSINIDKETNHMYSTQSDS----QKPEGFWINKLTPSG 207
            F+    + PK              V QS N D++ + +Y+TQ  S          + + I +L+  G
Sbjct: 7   FDFTNITPKLFTELRVADKTVLQSFNFDEKNHQIYTTQVASGLGKDNTQSYRITRLSLEG 66

Query: 208 DLISSMRIVQGGHGTTIGLERQSNGEMKIWLHHD-----GVAKLLQVAYKDNYVLDLEEA 262
              + SM +  GGHGT IG+E + NG + IW  +D         ++L+   YK    LD E +
Sbjct: 67  LQLDSMLLKHGGHGTNIGIENR-NGTIYIWSLYDKPNETDKSELVCFPYKAGATLD-ENS 124
```

```
Query: 263 KGLTDYTPQSLLNKHTFTPLIDEANDKLILRFGDGTIQVRSRADVKNHIDNVEKEMTIDN 322
           K L  ++        H  TP +D  N +L +R            + D KN+  N ++ +TI N
Sbjct: 125 KELQRFSNMPF--DHRVTPALDMKNRQLAIR----------QYDTKNN--NNKQWVTIFN 170

Query: 323 SE----NNDN-----------RWMQGIAVDGDDLYWLSGNSSVNSHVQIGKYSLTTGQKI 367
            +     N +N           ++QG  +D    LYW +G+++   S+  +          +
Sbjct: 171 LDDAIANKNNPLYTINIPDELHYLQGFFLDDGYLYWYTGDTNSKSYPNL--------ITV 222

Query: 368 YDYPFKLSYQDGINFPRD-------NFKEPEGICIYTNPKTKRKSLLLAMTNGGGGKRFH 420
           +D    K+  Q  I   +D         NF+EPEGIC+YTNP+T   KSL++ +T+G  G R
Sbjct: 223 FDSDNKIVLQKEITVGKDLSTRYENNFREPEGICMYTNPETGAKSLMVGITSGKEGNRIS 282

Query: 421 NLYGFFQLGEYEHF 434
            +Y +     YE+F
Sbjct: 283 RIYAYH---SYENF 293


>gi|142847 (M64050) DNase inhibitor [Bacillus subtilis]
          Length = 125

 Score = 51.9 bits (122), Expect = 1e-05
 Identities = 35/116 (30%), Positives = 55/116 (47%), Gaps = 10/116 (8%)

Query: 152 FELNELEPKFVMGFGGIRNAVNQSINIDKETNHMYSTQSDS----QKPEGFWINKLTPSG 207
           F+    + PK              V QS N D++ + +Y+TQ  S        + + I +L+  G
Sbjct: 7   FDFTNITPKLFTELRVADKTVLQSFNFDEKNHQIYTTQVASGLGKDNTQSYRITRLSLEG 66

Query: 208 DLISSMRIVQGGHGTTIGLERQSNGEMKIWLHHD-----GVAKLLQVAYKDNYVLD 258
            + SM +  GGHGT IG+E + NG + IW  +D        ++L+    YK     LD
Sbjct: 67  LQLDSMLLKHGGHGTNIGMENR-NGTIYIWSLYDKPNETDKSELVCFPYKAGATLD 121


>gi|4038407 (AF103943) factor C protein precursor [Streptomyces
          griseus]
          Length = 324

 Score = 39.1 bits (89), Expect = 0.10
 Identities = 61/269 (22%), Positives = 102/269 (37%), Gaps = 33/269 (12%)

Query: 172 VNQSINIDKETNHMYSTQSDSQKPEG---FWINKLTPSGDLISSMRIVQGGHGTTIGLER 228
           V QS    D      ++  Q  S  P+        I +L  SG+ +  M ++  GHG +IG +
Sbjct: 66  VQQSFTFDIVNRRLFVAQLKSGSPDDSGDLCITQLDFSGNKLGHMYLLGFGHGVSIGAQ- 124

Query: 229 QSNGEMKIWLHHDGVAKLLQVAYKDNYVLDLEEAKGLTDYTPQSLLNKHTFTP------- 281
               + +W   D          +        +     +     G T     S L KH    P
Sbjct: 125 PVGADTYLWTEVD-----VNSNARGTRLARFKWNNGATLSRTSSALAKHQPVPGATEMTC 179


Query: 282 LIDEANDKLILRFGDGTIQVRSRADVKNHIDNVEKEMTIDNSENNDNRWMQGIAVDGDDL 341
            ID  N+++ +R+     + +         +V +      V  +   D           QG A+ G  +
Sbjct: 180 AIDPVNNRMAIRYLTASGRRYGIYNVADIAAGVYDKPLSDVPHPTGLGTFQGYALYGSYV 239

Query: 342 YWLSGN-------SSVNSHVQIGKYSLTTGQKIYDYPFKLSYQDGINFPRDNFKEPEGIC 394
           Y L+GN        + NS+V        + TG  +       + G          F+EPEG+
Sbjct: 240 YQLTGNPYGPDNPNPGNSYVS--SVDVNTGALVQ----RAFTRAGSTL---TFREPEGMG 290

Query: 395 IYTNPKTKRKSLLLAMTNGGGGKRFHNLY 423
           IY     + + L L   +G  G R  NL+
Sbjct: 291 IYRTAAGEVR-LFLGFASGVAGDRRSNLF 318


Query= pt|110873 44AHJDORF003 Phage 44AHJD ORF |6626-8389|2 1
         (587 letters)

>gi|138123|sp|P04331|VG9_BPPH2 TAIL PROTEIN (LATE PROTEIN GP9)
          >gi|75850|pir||WMBPT9 gene 9 protein - phage phi-29
          >gi|215327 (M14782) tail protein [Bacteriophage phi-29]
          >gi|225364|prf||1301270D gene 9 [Bacillus sp.]
          Length = 599

 Score = 92.4 bits (226), Expect = 8e-18
 Identities = 126/618 (20%), Positives = 251/618 (40%), Gaps = 71/618 (11%)

Query: 5   TNFKFFYNTPFT-DYQNTIHFNSNKERDDYFLNGRHFKSLDYSKQPY-NFIRDRMEINVD 62
           TN +    + PF+ DY+NT  F S+  + ++F    R  +  + SK  +  F  ++  ++V
Sbjct: 9   TNVRILADVPFSNDYKNTRWFTSSSNQYNWF--NRKSRVYEMSKVTFMGFRENKPYVSVS 66
```

```
Query: 63  MQWHDAQGINYMTFLS-DFEDRRYYAFVNQIEYVNDVVVKIYFVIDTIMTYTQGNVLEQL 121
           +        +Y+ F + D+ ++ +YAFV ++E+ N  V  ++F ID + T+      ++
Sbjct: 67  LPIDKLYSASYIMFQNADYGNKWFYAFVTELEFKNSAVTYVHFEIDVLQTWMFDMKFQES 126

Query: 122 SNVNIERQHLSKRTYNYMLPMLRNNDDVLKVSNKNYVYNQMQQYLENLVLFQSSADLSKK 181
               I R+H+ K   +   P +   D+ L   ++  + +       + ++F      S
Sbjct: 127 F---IVREHV-KLWNDDGTPTINTIDEGLSYGSEYDIVSVENHKPYDDMMFLVIISKSIM 182

Query: 182 FGT--KKEPNLDTSKGTIYDNITSPVNLYVMEYGDFINFMDKMSAYPWITQNFQK----V 235
            GT  ++E  L+    ++ + +  P+  Y+  +     + D      +I  N       V
Sbjct: 183 HGTPGEEESRLNDINASL-NGMPQPLCYYIHPF-----YKDGKVPKTYIGDNNANLSPIV 236

Query: 236 QMLPKDFINTKDLEDVKTSEKITGLKTLKQGGKSKEWSLK-DLSL---------SFSNLQ 285
            ML   F     + D+  +  +T    LK   K+ + LK D  +            N+
Sbjct: 237 NMLTNIFSQKSAVNDI-VNMYVTDYIGLKLDYKNGDKELKLDKDMFEQAGIADDKHGNVD 295

Query: 286 EMMLSK-------------------KDEFKHMIRNEYMTIEFYDWNGNTMLLDAGKISQK 326
            + + K                   KD+   ++   Y   E  D+ GN M L    I+
Sbjct: 296 TIFVKKIPDYEALEIDTGDKWGGFTKDQESKLMMYPYCVTEITDFKGNHMNLKTEYINNS 355

Query: 327 TGVKLRTKSIIGYHNEVRVYPVDYNSAENDRPILAKNKEILIDTGSFLNTNITFNSFAQV 386
             +K++ +  +G  N+V     DYN+   D  +  N+        S +N N
Sbjct: 356 K-LKIQVRGSLGVSNKVAYSVQDYNA---DSALSGGNRLTASLDSSLINNNPN------- 404

Query: 387 PILINNGILGQSQQANRQ--KNAESQLITNRIDNVLNG---SDPKSRFYDAVSVASNLSP 441
            I I N  L    Q N+   +N +S ++ N I  ++ G   +   +    A+ +AS++
Sbjct: 405 DIAILNDYLSAYLQGNKNSLENQKSSILFNGIMGMIGGGISAGASAAGGSALGMASSV-- 462

Query: 442 TALFGKFNEEYNFYKQQQAEYKDLALQPPSVTESEMGNAFQIANSINGLTMKISVPSPKE 501
           T +           + QA+   D+A  PP +T++     AF   N   G+ +       +
Sbjct: 463 TGMTSTAGNAVLQMQAMQAKQADIANIPPQLTKMGGNTAFDYGNGYRGVYVIKKQLKAEY 522

Query: 502 ITFLQKYYMLFGFEVNDYNSFIEPINSMTVCNYLKCTGTYTIRDIDPMLMEQLKAILESG 561
              L  ++  +G+++N        + +    NY++    +  DI+   +++++  I ++G
Sbjct: 523 RRSLSSFFHKYGYKINRVKK--PNLRTRKAFNYVQTKDCFISGDINNNDLQEIRTIFDNG 580

Query: 562 VRFWHNDGSGNPMLQNPL 579
           + WH  D GN   ++N L
Sbjct: 581 ITLWHTDNIGNYSVENEL 598


>gi|138124|sp|P07534|VG9_BPPZA TAIL PROTEIN (LATE PROTEIN GP9)
           >gi|75849|pir||WMBP9Z gene 9 protein - phage PZA
           >gi|216058 (M11813) tail protein [Bacteriophage PZA]
           Length = 599

 Score = 81.9 bits (199), Expect = 1e-14
 Identities = 127/618 (20%), Positives = 248/618 (39%), Gaps = 71/618 (11%)

Query: 5   TNFKFFYNTPFT-DYQNTIHFNSNKERDDYFLNGRHFKSLDYSKQPYNFIRDRME-INVD 62
           TN +   + PF+ DY+NT  F S+  + ++F      +  + SK  +   R+    I+V
Sbjct: 9   TNVRILADVPFSNDYKNTRWFTSSSNQYNWF--NSKTRVYEMSKVTFQGFRENKSYISVS 66

Query: 63  MQWHDAQGINYMTFLS-DFEDRRYYAFVNQIEYVNDVVVKIYFVIDTIMTYTQGNVLEQL 121
           ++       +Y+ F + D+ ++ +YAFV ++EY N     ++F ID + T+   N+  Q
Sbjct: 67  LRLDLLYNASYIMFQNADYGNKWFYAFVTELEYKNVGTTYVHFEIDVLQTW-MFNIKFQE 125

Query: 122 SNVNIERQHLSKRTYNYMLPMLRNNDDVLKVSNKNYVYN--QMQQYLENLVLFQSSADLS 179
           S   I R+H+ K   +   P +   D+ L   ++  + +    + Y + + L   S  +
Sbjct: 126 SF--IVREHV-KLWNDDGTPTINTIDEGLNYGSEYDIVSVENHRPYDDMMFLVVISKSIM 182

Query: 180 KKFGTKKEPNLDTSKGTIYDNITSPVNLYVMEY-----------GD-------FINFMDK 221
                + E  L+    ++ + +  P+  Y+  +           GD        +N +
Sbjct: 183 HGTAGEAESRLNDINASL-NGMPQPLCYYIHPFYKDGKVPKTFIGDNNANLSPIVNMLTN 241

Query: 222 MSAYPWITQNFQKVQMLPKDFINTK--------DLEDVKTSEKITGLKTLKQGGKSKEWS 273
           + +      N   V M   D+I  K        +L+  K   + G+    K G     +
Sbjct: 242 IFSQKSAVNNI--VNMYVTDYIGLKLDYKNGDKELKLDKDMFEQAGIADDKHGNVDTIFV 299

Query: 274 LKDL---SLSFSNLQEMMLSKKDEFKHMIRNEYMTIEFYDWNGNTMLLDAGKISQKTGVK 330
            K     +L      +     KD+   ++   Y   E  D+ GN M L    I     +K
Sbjct: 300 KKIPDYETLEIDTGDKWGGFTKDQESKLMMYPYCVTEVTDFKGNHMNLKTEYIDNNK-LK 358

Query: 331 LRTKSIIGYHNEVRVYPVDYNSAENDRPILAKNKEILIDTGSFLNTNITFNSFAQVPILI 390
           ++ +  +G  N+V     DYN+  +    L+    +      L+T++  N+    + I+
```

```
Sbjct: 359 IQVRGSLGVSNKVAYSIQDYNAGGS----LSGGDRLTAS----LDTSLINNNPNDIAII- 409

Query: 391 NNGILGQSQQANRQ--KNAESQLITNRIDNVLNGSDPKSRFYDAVSVASNLSP------- 441
            N  L    Q N+    +N +S ++ N I  +L G          A + A    SP
Sbjct: 410 -NDYLSAYLQGNKNSLENQKSSILFNGIVGMLGGG------VSAGASAVGRSPFGLASSV 462

Query: 442 TALFGKFNEEYNFYKQQQAEYKDLALQPPSVTESEMGNAFQIANSINGLTMKISVPSPKE 501
            T +              +  QA+  D+A  PP +T+     AF   N   G+ +        +
Sbjct: 463 TGMTSTAGNAVLDMQALQAKQADIANIPPQLTKMGGNTAFDYGNGYRGVYVIKKQLKAEY 522

Query: 502 ITFLQKYYMLFGFEVNDYNSFIEPINSMTVCNYLKCTGTYTIRDIDPMLMEQLKAILESG 561
               L  ++  +G+++N          + +    NY++     +    DI+    +++++ I ++G
Sbjct: 523 RRSLSSFFHKYGYKINRVKK--PNLRTRKAYNYIQTKDCFISGDINNNDLQEIRTIFDNG 580

Query: 562 VRFWHNDGSGNPMLQNPL 579
            +  WH D  GN   ++N L
Sbjct: 581 ITLWHTDDIGNYSVENEL 598


>gi|1429238|emb|CAA67657| (X99260) tail protein [Bacteriophage B103]
          Length = 598

 Score = 77.6 bits (188), Expect = 2e-13
 Identities = 130/623 (20%), Positives = 240/623 (37%), Gaps = 86/623 (13%)

Query: 5   TNFKFFYNTPFT-DYQNTIHFNSNKERDDYFLNGRHFKSLDYSKQPYNFI---RDRMEIN 60
            T+ + F N PF+ DY++T  F +    + YF     + K    +     NF+         I
Sbjct: 9   TDVRIFSNVPFSNDYKSTRWFTNADAQYSYF----NAKPRVHVINECNFVGLKEGTPHIR 64

Query: 61  VDMQWHDAQGINYMTFLS-DFEDRRYYAFVNQIEYVNDVVVKIYFVIDTIMTYTQGNVLE 119
            V+ +  D         YM F +  + ++ +Y FV ++EYVN  V  +YF ID I T+   +
Sbjct: 65  VNKRIDDLYNACYMIFRNTQYSNKWFYCFVTRLEYVNSGVTNLYFEIDVIQTW-MFDFKF 123

Query: 120 QLSNVNIERQHLSKRTYNYMLPMLRNNDDVLKVSNKNYVYNQMQQYLENLVLFQSSADLS 179
            Q S + E Q +             P+    D+ L     + V    Q     ++F     S
Sbjct: 124 QPSYIVREHQEMWDANNE---PLTNTIDEGLNYGTEYDVVAVEQYKPYGDLMFMVCISKS 180


Query: 180 KKFGTKKEPNLDTSKGTIYDNITS---PVNLYVMEYGDFINFMDKMSAYPWITQNFQKVQ 236
            K   T   E         G I  NI        P++ YV  +         + D  S   P +T      +VQ
Sbjct: 181 KMHATAGET---FKAGEIAANINGAPQPLSYYVHPF-----YEDGSS--PKVTIGSNEVQ 230

Query: 237 ML-PKDFINTKDLEDVKTSEKITGLKT------LKQGGKSKEWSLKDLSLSFSNL----- 284
            +  P DF+      ++    +  ++     T         +      +K  SL+D        + +
Sbjct: 231 VSKPTDFLKNMFTQEHAVNNIVSLYVTDYIGLNIHYDESAKTMSLRDTMFEHAQIADDKH 290

Query: 285 --------------QEMMLSKKDEFKHMIRNEYMTIEFY--------DWNGNTMLLDAGK 322
                          +E  +     +F    NE    + Y         D+ GN + +
Sbjct: 291 PNVNTIYLKEVKEYEEKTIDTGYKFASFANNEQSKLLMYPYCVTTITDFKGNQIDIKNEY 350

Query: 323 ISQKTGVKLRTKSIIGYHNEVRVYPVDYNS---AENDRPILAKNKEILIDTGSFLNTNIT 379
            ++  + +K++ +  +G  N+V      DYN+       D+ + A             NT++
Sbjct: 351 VNG-SNLKIQVRGSLGVSNKVTYSVQDYNADTTLSGDQNLTAS-----------CNTSLI 398

Query: 380 FNSFAQVPILINNGILGQSQQANRQ--KNAESQLITNRIDNVLN---GSDPKSRFYDAVS 434
            N+    V I+   N  L    Q N+    +N +  ++ N +  ++L     G+    +     AV
Sbjct: 399 NNNPNDVAII--NDYLSAYLQGNKNSLENQKDSILFNGVMSMLGNGIGAVGSAATGSAVG 456

Query: 435 VASNLSPTALFGKFNEEYNFYKQQQAEYKDLALQPPSVTESEMGNAFQIANSINGLTMKI 494
            VAS  S T +              +  QA+  D+A  PP + +     A+   N   G+ +
Sbjct: 457 VAS--SATGMVSSAGNAVLQIQGMQAKQADIANTPPQLVKMGGNTAYDYGNGYRGVYVIK 514

Query: 495 SVPSPKEITFLQKYYMLFGFEVNDYNSFIEPINSMTVCNYLKCTGTYTIRDIDPMLMEQL 554
                 +    L  +   +G++ N          + +  +    NY++         I +++    ++++
Sbjct: 515 KQIKEEYRNILSDFSRKYGYKTNLVK--MPNLRTRESYNYVQTKDCNIIGNLNNEDLQKI 572

Query: 555 KAILESGVRFWHNDGSGNPMLQN 577
            + I +SG+  WH D  G+  L N
Sbjct: 573 RTIFDSGITLWHADPVGDYTLNN 595


>gi|215339 (M12456) p9 tail protein [Bacteriophage phi-29]
          >gi|224163|prf||1011232C protein p9,tail [Bacteriophage
          phi-29]
          Length = 335
```

```
 Score = 71.0 bits (171), Expect = 2e-11
 Identities = 64/293 (21%), Positives = 123/293 (41%), Gaps = 20/293 (6%)

Query: 292 KDEFKHMIRNEYMTIEFYDWNGNTMLLDAGKISQKTGVKLRTKSIIGYHNEVRVYPVDYN 351
            KD+    ++    Y    E   D+ GN M L        I+     +K++ +   +G   N+V         DYN
Sbjct: 57  KDQESKLMMYPYCVTEITDFKGNHMNLKTEYINNSK-LKIQVRGSLGVSNKVAYSVQDYN 115

Query: 352 SAENDRPILAKNKEILIDTGSFLNTNITFNSFAQVPILINNGILGQSQQANRQ--KNAES 409
            +   D   +    N+        S +N N           I  I  N  L    Q N+   +N +S
Sbjct: 116 A---DSALSGGNRLTASLDSSLINNNPN-------DIAILNDYLSAYLQGNKNSLENQKS 165

Query: 410 QLITNRIDNVLNG---SDPKSRFYDAVSVASNLSPTALFGKFNEEYNFYKQQQAEYKDLA 466
              ++ N I   ++ G     +     +    A+ +AS++   T +               +  QA+   D+A
Sbjct: 166 SILFNGIMGMIGGGISAGASAAGGSALGMASSV--TGMTSTAGNAVLQMQAMQAKQADIA 223

Query: 467 LQPPSVTESEMGNAFQIANSINGLTMKISVPSPKEITFLQKYYMLFGFEVNDYNSFIEPI 526
              PP +T+       AF     N     G+ +              +        L   ++    +G+++N               +
Sbjct: 224 NIPPQLTKMGGNTAFDYGNGYRGVYVIKKQLKAEYRRSLSSFFHKYGYKINRVKK--PNL 281

Query: 527 NSMTVCNYLKCTGTYTIRDIDPMLMEQLKAILESGVRFWHNDGSGNPMLQNPL 579
              +       NY++       +     DI+     +++++ I ++G+   WH  D   GN   ++N L
Sbjct: 282 RTRKAFNYVQTKDCFISGDINNNDLQEIRTIFDNGITLWHTDNIGNYSVENEL 334


>gi|1181968|emb|CAA87738.1| (Z47794) tail protein [Bacteriophage
          CP-1]
          Length = 230

 Score = 53.9 bits (127), Expect = 3e-06
 Identities = 29/113 (25%), Positives = 54/113 (47%), Gaps = 3/113 (2%)


Query: 1   MRKLTNFKFFYNTPF-TDYQNTIHFNSNKERDDYFLNGRHFKSLDYSKQPYNFIRDRMEI 59
            M++ T      +  +PF  DY N I+F + +  +D+F          + Y     + + +      I
Sbjct: 1   MQESTKIWLYAKSPFKNDYANVINFETRESMEDFFTKKNPHIEIVYEYDKFQYTQRNGSI 60

Query: 60  NVDMQWHDAQGINYMTFLSDFEDRRYYAFVNQIEYVNDVVVKIYFVIDTIMTY 112
            V   +       + + YM  F+++      R YYAFV   + Y+N++     +I  + +D     TY
Sbjct: 61  VVSGRVEKYENVTYMRFINN--GRTYYAFVFDVLYINEDATRIIYEVDVWNTY 111


>gi|1181970|emb|CAA87740.1| (Z47794) tail protein [Bacteriophage
          CP-1]
          Length = 586

 Score = 42.2 bits (97), Expect = 0.010
 Identities = 79/381 (20%), Positives = 139/381 (35%), Gaps = 92/381 (24%)

Query: 277 LSLSFSNLQEMMLSK--KDEFK---HMIRNEYMTIEFYDWNGNTMLLDAG----KISQKT 327
            L +++   +QE + S      KD+ +       ++ +E+   IE YD   GN+ +             I +
Sbjct: 187 LKIAYDQIQEGLRSYMGKDDLEIEVQLLNSEFTEIELYDIYGNSYVYQPQYLPRTIDEAH 246

Query: 328 GVKLRTKSIIGYHNEVRVYPVDYNSAEN----DRPIL----------------------- 360
             K+          +G   N+V  +    ++YN+A N       D+ IL
Sbjct: 247 KYKVIVSGSLGDSNQVHINFLEYNNANNVSYADKNILDLSLESGDWAEHNPEHFKYGLNDV 306

Query: 361 -AKNKEILIDT-GSFLNTNITFNSFAQVPILINNGILGQSQQANRQKNAESQLITNRIDN 418
             K+   IL D     S++ ++             Q+       N    +L QS     ++ A +          +
Sbjct: 307 TGKSVAILNDAEASYIQSHKNQMEHTQLTFKENRDMLKQSVDLSNKQVATANSQASYNAQ 366

Query: 419 VLNGSDPKSRFYDAVSVASNLSPTALFGKF-----------------NEEYNFYKQQQ-- 459
                   S    +++ +   S      N++       L G F                      N +YN       QQ
Sbjct: 367 FAVDSANINQWTEGASGILNVAGNLLTGNFGGALGGLASGGMKVFNANRDYNDKVVQQGF 426

Query: 460 -------------------------------AEYKDLALQPPSVTESEMGNAFQIANSIN 488
                                           A     DL    QP  SV +          AFQ   N +
Sbjct: 427 TSENNALKSQSNALANMKSKIALDQSIRAYNATMADLQNQPISVQQIGNDLAFQSGNRLT 486

Query: 489 GLTMKISVPSPKEITFLQKYYMLFGFEVNDY-NSFIEPINSMTVCNYLKCTGTY--TIRD 545
              +     K+S++     +   +         +Y      +G     VN  + N     +     +   S          NY+K             T+R
Sbjct: 487 DVYWKVSLAQKEIMGRANEYIKCYGVLVNWFTNDALSVMRSRKRFNYIKMINVNLGTLR- 545

Query: 546 IDPMLMEQLKAILESGVRFWH 566
            +     M    ++AI  +SGVR  W+
Sbjct: 546 ANQSHMNAIQAIFQSGVRIWN 566
```

```
Query= pt|110875 44AHJDORF005 Phage 44AHJD ORF |12643-13890|-1 1
         (415 letters)

>gi|3845203 (AE001399) GAF domain protein (cyclic nt signal
            transduct.) [Plasmodium falciparum]
            Length = 1245

 Score = 52.3 bits (123), Expect = 6e-06
 Identities = 59/246 (23%), Positives = 105/246 (41%), Gaps = 27/246 (10%)

Query: 174  ESIDRNHGNVDYIGFPKMFLLGNAVNFSSPILSNLNIYNLLQKHKMNTSRLYKNIFLEMR 233
            +S D N+ N +       +   N+V FS+    N  IY++L     N   +YK +  E+
Sbjct: 854  DSSDNNNNNNNNNNNNNNYNNNNSVIFST----NEKIYDML-----NRDNIYKKVKKEIF 904

Query: 234  RNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYNLADDNLRNHINQNGDFFYIKTDDKYI-- 291
              D + +    +   +N + M     + N  N  ++N+ N+ N NGD  Y     KY
Sbjct: 905  EGDSIIKTMENKPNLTNKNYMNNDNIDNNNNNNNNNNIDNNNNNNGDNIYNDDLKKYYLN 964

Query: 292  KVMYNVTTFMTNIIVVPYTKQYEFCTKIR-DIDNHVTYLRDDMFYKENMERYYYNPSNLH 350
              ++N   ++ + + +   K  E   K+   I   +  L   +F+K NM     + + L+
Sbjct: 965  TSIFNKDLYVKHFVDIIMNKSLEEIIKMNVYISERINSL---LFHKGNM---LNDVTKLY 1018

Query: 351  FDNAYSKNYVVDNDRYLYLDMNKIIKFHIKNEMKKNMSEFERKEKIYEDN----YIENTK 406
              NAY +     N         K I F  + E K +M  F+  +KIY+ N    +  N K
Sbjct: 1019 MSNAYGEKCFFFN-----FPQIKEIIFVNEYEKKMDMKYFKMLKKIYKYNLNKIFSNNYK 1073

Query: 407  KYLMKQ 412
             +++K+
Sbjct: 1074 FFIIKK 1079


>gi|3758843|emb|CAB11128.1| (Z98551) predicted using hexExon;
            MAL3P6.23 (PFC0820w), Hypothetical protein, len: 4982 aa
            [Plasmodium falciparum]
            Length = 4981

 Score = 49.2 bits (115), Expect = 5e-05
 Identities = 67/287 (23%), Positives = 110/287 (37%), Gaps = 60/287 (20%)

Query: 127  ITDLNSATDLKYHSNFLKHYPIIIYDEFLALEDDYLIDEWDKLKT----IYESIDRNHGN 182
            I D+N + D+  +   +++   I YD           +++DK++     IY +ID++  N
Sbjct: 3619 IMDINKSKDISKNMEIVQN---IEYD-----------NKYDKIRNDMDAIYMAIDKDMDN 3664

Query: 183  VDYIGFPKMFLLGNAVNFSSPILSNLNIYNL----LQKHKMNTSRLYKNIFLEMRRNDYV 238
            +  I   + F L    N  S   +N   YNL    ++  K N  R Y N F     +D
Sbjct: 3665 IGIINCMRYFNLYKNYNNLSNECNNRE-YNLNELYMEDIKRNMKR-YDNNFNINHYDDNN 3722

Query: 239  NEKRNTRAFNSNDDAMTTGEFEFNEYNLADDNLRNHINQNGDFFYIKTDDKYIKVMYNVT 298
            N   N    N+N++         N  N  ++N  N+ N NG  F+   D
Sbjct: 3723 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGCFFFHVD----------- 3771

Query: 299  TFMTNIIVVPYTKQYEFCTKIRDIDNHVTYLRDDMFYKENMERYYYNPSNLHFDNAYSKN 358
                        K   FCTK             ++F  +N+E    N  N    N Y+ N
Sbjct: 3772 ------------KDLFFCTK------------KNIFPCKNIETVCKNEYNKKIYNNYTCN 3807

Query: 359  YVVDNDRYLYLDMNKIIKFHIKNEMKKNMSEFERKEK-IYEDNYIEN 404
              V+N       + ++IK +   +   N  E+ + EK +Y  +  EN
Sbjct: 3808 ISVNNTLNCLNIIKELIKLNNNKKKILNYYEYHKVEKLLYYRHSFEN 3854


 Score = 35.6 bits (80), Expect = 0.70
 Identities = 62/290 (21%), Positives = 121/290 (41%), Gaps = 65/290 (22%)

Query: 2    VKQNRLDMVRDYQNAVN--HVRKKIPDKYNQIELVDELMNDDIDYYISISNRSDGKSFNY 59
            +K+N ++     +N +N  +V++   DK N I           D++I+ SN +  +SF
Sbjct: 4445 IKRNNINKSNIKRNNINKSNVKRSNTDKSNVIS----------DFHIT-SNNNITRSFT- 4492

Query: 60   VSFFIYLAIKLDIKFTLLSRHYTLRDAYRDFIEEIIDENPLFKSKRVTFRSARDYLAIIY 119
                   A   D  F  LS   TL  +Y +F   + +                    I
Sbjct: 4493 -------ATLTDSIFNTLSE--TLNYSYDNFFSNMDN--------------------IKI 4523

Query: 120  QDKEIGVITDLNSATDLKYHSNFLKHYPIIIYDEFL-----ALEDDYLIDEWDKLKTIYE 174
            +  EI  ITD++     +YH N+LK     + +E++     + +D  + DE   ++T+ E
Sbjct: 4524 KKNEINNITDVDYGNKKEYHENYLKVKQNKVNEEYIEETFKSDKDCSIKDEACTIRTLSE 4583
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Query: 175  S--IDRNHGNVDYIGFPKMFLLGNAVNFSSPILSNLNIYNLLQKHKMN--TSRLYKNIFL 230
            S  I  N  N+D           + +  + S P   N++  N ++K+ +N     R+ KN
Sbjct: 4584 SCNISENISNID---------MDDEDHISFPNGRNVHDNNYMKKNHVNYDKMRVGKNKIP 4634

Query: 231  EMRRNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYNLADDNLRNHINQNGD 280
                 D + +++  +     +D  M++ ++    E ++ +  L  +   NG+
Sbjct: 4635 SFTHFDKILDEKKKK----SDKDMSSSKWLEREEHIKEIKLEKNEYMNGN 4680


 Score = 34.0 bits (76), Expect = 2.0
 Identities = 47/211 (22%), Positives = 84/211 (39%), Gaps = 32/211 (15%)

Query: 210  IYNLLQKHKMNTSRLYKNIFLEMRRNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYNLADD 269
            I++LLQK         LY+N+ +              R     +  N+    T  E ++ + ++
Sbjct: 918  IFSLLQKDSSPLLVLYENVHI-----------REGEKYGRNE--ATDNEVDYKKGDIIKH 964

Query: 270  NLRNHINQNGDFFYIKTD---DKYIKVMYNVTTFMTNIIVVPYTKQYEFCTKIRDIDNHV 326
            N+ N     + D +          D+  K MY      +       V         E    K  D+ N+
Sbjct: 965  NVTNEHGNHSDSYPYGNSLNLDRKPKNMYE-DIYKEKGFVKSDCSNIEI--KKNDMINND 1021


Query: 327  TYLRDDMFYKENMERYYYNPSNLHFDNAYSKNYVVDNDRYLYLDMNKII----KFHIKNE 382
             Y +++ FY+++       Y+     +       YV++      +YL +N ++        F +KN+
Sbjct: 1022 VYKKNE-FYEDSRINMIYDEDEIKTWFLIPHKYVIN---IIYLFLNILLTDESNFKLKNK 1077

Query: 383  MKKNMSEFERKEKIYEDN-----YIENTKKY 408
                    E K  IYEDN       ++N KKY
Sbjct: 1078 KYGYFVNEETKGTIYEDNNGLQEILKNGKKY 1108


 Score = 33.6 bits (75), Expect = 2.7
 Identities = 42/198 (21%), Positives = 77/198 (38%), Gaps = 42/198 (21%)

Query: 222 SRLYKNIFLEMR---RNDYVNEKRNTRAF-----------NSNDDAMTTGEFEFNEYNLA 267
            S LY  I++  +   +N  +  K+NT  +            N+++D  TT   E +  +
Sbjct: 411 SVLYSIIYMNKKYKKKNFIITNKKNTNVYFENDVIQLSVENTSEDTFTTNTRESSLNSGM 470

Query: 268 DDNLRNHINQNGDFFYIKTDDKYIKVMYNVTTFMTNIIVVPYTKQYEFCTKIRDIDNHVT 327
            +++R  +N   D     +DDK    ++Y         N       YTK  E
Sbjct: 471 MNDMRYSVNNYADEKVYHSDDKSDHLIYKHVHDEKNKYDEMYTKTKE------------- 517

Query: 328 YLRDDMFYKENMERYYYNPSNLHFDNAYSKNYVVDNDRYLYLDMNKIIKFHIKNEMKKNM 387
             +++ YK N+          +    N    K          LD+ K I   H+KN+ + N
Sbjct: 518 --NENIIYKSNIVDKKTCDISSEMVNGKDK-----------LDVEKYIGSHVKND-ENNK 563

Query: 388 SEFERK-EKIYEDNYIEN 404
            + ++K + + +  YI+N
Sbjct: 564 EKLKKKIDNVNKKEYIDN 581
```

>gi|3845297 (AE001421) hypothetical protein [Plasmodium falciparum]
Length = 2380

```
 Score = 48.0 bits (112), Expect = 1e-04
 Identities = 87/390 (22%), Positives = 160/390 (40%), Gaps = 65/390 (16%)

Query: 20   VRKKIPDKYNQIELVDELMNDDIDYYISISNRSDGKSFNYVSFF-----IYLAIKLDIKF 74
            +++K  +K ++      +  +N D + ++     R     K+ NY++            +YL  I  DI
Sbjct: 1049 LQRKNMNKCSKNRNRNRYINKDSNIHLMNLIRIKFKNLNYMNMNSFEIELYLKINNDIFL 1108

Query: 75   TLLSRHYTLRDAYR------DFIEEIIDEN-PLFKSKRVTFRSARDYLAIIYQDKEIGVI 127
                  +Y +++ Y          + + +     EN    +  +++ ++    +         Y +K+
Sbjct: 1109 QFNKHNYNVQNFYNFSITLINIMSKYYSENFYAYNLEKIVYKFLLNNKNFEYIEKQYSSK 1168

Query: 128  TDLNSATDLKYHSNFLKHYPIIIYDEFLA----LEDDYLIDEWDKLKTIYESIDRNHGNV 183
            D+N   D+  ++  +K+  II    EFL       L+ D  I   + KLKT            ++
Sbjct: 1169 EDMNEL-DILVNTYDMKYDKII---EFLKNNGYLKIDRYIYFYPKLKT----------DI 1214

Query: 184  DYIGFPKMFLLGNAVNFSSPILSNLNIYNLLQKHKMNTSRLY------KNIF--LEMRRN 235
                  F ++FL  N +      L   NI  +++  K      + Y          K IF  + M+ +
Sbjct: 1215 ILFFFKEIFLNDNILKIDRKFLKK-NITIMIEVLKEIFFKEYVKRCITKVIFFPVHMKEH 1273

Query: 236  DYVNEKR--------NTRAFNSNDDAMTTGEFEFNEYNLADDNLRNHINQNGDFFYIKTD 287
            D+V  K            N+  FN+  D       +    N YN   D+   N+ N N     +Y K
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```
Sbjct: 1274 DHVMNKNYYNNQYVNNSNMFNTRGDHNNNNQTNDNHYNHHYDDTHNNNNNNNSKYY-KNK 1332

Query: 288  DKYIKVMYNVTTFMTNIIV---VPYTKQYEFCTKIRDIDNHVTYLRDDMFYKEN----ME 340
            +K  K+MY        +++ +   V    K  +    K   I  +  Y+  ++     N    +
Sbjct: 1333 NKN-KIMYEKERKSSSLFISNNVQDVKPIKHYLKYSSIYKNFIYIISEIKNFNNKITKIN 1391

Query: 341  RY-YYNPSNLHFDNAYSKNYVVDNDRYLYL 369
            RY YYN  NL+ D+          ND YL+L
Sbjct: 1392 RYNYYNYMNLNIDDL--------NDAYLFL 1413


 Score = 32.5 bits (72), Expect = 6.0
 Identities = 46/183 (25%), Positives = 73/183 (39%), Gaps = 26/183 (14%)

Query: 225 YKNIFLEMRRNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYNLADDNLRNHINQNGDFFYI 284
            +KNI   ++   ++N   +    NSN +   +      N  N+  +N  N IN +      I
Sbjct: 27  HKNINKNIKNKKFINIDNSNNCNNSNSNNSNSNNNNNNNNIVRNN-NNFINADKKKNVI 85

Query: 285 KTDDKYIKVMYNVTTFMTNIIVVPYTKQYEFCTKIRDIDNHVTYLRDDMFYKENMERYYY 344
              +D  IK     V     NI     Y    ++     + D+ N+        + +  KE   ER
Sbjct: 86  LNEDDDIKNKELVDESFVNIFF--YENYFKNLFNLNDVSNNKVI--NIIEQKEGDER--- 138

Query: 345 NPSNLHFDNAYSKNYVVDNDRYLYLDMNKIIKFHIKNEMKKNMSEFERKEKIYEDNYIEN 404
            N  N     N  +KN V DN         +NK      IKN    +N++E         Y  N++ +
Sbjct: 139 NADN----NLKNKNIVRDN-------INK-----IKN--TRNVNEILIYNNKYIINFLND 180

Query: 405 TKK 407
            T K
Sbjct: 181 TTK 183


>gi|4493936|emb|CAB38972.1| (AL034556) predicted using hexExon;
          MAL3P5.6 (PFC0600w), Hypothetical protein, len: 250 aa
          [Plasmodium falciparum]
          Length = 249

 Score = 47.3 bits (110), Expect = 2e-04
 Identities = 53/215 (24%), Positives = 87/215 (39%), Gaps = 30/215 (13%)

Query: 209 NIYNLLQKHKMNTSRLYKNIFLEMRRNDYVNEKRNTRAFNSNDDAMTTGEFEF--NEYNL 266
            NIYN L++         YKN         N ++    +N    N+N          EFE    N YN
Sbjct: 13  NIYNKLEEK-------YKNFLKLKNMNSHMGASQNMNV-NNNYTMNELEEFEKINNNYNN 64

Query: 267 ADDNLRNHINQNGDFFYIKTD-----DKYIKVMYNVTTFMTNIIVVPYTKQYEFCTKIRD 321
             ++N+ N+IN   D+  IK           +K ++  YN         + I     T +++
Sbjct: 65  NNNNINNNINNYYDYMNIKVSQSVQHNKRLQDFYNNKNSFQHYIKKLKTCRFDADDIRNL 124

Query: 322 IDNHVTYLRDDMFYK-----ENMERYYYNPSNLHFDNAYSKNYVVDNDRYLYLDMNKIIK 376
            ++   + Y RD+     K        EN +      N +          N+ S NY  DN+  LY   +N++ K
Sbjct: 125 LEKRLAYERDNTLIKNIQEEENKKGIGINGNFGSESNSSSSNY--DNNYLLYRKINRLNK 182

Query: 377 FHIKNEMKKNMSEFERKEKIYEDNYIENTKKYLMK 411
             +       ++            KI            KKY++K
Sbjct: 183 TNTNKSKNRSRKRKRINSKI--------DKKYIIK 209


>gi|3845165 (AE001390) hypothetical protein [Plasmodium falciparum]
          Length = 1247

 Score = 45.7 bits (106), Expect = 6e-04
 Identities = 52/239 (21%), Positives = 94/239 (38%), Gaps = 38/239 (15%)

Query: 206 SNLNIYNLLQKHKMNTSRLYKNIFLEMRRNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYN 265
            +N N +N ++K K     R      I        +N      + +N       ++N+D               E N  N
Sbjct: 474 NNTNKWNEIKKRKKKFKREKNKIINNSFQNQEAEDDKNNNNNDNNNDNHNDNNNENNNEN 533

Query: 266 LADDNLRNHINQNGDFFYI-KTDDKYIK----VMYNVTTFMTNIIVVPYTKQYEFCTKIR 320
              D+N   N+ + N D    I      D+ Y            +YN  T         ++        YTK + +     +
Sbjct: 534 NNDNNNENNNDINNDINNIHNNDNNYYNNDNINLYNEMTKKKCMLDNSYTKYFFYIFTL- 592

Query: 321 DIDNHVTYLRDDMFYKENME--------RYYYN----------------PSNLHFDNAYS 356
              + +   ++ + FY++N +             ++YYN                                 +      N
Sbjct: 593 ---DMLPSIKFETFYEKNTDHKNFNENYKFYYNTDDDTDIINAIKKKNVKNKKKNGNIVI 649

Query: 357 KNYVVDNDRYLYLDMNKIIKFHIKNEMKKNMSEFER----KEKIYEDNYIENTKKYLMK 411
            KNY+   N+ Y YL+ N+    + I   + K        +E        K+ I+  ++Y E    K     K
```

```
Sbjct: 650 KNYINHNE-YSYLEYNENKNYEINKKEKLLTENYEYDMYIKDNIHYNDYSEGDGKQTKK 707


 Score = 41.0 bits (94), Expect = 0.016
 Identities = 58/245 (23%), Positives = 96/245 (38%), Gaps = 43/245 (17%)

Query: 207 NLNIYNLLQKHKMNTSRLYKNIFLEMRRNDYVNEKRNTRAFNSNDDAMTTGEFEFNEYNL 266
           N+N+YN + K K        Y  F  +   D +   +     + N D      E      YN
Sbjct: 564 NINLYNEMTKKKCMLDNSYTKYFFYIFTLDMLPSIKFETFYEKNTDHKNFNENYKFYYNT 623

Query: 267 ADD----------NLRNHINQNGDPF---YIKTDDKYIKVMYNVT-TFMTNIIVVPYTKQ 312
            DD          N++N    +NG+        YI  ++ Y  + YN     + N     T+
Sbjct: 624 DDDTDIINAIKKKNVKNK-KKNGNIVIKNYINHNE-YSYLEYNENKNYEINKKEKLLTEN 681

Query: 313 YEFCTKIRDIDNHVTYLRDDMFYKENMERYYYNPSNLHFDNAYSK--------NYV--VD 362
           YE+   I+D  ++  Y   D     +      + YN +N    +N Y K       +Y+  VD
Sbjct: 682 YEYDMYIKDNIHYNDYSEGDGKQTKKASSFLYNNNN---NNKYKKEDNKTQIISYMDHVD 738

Query: 363 NDR---------YLYLDMNKIIKFHIK-NEM----KKNMSEFERKEKIYEDNYIENTKKY 408
           N+                 Y + +++  F +K N+M     K+    F  +E I   +  +EN  K+
Sbjct: 739 NENGVKGLKKRNLFYNNSDQLYNFDVKDNDMIKYEKRQSKNFVEEEFINGNRKMENEDKH 798

Query: 409 LMKQY 413
           L K Y
Sbjct: 799 LKKHY 803


Query= pt|110877 44AHJDORF007 Phage 44AHJD ORF |2044-3027|1 1
         (327 letters)

>gi|1181960|emb|CAA87731.1| (Z47794) connector protein
          [Bacteriophage CP-1]
          Length = 337

 Score = 45.7 bits (106), Expect = 5e-04
 Identities = 44/184 (23%), Positives = 84/184 (44%), Gaps = 13/184 (7%)

Query: 127 QIHKLYDNCMSGNFVVMQNKPIQYNSDIEIIEHYTDELAEVALSRFSLIMQAKFSK--IF 184
           ++HK     + +    +V+ N       Y    I  +E + ++LA++ L+    L   A++ +   IF
Sbjct: 125 ELHKDNPDKIKRPCIVIPNNNF-YEPYIGYLELFCEKLADIELT-IQLNRNAQITPYFIF 182

Query: 185 KSEINDESINQLVSEIYNGAPFVKMSPMFNAD--------DDIIDLTSNSVIPALTEMKR 236
               N  S+   + ++I  N  P V ++   + D          D I +          L ++
Sbjct: 183 ADNTNVLSMKNIFNKIANFEPVVYLNKQKDQDGQDSFKQLSDYIQVFRTDAPFLLDKLHD 242

Query: 237 EYQNKISELSNYLGINSLAVDKESGVSDEEAKSNRGFTTSNSNIYLKGREP-ITFLSKRY 295
           E    +++L   ++GIN+    DK+   +    EA SN G   ++N   +  K R     +  ++K Y
Sbjct: 243 EKLRVMNQLLTFIGINNNPSDKKERLVVSEAISNNGVISANIEVGWKSRRKFVELINKCY 302

Query: 296 GLDI 299
           GL+I
Sbjct: 303 GLEI 306


>gi|1429239|emb|CAA67658| (X99260) upper collar protein
          [Bacteriophage B103]
          Length = 308

 Score = 44.9 bits (104), Expect = 8e-04
 Identities = 40/159 (25%), Positives = 73/159 (45%), Gaps = 11/159 (6%)

Query: 150 YNSDIEI-----IEHYTDELAEVA-LSRFSLIMQAKFSKIFKSEINDESINQLVSEIYNG 203
           YN+D++          +E +  +LAE+  +    +   Q      I  ++ N   S+  + ++
Sbjct: 121 YNNDLKCSTLPALEMFAQDLAELKEIIAVNQNAQKTPVLIAANDNNQLSLKNIYNQYEGN 180

Query: 204 APFVKMSPMFNADD-DIIDLTSNSVIPALTEMKREYQNKISELSNYLGINSLAVDKESGV 262
           AP + +     + D+ +    +    V+ L   K    N   E+ YLGI +   ++K+  +
Sbjct: 181 APVIFVHESLDLDNLKVFKTDAPYVVDKLNAQKNAVWN---EVMTYLGIKNANLEKKERM 237

Query: 263 SDEEAKSNRGFTTSNSNIYLKGR-EPITFLSKRYGLDIK 300
               E SN      S+ NIYLK R E     +S+ YGL++K
Sbjct: 238 VTSEVDSNDEQIESSGNIYLKARQEACNKISELYGLNLK 276


>gi|137915|sp|P07535|VG10_BPPZA UPPER COLLAR PROTEIN (CONNECTOR
          PROTEIN) (LATE PROTEIN GP10) >gi|75851|pir||WMBP10 gene
```

```
          10 protein - phage PZA >gi|216059 (M11813) upper collar
          protein [Bacteriophage PZA]
          Length = 309

 Score = 43.8 bits (101), Expect = 0.002
 Identities = 38/160 (23%), Positives = 75/160 (46%), Gaps = 13/160 (8%)

Query: 150 YNSDIEI-----IEHYTDELAEVALSRFSLIMQAKFSKIF--KSEINDESINQLVSEIYN 202
           YN+D+        +E +  ELAE+      S+    A+ + +     ++ N  S+ Q+ ++
Sbjct: 122 YNNDMSFPTTPTLELFAAELAELK-EIISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEG 180

Query: 203 GAPFVKMSPMFNADD-DIIDLTSNSVIPALTEMKREYQNKISELSNYLGINSLAVDKESG 261
           AP +         ++D  ++       + V+  L   K     N   E+  +LGI +  ++K+
Sbjct: 181 NAPVIFAHEALDSDSIEVFKTDAPYVVDKLNAQKNAVWN---EMMTFLGIKNANLEKKER 237

Query: 262 VSDEEAKSNRGFTTSNSNIYLKGR-EPITFLSKRYGLDIK 300
           +  +E  SN       S+  ++LK R E      +++ YGLD+K
Sbjct: 238 MVTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLDVK 277


>gi|137914|sp|P04332|VG10_BPPH2 UPPER COLLAR PROTEIN (CONNECTOR
          PROTEIN) (LATE PROTEIN GP10) >gi|75852|pir||WMBPC9 gene
          10 protein - phage phi-29 >gi|215328 (M14782) upper
          collar protein [Bacteriophage phi-29] >gi|215340
          (M12456) p10 connector protein [Bacteriophage phi-29]
          >gi|224161|prf||1011232A protein p10,connector
          [Bacteriophage phi-29] >gi|225365|prf||1301270E gene 10
          [Bacteriophage phi-29]
          Length = 309

 Score = 41.4 bits (95), Expect = 0.009
 Identities = 37/160 (23%), Positives = 75/160 (46%), Gaps = 13/160 (8%)

Query: 150 YNSDIEI-----IEHYTDELAEVALSRFSLIMQAKFSKIF--KSEINDESINQLVSEIYN 202
           YN+D+        +E +  ELAE+      S+    A+ + +     ++ N  S+ Q+ ++
Sbjct: 122 YNNDMAFPTTPTLELFAAELAELK-EIISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEG 180

Query: 203 GAPFVKMSPMFNADD-DIIDLTSNSVIPALTEMKREYQNKISELSNYLGINSLAVDKESG 261
           AP +         ++D  ++       + V+  L   K     N   E+  +LGI +  ++K+
Sbjct: 181 NAPVIFAHEALDSDSIEVFKTDAPYVVDKLNAQKNAVWN---EMMTFLGIKNANLEKKER 237

Query: 262 VSDEEAKSNRGFTTSNSNIYLKGR-EPITFLSKRYGLDIK 300
           +  +E  SN       S+  ++LK R E      +++ YGL++K
Sbjct: 238 MVTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLNVK 277

Query= pt|110878 44AHJDORF008 Phage 44AHJD ORF |3020-3775|2 1
         (251 letters)

>gi|4982468|gb|AAD30963.2| (AF118151) SNF1/AMP-activated kinase
          [Dictyostelium discoideum]
          Length = 718

 Score = 52.3 bits (123), Expect = 3e-06
 Identities = 28/118 (23%), Positives = 56/118 (46%), Gaps = 5/118 (4%)

Query: 121 YLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYV----SLPQSEVNIDVDN 176
           +   + GF    N ++ SN +    +N N   +  N+     T N N  +      ++  + +N + +N
Sbjct: 382 FTTTTGFNPTNSNSISNNNNNNNNNNNNTTNNNNNTTNNNNSIINNNNINNNNINNNNNN 441

Query: 177 TTLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLID-NIDKAYD 233
                +NN I+N      N ++N +N N    N N    N+  +  T+ + I   N++ +Y+
Sbjct: 442 NNNNINNNNIINNNNNNNNNNNNNNNNNNNNNNNNNSSISGGTEVFSISPNLNNSYN 499


 Score = 37.5 bits (85), Expect = 0.094
 Identities = 17/111 (15%), Positives = 45/111 (40%)

Query: 130 HNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDN 189
           +N +  +N +   +N N  + +N++ ++       +     P     + + +++     N+   ++
Sbjct: 456 NNNNNNNNNNNNNNNNNNNNNNNSSISGGTEVFSISPNLNNSYNSNSSGNSNGSNSNNNS 515

Query: 190 GKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKKILN 240
                N  +N +N N   N N    N            ID+++ + +    + N
Sbjct: 516 NNNTNNDNNNNNNNNNNNNNNNNNNNNNNNNNNNCIDSVNNSLNNENDVNN 566
```

```
 Score = 32.8 bits (73), Expect = 2.4
 Identities = 31/140 (22%), Positives = 57/140 (40%), Gaps = 14/140 (10%)

Query: 109 LNVVYSSSEVEKYLQSQGFTEHNEDTTS---NTDETSNQNATSLDNSTGMTANRNAYVSL 165
           LN  Y+S+        S       N +T +    N +   +N N   + +N+       N N   +
Sbjct: 494 LNNSYNSNSSGNSNGSNSNNNSNNNTNNDNNNNNNNNNNNNNNNNNNNNNNNNNNNNCIDS 553

Query: 166 PQSEVN--IDVDNTTLRFADNNTIDNGKTVNKSS--------NESNQNAKRNQNQKGNAK 215
              + +N    DV+N+ +    +NN  D+G    N           ++ N N +    N  GN
Sbjct: 554 VNNSLNNENDVNNSNINNNNNNNSDDGSNNNSYEGGGDVLLLSDLNGNNQLGGNDNGNVV 613

Query: 216 GTQFTKQYLIDNIDKAYDLR 235
                Q L++++D    D++
Sbjct: 614 NLNNNFQ-LLNSLDLNSDIQ 632


 Score = 31.7 bits (70), Expect = 5.4
 Identities = 25/115 (21%), Positives = 48/115 (41%), Gaps = 10/115 (8%)

Query: 130 HNEDTTSNTDETSNQNATSLDNST---GMTAN-RNAYVSLPQSEVNIDVDNTTLRFADNN 185
           +N +   +N +   +N N +S+     T       ++ N  N+Y S     S  N +  N+       +N
Sbjct: 462 NNNNNNNNNNNNNNNNNSSISGGTEVFSISPNLNNSYNS--NSSGNSNGSNSNNNSNNNT 519

Query: 186 TIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKKILN 240
             DN      N ++N +N N      N N    N                    + ++++   D+    +N
Sbjct: 520 NNDN----NNNNNNNNNNNNNNNNNNNNNNNNNCIDSVNNSLNNENDVNNSNIN 570


 Score = 31.7 bits (70), Expect = 5.4
 Identities = 15/104 (14%), Positives = 43/104 (40%)

Query: 110 NVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSE 169
           N+  +++       + +      +N +   +N +   +N N   + +N+      + +        V
Sbjct: 434 NINNNNNNNNNNINNNNIINNNNNNNNNNNNNNNNNNNNNNNNNNNSSISGGTEVFSISPN 493

Query: 170 VNIDVDNTTLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGN 213
           +N     ++ +      ++ +  +N       N +++ +N N      N N     N
Sbjct: 494 LNNSYNSNSSGNSNGSNSNNNSNNNTNNDNNNNNNNNNNNNNNN 537


 Score = 30.9 bits (68), Expect = 9.2
 Identities = 16/84 (19%), Positives = 34/84 (40%)

Query: 130 HNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDN 189
           +N +  +N +   +N N   + +N+       +          S+  +  N       N++        +N+ +N
Sbjct: 455 NNNNNNNNNNNNNNNNNNNNNNNNNSSISGGTEVFSISPNLNNSYNSNSSGNSNGSNSNNN 514

Query: 190 GKTVNKSSNESNQNAKRNQNQKGN 213
                + N +N N    N N    N
Sbjct: 515 SNNNTNNDNNNNNNNNNNNNNNNN 538


>gi|1730077|sp|P18160|KYK1_DICDI NON-RECEPTOR TYROSINE KINASE SPORE
          LYSIS A (TYROSINE-PROTEIN KINASE 1) >gi|974334 (U32174)
          non-receptor tyrosine kinase [Dictyostelium discoideum]
          Length = 1584

 Score = 46.5 bits (108), Expect = 2e-04
 Identities = 29/106 (27%), Positives = 48/106 (44%), Gaps = 4/106 (3%)

Query: 130 HNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNID---VDNTTLRFADN-N 185
           +NED +SN +   +N N   + +N+       N N      +       +  N +       ++NTT          N N
Sbjct: 442 NNEDISSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNSNSSNTNNNNINNTTNNNNSNSN 501

Query: 186 TIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKA 231
           +N      N +SN +N N      N N      N           TK+    I  + D++
Sbjct: 502 NNNNNNNSNSNSNSNNNNINNNNNNNNNNNIYLTKKPSIGSTDES 547


 Score = 34.0 bits (76), Expect = 1.1
 Identities = 20/117 (17%), Positives = 46/117 (39%)

Query: 87  NRQTVEAFGMQVITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETSNQNA 146
           N       G  IT   T       + + ++ ++        +      +N +   +N +   +N N
```

```
Sbjct: 415 NNNNNNIIGNGKITTTTTTTSTSPSSINNNEDISSNNNNNNNNNNNNNNNNNNNNNNNNNNN 474

Query: 147 TSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNGKTVNKSSNESNQN 203
           + ++++ T N N  +    +  N + +N         N+  +N    N ++N +N N
Sbjct: 475 NNNNSNSSNTNNNNINNTTNNNNSNSNNNNNNNNSNSNSNSNNNNINNNNNNNNNNN 531


 Score = 33.2 bits (74), Expect = 1.8
 Identities = 18/88 (20%), Positives = 35/88 (39%)

Query: 130 HNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDN 189
           +N + ++N +  +N N          T  T    +  S+  +E      +N      +NN  +N
Sbjct: 405 NNNNNSNNNNNNNNNNIIGNGKITTTTTTTSTSPSSINNNEDISSNNNNNNNNNNNNNNN 464

Query: 190 GKTVNKSSNESNQNAKRNQNQKGNAKGT 217
               N ++N +N N+  +      N   T
Sbjct: 465 NNNNNNNNNNNNNSNSSNTNNNNINNT 492


 Score = 32.5 bits (72), Expect = 3.1
 Identities = 18/94 (19%), Positives = 37/94 (39%)

Query: 120 KYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTL 179
           K + S       N +  +N++  +N N  ++  +  +T          S        N D+ +
Sbjct: 392 KNVNSTSILVPNGNNNNNSNNNNNNNNNNIIGNGKITTTTTTTSTSPSSINNNEDISSNNN 451

Query: 180 RFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGN 213
              +NN  +N     N ++N +N N    + +  N
Sbjct: 452 NNNNNNNNNNNNNNNNNNNNNNNNNNNSNSSNTN 485


 Score = 32.5 bits (72), Expect = 3.1
 Identities = 24/110 (21%), Positives = 44/110 (39%), Gaps = 10/110 (9%)

Query: 138 TDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNGK------ 191
           T  T++ + +S++N+  +++N N    +    + N + +N       +NN   N
Sbjct: 429 TTTTSTSPSSINNNEDISSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNSNSSNTNNNN 488

Query: 192 ----TVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKK 237
             T N +SN +N N   N N   N+          +N +    L KK
Sbjct: 489 INNTTNNNNSNSNNNNNNNNSNSNSNSNNNNINNNNNNNNNNNNIYLTKK 538


>gi|3758855|emb|CAB11140.1| (Z98551) predicted using hexExon;
          MAL3P6.11 (PFC0760c), Hypothetical protein, len: 3395 aa
          [Plasmodium falciparum]
          Length = 3394

 Score = 46.5 bits (108), Expect = 2e-04
 Identities = 52/202 (25%), Positives = 96/202 (46%), Gaps = 32/202 (15%)

Query: 21  FNEFVNDNKLTFYDDEFQFMQKMLKFD-KDVLAIVNEKVFKGFSLKDELSDL--LFKKSF 77
            F ++ ++ K T   D+   M+K  K D  DV  + NEK++    L ++L+ +  + KK
Sbjct: 665 FEKYCSNIKNTLIRDD---MKKFRKPDISDVHILHNEKIYLEKLLNEKLNYIKDIEKKLD 721

Query: 78  TIHFLDREINRQTVEAFGMQV-----ITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNE 132
            +H +    IN+   + + +QV       I V  +  DY  +  S + + K    +   +N
Sbjct: 722 ELHGV---INKNKEDIYILQVEKQTLIKVISSVYDYTKME-SENHIFKMNTTWNKMLNNV 777

Query: 133 DTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNGKT 192
             +SN D  +NQN  +++N+  +  N+N              N +++N      + N  +N
Sbjct: 778 HMSSNKDY-NNQNNQNIENNQNIENNQN----------NQNIEN------NQNIENNQNN 820

Query: 193 VNKSSNESNQNAKRNQNQKGNA 214
             N  +N++NQN + NQN + NA
Sbjct: 821 QNNQNNQNNQNNQNNQNNQNNA 842


 Score = 33.6 bits (75), Expect = 1.4
 Identities = 46/221 (20%), Positives = 89/221 (39%), Gaps = 37/221 (16%)

Query: 10  DFIKSELIKKGFNEFVNDNKLTFYDDEFQFMQKMLKFDKDVLAIVNEKVFKGFSLKDELS 69
            D +K E  K  N    + +L  Y +  + M+K  K           + V K  SL
Sbjct: 367 DSLKIEYNKSKTNIQQLNEQLVNYKNFIKEMEKKYK----------QLVVKNNSLFSITH 416

Query: 70  DLLFKKSFTIHFLDREINRQTVEAFGMQVITVCITH---EDYLNVVYSSSEVEKYLQSQG 126
```

```
                D +  K+  I  + R  + + +     ++  + I H   +D+L+V+Y    + + L +
Sbjct: 417 DFINLKNSNIIIIRRTSDMKQI----FKMYNLDIEHFNEQDHLSVIY----IYEILYNTN 468

Query: 127 FTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNT 186
             +N D  +N D  +N N  + +N+     N N          N + +N  +
Sbjct: 469 -DNNNNDNDNNNDNNNNNNNNNDNNNNNNDNNNN---------NNNYNNIMM------M 512

Query: 187 IDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDN 227
            I+N  + N  ++ +  N + N N + N    + + +Y I+N
Sbjct: 513 IENMNSGNHPNSNNLHNYRHNTNDENNLSSLKTSFRYKINN 553
```

```
 Score = 32.8 bits (73), Expect = 2.4
 Identities = 28/122 (22%), Positives = 53/122 (42%), Gaps = 2/122 (1%)

Query: 119  EKYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNID-VDNT 177
             E Y  S  +  +++     N +  +N +  + DN+       N N    ++      +N D ++N
Sbjct: 2838 ENYPVSTHYDNNDDINKDNINNDNNNDNINDDNNNDNINNDNNNDNINNDNINNDNINND 2897

Query: 178  TLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKK 237
                 +N+  +NG       SSN ++ N    N N K N +G   +  +  +  +  YD   K
Sbjct: 2898 NNNDNNNDNSNNGFVCELSSNINDFNNILNVN-KDNFQGINKSNNFSTNLSEYNYDAYVK 2956

Query: 238  IL 239
             I+
Sbjct: 2957 IV 2958
```

```
 Score = 32.5 bits (72), Expect = 3.1
 Identities = 46/249 (18%), Positives = 101/249 (40%), Gaps = 31/249 (12%)

Query: 9    YDFIKSELIKKGFNEFVNDNKLTFYDDEFQFMQKMLKFDKDVLAIVNEKVFKGFSLKDEL 68
             Y+++K    ++    N    N NK         E     Q++ K+  + + + +E    K     L++
Sbjct: 2150 YNYVK---VQNATNREDNKNK------ERNLSQEIYKYINENIDLTSELEKKNDMLENYK 2200

Query: 69   SDL------LFKKSFTIHFLDREINRQTVEAFGMQVITVCITHEDYLNVVYSSSEVEKYL 122
             ++L       ++K +  I  L        +          M+    + +          N +     E+ + L
Sbjct: 2201 NELKEKNEEIYKLNNDIDMLSNNCKKLKESIMMMEKYKIIMN-----NNIQEKDEIIENL 2255

Query: 123  QSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTAN----RNAYVSLPQSE----VNIDV 174
             +++ +     +D  +N             +  ++S  M+ +      N + +L +S         N+D+
Sbjct: 2256 KNK-YNNKLDDLINNYSVVDKSIVSCFEDSNIMSPSCNDILNVFNNLSKSNKKVCTNMDI 2314

Query: 175  DNTTLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDL 234
              N  +      ++I+N    +N   +N +N N     N N    N K          YL++N+     D
Sbjct: 2315 CNENMDSI--SSINNVNNINNVNNINNVNNINNVNNINNVKNIVDINNYLVNNLQLNKDN 2372

Query: 235  RKKILNEFD 243
                 I+ +F+
Sbjct: 2373 DNIIIIKFN 2381
```

```
 Score = 32.1 bits (71), Expect = 4.1
 Identities = 20/103 (19%), Positives = 48/103 (46%), Gaps = 2/103 (1%)

Query: 115  SSEVEKYLQSQGFTEHNEDTTSNTDETSNQN--ATSLDNSTGMTANRNAYVSLPQSEVNI 172
             +++ EKY         EH  +    N D  +N+N       L ++   ++ + N     S   ++E+
Sbjct: 3264 NNDEEKYSCHDDKNEHTNNDLLNIDHDNNKNNITDELYSTYNVSVSHNKDPSNKENEIQN 3323

Query: 173  DVDNTTLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAK 215
              +    +        D N   ++      N   ++E+++N  +  ++N  +  +  K
Sbjct: 3324 LISIDSSNENDENDENDENDENDENDENDENDENDENDEK 3366
```

```
 Score = 30.9 bits (68), Expect = 9.2
 Identities = 27/118 (22%), Positives = 53/118 (44%), Gaps = 15/118 (12%)

Query: 104  THEDYLNVVYSSSEV----EKYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANR 159
             T+ D LN+ + +++        E Y           HN+D ++  +E    QN   S+D+S        N
Sbjct: 3280 TNNDLLNIDHDNNKNNITDELYSTYNVSVSHNKDPSNKENEI--QNLISIDSSNENDEND 3337

Query: 160  NAYVSLPQSEVNIDVDNTTLRFADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
                 +++ N + D           D N  ++      N      +E+++N +  ++N    N +GT
Sbjct: 3338 EN----DENDENDEN-----DENDENDENDEKDENDENDENDENFDNNNEGT 3386
```

```
>gi|585795|sp|P21538|REB1_YEAST DNA-BINDING PROTEIN REB1 (QBP)
          >gi|626139|pir||S45907 DNA-binding protein REB1 - yeast
          (Saccharomyces cerevisiae) >gi|536280|emb|CAA84992|
          (Z35918) ORF YBR049c [Saccharomyces cerevisiae]
          >gi|559944|emb|CAA86391| (Z46260) REB1 DNA-binding
          protein [Saccharomyces cerevisiae]
          Length = 810

 Score = 45.7 bits (106), Expect = 3e-04
 Identities = 34/158 (21%), Positives = 72/158 (45%), Gaps = 14/158 (8%)

Query: 83  DREINRQTVEAFGMQVITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETS 142
            D+  N+++VE    ++ + V + H+++    +++       K+ + Q    E + D    N ++ S
Sbjct: 7   DKNANQESVEEAVLKYVGVGLDHQNHDPQLHTKDLENKHSKKQNIVESSSDVDVNNNDDS 66

Query: 143 NQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTID---NGKTVNKSSNE 199
            N+N  + D+S  ++A          L  +E + +VD+         N  +D        N+  +E
Sbjct: 67  NRNEDNNDDSENISA-------LNANESSSNVDHANSNEQHNAVMDWYLRQTAHNQQDDE 119

Query: 200 SNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKK 237
             ++N   N    GN     F++   ++   +D   D  KK
Sbjct: 120 DDEN--NNNTDNGNDSNNHFSQSDIV--VDDDDDKNKK 153


>gi|172372 (M58728) DNA-binding protein [Saccharomyces cerevisiae]
          Length = 809

 Score = 45.7 bits (106), Expect = 3e-04
 Identities = 34/158 (21%), Positives = 72/158 (45%), Gaps = 14/158 (8%)

Query: 83  DREINRQTVEAFGMQVITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETS 142
            D+  N+++VE    ++ + V + H+++    +++       K+ + Q    E + D    N ++ S
Sbjct: 7   DKNANQESVEEAVLKYVGVGLDHQNHDPQLHTKDLENKHSKKQNIVESSNDVDVNNNDDS 66

Query: 143 NQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTID---NGKTVNKSSNE 199
            N+N  + D+S  ++A          L  +E + +VD+         N  +D        N+  +E
Sbjct: 67  NRNEDNNDDSENISA-------LNANESSSNVDHANSNEQHNAVMDWYLRQTAHNQQDDE 119

Query: 200 SNQNAKRNQNQKGNAKGTQFTKQYLIDNIDKAYDLRKK 237
             ++N   N    GN     F++   ++   +D   D  KK
Sbjct: 120 DDEN--NNNTDNGNDSNNHFSQSDIV--VDDDDDKNKK 153


>gi|2952545 (AF051898) coronin binding protein [Dictyostelium
          discoideum]
          Length = 560

 Score = 44.9 bits (104), Expect = 6e-04
 Identities = 26/83 (31%), Positives = 39/83 (46%), Gaps = 5/83 (6%)

Query: 131 NEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNG 190
            N +  +N      +N N+ S +NS     +N N+  + P      N D DN T      +NNT +N
Sbjct: 404 NNNNNNNIINNNNSNSNSNNNSNN-NSNNNSNRNSPNHNNNGDNDNNT----NNNTNNNN 458

Query: 191 KTVNKSSNESNQNAKRNQNQKGN 213
                N ++N +N N    N N   N
Sbjct: 459 NNNNNNNNNNNNNNNNNNNNNNN 481


 Score = 41.4 bits (95), Expect = 0.006
 Identities = 22/88 (25%), Positives = 43/88 (48%), Gaps = 6/88 (6%)

Query: 130 HNEDTTSNTDETSNQNATSLDN---STGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNT 186
            +  ++ +N++  SN N+ + +N    + G  AN++   + P + +N + DN         +NN
Sbjct: 337 NRNNSNNNSNNNSNNNSNNSNNRNITNGSNANKS---NSPNNNLNTNNDNKNNNSNNNNN 393

Query: 187 IDNGKTVNKSSNESNQNAKRNQNQKGNA 214
             +N        S+N +N N    N N   N+
Sbjct: 394 SNNNSNNGNSNNNNNNNIINNNNSNSNS 421


 Score = 40.6 bits (93), Expect = 0.011
 Identities = 24/101 (23%), Positives = 41/101 (39%), Gaps = 2/101 (1%)

Query: 115 SSEVEKYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDV 174
            S+      L +      ++N      +N      ++ N   S +N+          N N     S       +  N +
```

```
Sbjct: 370 SNSPNNNLNTNNDNKNNNSNNNNNSNNNSNNGNSNNNNNNNIINNNNSNSNSNNNSNNNS 429

Query: 175 DNTTLRFADN--NTIDNGKTVNKSSNESNQNAKRNQNQKGN 213
           +N + R + N  N  DN    N ++N +N N   N N   N
Sbjct: 430 NNNSNRNSPNHNNNGDNDNNTNNNTNNNNNNNNNNNNNNNN 470


 Score = 40.2 bits (92), Expect = 0.014
 Identities = 21/80 (26%), Positives = 39/80 (48%), Gaps = 9/80 (11%)

Query: 130 HNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDN 189
           +N D  +NT+   +N N  + +N+      N N          N + +N     +ADN+  ++
Sbjct: 442 NNGDNDNNTNNNTNNNNNNNNNNNNNNNNNN---------NNNNNNNNNNYADNSNNNS 492

Query: 190 GKTVNKSSNESNQNAKRNQN 209
             + N +SN +N N   +N+N
Sbjct: 493 SNSNNNNSNSNNNNDNKNEN 512


 Score = 39.5 bits (90), Expect = 0.024
 Identities = 26/111 (23%), Positives = 44/111 (39%), Gaps = 20/111 (18%)

Query: 112 VYSSSEVEKYLQSQ--GFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSE 169
           VY +     K+ ++    G    +N ++ +N++  SN N    ++N       N N
Sbjct: 296 VYCTHHHTKFYETHRNGLLNNNNNSNNNSNSNSNSNNNNGINNRNNSNNNSN--------- 346

Query: 170 VNIDVDNTTLRFADNNTIDNGKTVNKSS------NESNQNAKRNQNQKGNA 214
              +  N      ++N  I NG    NKS+        N +N N   N N    N+
Sbjct: 347 ---NNSNNNSNNSNNRNITNGSNANKSNSPNNNLNTNNDNKNNNSNNNNNS 394


 Score = 37.5 bits (85), Expect = 0.094
 Identities = 24/96 (25%), Positives = 41/96 (42%), Gaps = 1/96 (1%)

Query: 124 SQGFTEHNEDTTSNTDETSNQNATSLDNSTGM-TANRNAYVSLPQSEVNIDVDNTTLRFA 182
           S     + +N +  SN +  ++ N     DN+T    T N N    +     +  N + +N
Sbjct: 421 SNNNSNNNSNNNSNRNSPNHNNNGDNDNNTNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Query: 183 DNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQ 218
           +NN  DN      + +SN +N N+   N + K       Q
Sbjct: 481 NNNYADNSNNNSSNSNNNNSNSNNNNDNKNENSDNQ 516


 Score = 35.6 bits (80), Expect = 0.36
 Identities = 25/99 (25%), Positives = 42/99 (42%), Gaps = 18/99 (18%)

Query: 130 HNEDTTSNTDETSNQNATSLDNST-GMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTID 188
           +N +    SN +    +N N ++  N T G  AN++    + P + +N + DN       +NN  +
Sbjct: 339 NNSNNNSNNNSNNNSNNSNNRNITNGSNANKS---NSPNNNLNTNNDNKNNNSNNNNNSN 395

Query: 189 NGKTV--------------NKSSNESNQNAKRNQNQKGN 213
           N                N S++ SN N+ N N   N
Sbjct: 396 NSNNGNSNNNNNNNIINNNNSNSNSNNNSNNNSNNNSN 434


 Score = 35.2 bits (79), Expect = 0.47
 Identities = 21/94 (22%), Positives = 42/94 (44%), Gaps = 5/94 (5%)

Query: 124 SQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFAD 183
           + G    +   ++ +N    T+N N   +  N+        N N+  +         N + +N   +    +
Sbjct: 362 TNGSNANKSNSPNNNLNTNNDNKNNNSNN-----NNNSNNNSNNGNSNNNNNNNIINNNN 416

Query: 184 NNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
           +N+  N  + N S+N SN+N+   + N   N    T
Sbjct: 417 SNSNSNNNSNNNSNNNSNRNSPNHNNNGDNDNNT 450


 Score = 35.2 bits (79), Expect = 0.47
 Identities = 29/118 (24%), Positives = 53/118 (44%), Gaps = 12/118 (10%)

Query: 115 SSEVEKYLQS-QGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNID 173
           SS+ E  ++  +GF + +  T+N  ++N      D S+G + +  + V+ P+S +N
Sbjct: 114 SSDSEADIEDDKGFQD--KPITTNNSGSNNPLKNLKDYSSGSSGSSRSGVNQPRSNINNS 171

Query: 174 VDNTTLRFADNNT---------IDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQ 222
             D    + +N++           I  +  T  +  NQN    +NQNQ  N    Q +Q
```

```
Sbjct: 172 NDKYKSKSSSSNSNSSSSGGSLISSLLTGGNTYQNQNQNQNQNQNQNNNQSQLQQQQQ 229


 Score = 34.4 bits (77), Expect = 0.81
 Identities = 24/94 (25%), Positives = 38/94 (39%), Gaps = 12/94 (12%)

Query: 131 NEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNG 190
           N +T +N +  +N N  + +N+     N N       S  N    N       +NN+  N
Sbjct: 451 NNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNYADNSNNNSSNSN------NNNSNSNN 504

Query: 191 KTVNKSSNESNQNAKR------NQNQKGNAKGTQ 218
              NK+ N  NQ+  R       ++NQK  +   Q
Sbjct: 505 NNDNKNENSDNQSVLRSNEKFTDENQKNGSDDQQ 538


 Score = 33.6 bits (75), Expect = 1.4
 Identities = 22/90 (24%), Positives = 35/90 (38%)

Query: 124 SQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFAD 183
           S       N     SN +++++ N      N+      N N      +     +  N + +N
Sbjct: 353 SNNSNNRNITNGSNANKSNSPNNNLNTNNDNKNNNSNNNNNSNNNSNNGNSNNNNNNNII 412

Query: 184 NNTIDNGKTVNKSSNESNQNAKRNQNQKGN 213
           NN    N  + N S+N SN N+ RN      N
Sbjct: 413 NNNNSNSNSNNNSNNNSNNNSNRNSPNHNN 442


>gi|535260|emb|CAA82996| (Z30339) STARP antigen [Plasmodium
           reichenowi]
           Length = 655

 Score = 44.5 bits (103), Expect = 7e-04
 Identities = 31/114 (27%), Positives = 47/114 (41%), Gaps = 14/114 (12%)

Query: 128 TEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVN------IDVDNTTLRF 181
           T++N    T  TD  +       + +N+T    A  N     +    ++ N          D +NT   +
Sbjct: 433 TDNNNTNTKATDSNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKA 492

Query: 182 ADNNTI-----DNGKTVNKSSNESNQNAKRNQNQKGNAKGT---QFTKQYLIDN 227
            DNN        DN  T  K+++ +N N K    N  N K T      T QY+  N
Sbjct: 493 TDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNNTNQYVFAN 546


 Score = 44.5 bits (103), Expect = 7e-04
 Identities = 30/103 (29%), Positives = 44/103 (42%), Gaps = 13/103 (12%)

Query: 128 TEHNEDTTSNTDETSNQNATSLDNS----TGMTANRNAYVSLPQSEVN----IDVDNTTL 179
           T++N    T  TD+++N +  +  + DN+     T  T N N          S       D +NT
Sbjct: 401 TDNNNTDTKATDKSNNTDTKATDNNNNNTDTKATDNNNTNTKATDSNNTNTKATDNNNTNT 460

Query: 180 RFADNNTI-----DNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
           + DNN       DN  T  K+++ +N N K    N  N K T
Sbjct: 461 KATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKAT 503


 Score = 42.6 bits (98), Expect = 0.003
 Identities = 27/96 (28%), Positives = 43/96 (44%), Gaps = 10/96 (10%)

Query: 128 TEHNEDTTSNTDETSNQNATSLD-NSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNT 186
           T++N +T +    + +N   + D N+T     A N    +    ++ N    NT  +  DNN
Sbjct: 422 TDNNNNTDTKATDNNNTNTKATDSNNTNTKATDNNNTNTKATDNN----NTNTKATDNNN 477

Query: 187 I-----DNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
                  DN  T  K+++ +N N K    N  N K T
Sbjct: 478 TNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKAT 513


 Score = 41.8 bits (96), Expect = 0.005
 Identities = 35/150 (23%), Positives = 59/150 (39%), Gaps = 9/150 (6%)

Query: 85  EINRQTVEAFGMQVITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETSNQ 144
           E N+  ++ G   T+     +N     +      E    + +Q  T +N  TT+ +       N
Sbjct: 118 ETNKTNIKLTGNNSTTINTNLTENTNA--TKKLTENVITNQILTGNNNTTTNTSSTEHNN 175

Query: 145 NATSLDNSTGMTANRNAYVSLPQSEVNIDVDNTTLRFADNNTIDNGKTVNKSSNESNQNA 204
           N  +  NSTG T+              NI + N  L   +N T +   T + ++  +N N+
```

```
Sbjct: 176 NINTNTNSTGNTSTTKKLTE------NI-ITNQILTGNNNTTTNTSSTEHNNNINTNTNS 228

Query: 205 KRNQNQKGNAKGTQFTKQYLIDNIDKAYDL 234
             N N    N       T +    DNI+    +L
Sbjct: 229 TDNSNTNTNLTDITTTTKKWTDNINTTQNL 258


 Score = 41.8 bits (96), Expect = 0.005
 Identities = 30/101 (29%), Positives = 43/101 (41%), Gaps = 13/101 (12%)

Query: 130 HNEDTTSNTDETSNQNATSLDNS-TGMTANRNAYVSLPQSEVNIDV------DNTTLRFA 182
           +N DT S  ++ ++  AT  DN+ T  T N N   +        N D        +NT   +
Sbjct: 363 NNTDTISTDNDNTDTKATDNDNTDTKATDNNNNTDTKATDNNNTDTKATDKSNNTDTKAT 422

Query: 183 DNN------TIDNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
           DNN         DN  T  K+++ +N N K   N   N K T
Sbjct: 423 DNNNNTDTKATDNNNTNTKATDSNNTNTKATDNNNTNTKAT 463


 Score = 40.6 bits (93), Expect = 0.011
 Identities = 31/121 (25%), Positives = 47/121 (38%), Gaps = 31/121 (25%)

Query: 128 TEHNEDTTSNTDETSNQNAT-----SLDNSTGMTANRNAYVSLPQSEVN----------- 171
           TEHN +   +NT+ T N + T        ++  +   +T N N    +    +E N
Sbjct: 171 TEHNNNINTNTNSTGNTSTTKKLTENIITNQILTGNNNTTTNTSSTEHNNNINTNTNSTD 230

Query: 172 --------IDVDNTTLRFADN-------NTIDNGKTVNKSSNESNQNAKRNQNQKGNAKG 216
                    D+  TT ++ DN          T  N  TV+   +N +N N K   N   N K
Sbjct: 231 NSNTNTNLTDITTTTKKWTDNINTTQNLTTSTNTTTVSTDNNNNNINTKPTDNNNTNIKS 290

Query: 217 T 217
           T
Sbjct: 291 T 291


 Score = 38.3 bits (87), Expect = 0.055
 Identities = 28/98 (28%), Positives = 41/98 (41%), Gaps = 10/98 (10%)

Query: 128 TEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVNIDVD-NTTLRFADNNT 186
           TEHN +   +NT+  S   N+ +  N T +T       +     + N+       NTT    DNN
Sbjct: 216 TEHNNNINTNTN--STDNSNTNTNLTDITTTTKKWTDNINTTQNLTTSTNTTTVSTDNNN 273


Query: 187 -------IDNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
                  DN  T  KS++   N    K   N+   + K T
Sbjct: 274 NNINTKPTDNNNTNIKSTDNYNTGTKETDNKNTDIKAT 311


 Score = 37.5 bits (85), Expect = 0.094
 Identities = 31/106 (29%), Positives = 45/106 (42%), Gaps = 18/106 (16%)

Query: 128 TEHNEDTTSNTDETSNQN----ATSLDNSTGMTANRNAYVSLPQSEVN-------IDVDN 176
           T++N +T    +T  T N N       AT     N+T    A  N    +    ++ N          D +N
Sbjct: 390 TDNNNNT--DTKATDNNNTDTKATDKSNNTDTKATDNNNNTDTKATDNNNTNTKATDSNN 447

Query: 177 TTLRFADNN-----TIDNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
           T   +  DNN         DN  T  K+++ +N N K   N   N K T
Sbjct: 448 TNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKAT 493


 Score = 35.2 bits (79), Expect = 0.47
 Identities = 24/109 (22%), Positives = 46/109 (42%), Gaps = 6/109 (5%)

Query: 128 TEHNEDTTSNTDETSNQNATSLDNSTGMTANRNAYVSLPQSEVN------IDVDNTTLRF 181
           T++N    T  TD  +       + +N+T    A  N    +    ++ N          D +NT   +
Sbjct: 473 TDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKATDNNNTNTKA 532

Query: 182 ADNNTIDNGKTVNKSSNESNQNAKRNQNQKGNAKGTQFTKQYLIDNIDK 230
            DNN    N          + +E++    + K N++     N++    +    K    +     +DK
Sbjct: 533 TDNNNNTNQYVFANNYDETTSDDKLNKDSCDNSEEKENIKSMINAYLDK 581


 Score = 34.4 bits (77), Expect = 0.81
 Identities = 26/126 (20%), Positives = 46/126 (35%), Gaps = 7/126 (5%)
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```
Query: 99  ITVCITHEDYLNVVYSSSEVEKYLQSQGFTEHNEDTTSNTDETSNQNATSLDNSTGMTAN 158
           IT   T+ + ++   S + V     S   T   +++ +N   T N N  ++      T
Sbjct: 318 ITTDNTNTNVISTDNSKTNVISKDNSNTHTISTDNSKTNVISTDNNNTDTISTDNDNTDT 377

Query: 159 RNAYVSLPQSEVNIDVDNTTLRFADNNTID-------NGKTVNKSSNESNQNAKRNQNQK 211
           +        ++   + +NT  +  DNN  D       N      + N +N + K   N
Sbjct: 378 KATDNDNTDTKATDNNNNTDTKATDNNNTDTKATDKSNNTDTKATDNNNNTDTKATDNNN 437

Query: 212 GNAKGT 217
            N K T
Sbjct: 438 TNTKAT 443


 Score = 34.4 bits (77), Expect = 0.81
 Identities = 30/100 (30%), Positives = 44/100 (44%), Gaps = 14/100 (14%)

Query: 131 NEDTTSNTDETSNQNATSLDNS-TGMTANRNAY---VSLPQSEVNI---DVDNTTLRFAD 183
           N + T  TD T N N  S DNS T + +  N+    +S   S+ N+   D +NT     D
Sbjct: 313 NNNITITTDNT-NTNVISTDNSKTNVISKDNSNTHTISTDNSKTNVISTDNNNTDTISTD 371

Query: 184 NNTIDNGKTVNKSS------NESNQNAKRNQNQKGNAKGT 217
           N+  D   T N ++      N +N + K   N   + K T
Sbjct: 372 NDNTDTKATDNDNTDTKATDNNNNTDTKATDNNNTDTKAT 411


 Score = 34.4 bits (77), Expect = 0.81
 Identities = 28/101 (27%), Positives = 41/101 (39%), Gaps = 15/101 (14%)

Query: 131 NEDTTSNTDETSNQNATSLDNSTGMTA--NRNAYVSLPQSEVNIDV------DNTTLRFA 182
           N DT +  ++ ++  AT  +N+T   A  N N          N D       +NT  +
Sbjct: 374 NTDTKATDNDNTDTKATDNNNNTDTKATDNNNTDTKATDKSNNTDTKATDNNNNTDTKAT 433

Query: 183 DNNTIDNGK------TVNKSSNESNQNAKRNQNQKGNAKGT 217
           DNN   N K      T  K+++ +N N K   N   N K T
Sbjct: 434 DNNN-TNTKATDSNNTNTKATDNNNTNTKATDNNNTNTKAT 473


 Score = 32.5 bits (72), Expect = 3.1
 Identities = 30/110 (27%), Positives = 40/110 (36%), Gaps = 23/110 (20%)

Query: 131 NEDTTSNTDETSNQNATSLDNS-----TGMTANRNAYVSLPQS----EVNIDVDNTTLRF 181
           N +TT N   ++N    S DN+     T  T N N  +    +        D  NT ++
Sbjct: 251 NINTTQNLTTSTNTTTVSTDNNNNNINTKPTDNNNTNIKSTDNYNTGTKETDNKNTDIKA 310

Query: 182 ADNNTI--------------DNGKTVNKSSNESNQNAKRNQNQKGNAKGT 217
            DNN I              DN KT   S + SN +     N K N   T
Sbjct: 311 TDNNNITITTDNTNTNVISTDNSKTNVISKDNSNTHTISTDNSKTNVIST 360


>gi|1429240|emb|CAA67659| (X99260) lower collar protein
          [Bacteriophage B103]
          Length = 293

 Score = 43.8 bits (101), Expect = 0.001
 Identities = 53/204 (25%), Positives = 79/204 (37%), Gaps = 42/204 (20%)

Query: 56  EKVFKG----FSLKDELSDLLFKKSFTIHFLD----REINRQTVEAFGMQVITVCITHED 107
           EK+ KG    F  +  + D  ++K F  HF+     REI  +T   F   + T  I +
Sbjct: 26  EKIEKGRPKLFDFQYPIFDESYRKVFETHFIRNFYMREIGFETEGLFKFNLETWLIINMP 85

Query: 108 YLNVVYSSSEVEKY-------LQSQGFTEH------NEDTT--------SNTDETSNQNA 146
           Y N ++ S E+ KY       L + G  ++      N DTT        SNT  +   NA
Sbjct: 86  YFNKLFES-ELIKYDPLENTRLNTTGNKKNDTERNDNRDTTGSMKADGKSNTKTSDKTNA 144

Query: 147 TSLDNSTGMTA--------NRNAYVSLPQSEVNIDVDN--TTLRFADNNTIDNGKTVNKS 196
           T      G T         NR      P S +N+  ++   TL +A  + I+   T NK
Sbjct: 145 TGSSKEDGKTTGSVTDDNFNRKIDSDQPDSRLNLTTNDGQGTLEYA--SAIEENNTNNKR 202

Query: 197 SNESNQNAKRNQNQKGNAKGTQFT 220
           +     N   +   +    GT  T
Sbjct: 203 NTTGTNNVTSSAESESTGSGTSDT 226


Query= pt|110879 44AHJDORF009 Phage 44AHJD ORF |5744-6496|2 1
         (250 letters)
```

```
>gi|2764981|emb|CAA69021.1| (Y07739) N-acetylmuramoyl-L-alanine
          amidase [Staphylococcus phage Twort]
          Length = 467

 Score =  180 bits (452), Expect = 1e-44
 Identities = 89/157 (56%), Positives = 109/157 (68%), Gaps = 8/157 (5%)

Query: 1   MKSQQQAKEWIYKHEGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDAINNDFK 60
            MK+ +QA+ +I       G DFDG YG+QCMDL+V Y+Y++TDGK+RMWGNAKDAINN F
Sbjct: 1   MKTLKQAESYIKSKVNTGTDFDGLYGYQCMDLAVDYIYHVTDGKIRMWGNAKDAINNSFG 60

Query: 61  GLATVYKNTPSFKPQLGDVAVYTNGQ---YGHIQCVLS----GNLDYYTCLEQNWLGGGF 113
            G ATVYKN P+F+P+ GDV V+T G     YGHI  V +    G+L Y T LEQNW G G
Sbjct: 61  GTATVYKNYPAFRPKYGDVVVWTTGNFATYGHIAIVTNPDPYGDLQYVTVLEQNWNGNGI 120

Query: 114 DGWEKATIRTHYYDGVTHFIRPKFSGSNS-KALETSK 149
               E ATIRTH Y G+THFIRP F+  +S K  +T K
Sbjct: 121 YKTELATIRTHDYTGITHFIRPNFATESSVKKKDTKK 157


 Score = 61.7 bits (147), Expect = 6e-09
 Identities = 41/125 (32%), Positives = 57/125 (44%), Gaps = 8/125 (6%)

Query: 125 YYDGVTHFIRPKFSGSNSKALETSKVNTFGKWKRNQYGTYYRNENGTFTC-GFLPIFARV 183
            YY+G T     P        +K      + +T G W  N YGTYY++E+ TF C      I  R
Sbjct: 346 YYEGKTPV--PTVVNQKAKTKPVKQSSTSG-WNVNNYGTYYKSESATFKCTARQGIVTRY 402

Query: 184 GSPKLSEPNGYWFQPNGYTPYNEVCLSDGYVWIGYNWQGTR-YYLPVRQWNGKTGNSYSV 242
              P  + P            Y+ VC  DGYVWI +    G +  ++PVR W+    N+  +
Sbjct: 403 TGPFTTCPQAGVLYYGQSVTYDTVCKQDGYVWISWTTNGGQDVWMPVRTWD---KNTDIM 459

Query: 243 GIPWG 247
            G  WG
Sbjct: 460 GQLWG 464


>gi|113675|sp|P24556|ALYS_STAAU AUTOLYSIN
          (N-ACETYLMURAMOYL-L-ALANINE AMIDASE)
          >gi|79887|pir||JQ1147 N-acetylmuramoyl-L-alanine amidase
          (EC 3.5.1.28) - Staphylococcus aureus >gi|153067
          (M76714) peptidoglycan hydrolase [Staphylococcus aureus]
          Length = 481

 Score =  118 bits (292), Expect = 6e-26
 Identities = 56/117 (47%), Positives = 68/117 (57%), Gaps = 1/117 (0%)

Query: 135 PKFSGSNSKALETSKVNTFGK-WKRNQYGTYYRNENGTFTCGFLPIFARVGSPKLSEPNG 193
            P  + SN  +  ++ V      WKRN+YGTYY  E+  FT G  PI  R   P LS P G
Sbjct: 365 PVATVSNESSASSNTVKPVASAWKRNKYGTYYMEESARFTNGNQPITVRKVGPFLSCPVG 424

Query: 194 YWFQPNGYTPYNEVCLSDGYVWIGYNWQGTRYYLPVRQWNGKTGNSYSVGIPWGVFS 250
            Y FQP GY  Y EV L DG+VW+GY W+G RYYLP+R WNG     +  +G  WG  S
Sbjct: 425 YQFQPGGYCDYTEVMLQDGHVWVGYTWEGQRYYLPIRTWNGSAPPNQILGDLWGEIS 481


 Score = 78.0 bits (189), Expect = 7e-14
 Identities = 48/109 (44%), Positives = 62/109 (56%), Gaps = 6/109 (5%)

Query: 15  EGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDA-INNDFKGLATVYKNTPSFK 73
            EG    + D  YGFQC D + A  + +  G +     AKD    N+F GLATVY+NTP F
Sbjct: 18  EGKQFNVDLWYGFQCFDYANAG-WKVLFGLLLKGLGAKDIPFANNFDGLATVYQNTPDFL 76

Query: 74  PQLGDVAVYTNGQ---YGHIQCVLSGNLDYYTCLEQNWLGGGF-DGWEK 118
            Q GD+ V+ +     YGH+  V+   LDY    EQNWLGGG+ DG E+
Sbjct: 77  AQPGDMVVFGSNYGAGYGHVAWVIEATLDYIIVYEQNWLGGGWTDGIEQ 125


>gi|1763243 (U72397) amidase [bacteriophage 80 alpha]
          Length = 481

 Score =  118 bits (292), Expect = 6e-26
 Identities = 56/117 (47%), Positives = 68/117 (57%), Gaps = 1/117 (0%)

Query: 135 PKFSGSNSKALETSKVNTFGK-WKRNQYGTYYRNENGTFTCGFLPIFARVGSPKLSEPNG 193
            P  + SN  +  ++ V      WKRN+YGTYY  E+  FT G  PI  R   P LS P G
Sbjct: 365 PVATVSNESSASSNTVKPVASAWKRNKYGTYYMEESARFTNGNQPITVRKVGPFLSCPVG 424
```

```
Query: 194 YWFQPNGYTPYNEVCLSDGYVWIGYNWQGTRYYLPVRQWNGKTGNSYSVGIPWGVFS 250
           Y FQP GY  Y EV L DG+VW+GY W+G RYYLP+R WNG    +  +G  WG  S
Sbjct: 425 YQFQPGGYCDYTEVMLQDGHVWVGYTWEGQRYYLPIRTWNGSAPPNQILGDLWGEIS 481


 Score = 83.5 bits (203), Expect = 2e-15
 Identities = 50/115 (43%), Positives = 65/115 (56%), Gaps = 6/115 (5%)

Query: 9   EWIYKHEGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDA-INNDFKGLATVYK 67
           EW+   EG   + D  YGFQC D + A  + +  G +      AKD    N+F GLATVY+
Sbjct: 12  EWLKTSEGKQFNVDLWYGFQCFDYANAG-WKVLFGLLLKGLGAKDIPFANNFDGLATVYQ 70

Query: 68  NTPSFKPQLGDVAVYTNGQ---YGHIQCVLSGNLDYYTCLEQNWLGGGF-DGWEK 118
           NTP F  Q GD+ V+ +      YGH+  V+   LDY     EQNWLGGG+ DG E+
Sbjct: 71  NTPDFLAQPGDMVVFGSNYGAGYGHVAWVIEATLDYIIVYEQNWLGGGWTDGIEQ 125


>gi|4574237|gb|AAD23962.1|AF106851_1 (AF106851) LytN [Staphylococcus
           aureus]
           Length = 383

 Score = 84.3 bits (205), Expect = 9e-16
 Identities = 48/128 (37%), Positives = 68/128 (52%), Gaps = 7/128 (5%)

Query: 15  EGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDAINNDFKGLATVYKNTPSFKP 74
           E  G DFDG+YG+QC DL   Y  ++    ++ +G         N+F   A +Y NTP+FK
Sbjct: 252 ENRGWDFDGSYGWQCFDLVNVYWNHLYGHGLKGYGAKDIPYANNFNSEAKIYHNTPTFKA 311

Query: 75  QLGDVAVYT---NGQYGHIQCVLSGNLD----YYTCLEQNWLGGGFDGWEKATIRTHYYD 127
           + GD+ V++    G YGH  VL+G+ D     +  L+QNW  GG+  E A   H Y+
Sbjct: 312 EPGDLVVFSGRFGGGYGHTAIVLNGDYDGKLMKFQSLDQNWNNGGWRKAEVAHKVVHNYE 371

Query: 128 GVTHFIRP 135
                FIRP
Sbjct: 372 NDMIFIRP 379


>gi|3767593|dbj|BAA33856.1| (AB015195) LytN [Staphylococcus aureus]
           Length = 383

 Score = 84.3 bits (205), Expect = 9e-16
 Identities = 48/128 (37%), Positives = 68/128 (52%), Gaps = 7/128 (5%)

Query: 15  EGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDAINNDFKGLATVYKNTPSFKP 74
           E  G DFDG+YG+QC DL   Y  ++    ++ +G         N+F   A +Y NTP+FK
Sbjct: 252 ENRGWDFDGSYGWQCFDLVNVYWNHLYGHGLKGYGAKDIPYANNFNSEAKIYHNTPTFKA 311

Query: 75  QLGDVAVYT---NGQYGHIQCVLSGNLD----YYTCLEQNWLGGGFDGWEKATIRTHYYD 127
           + GD+ V++    G YGH  VL+G+ D     +  L+QNW  GG+  E A   H Y+
Sbjct: 312 EPGDLVVFSGRFGGGYGHTAIVLNGDYDGKLMKFQSLDQNWNNGGWRKAEVAHKVVHNYE 371

Query: 128 GVTHFIRP 135
                FIRP
Sbjct: 372 NDMIFIRP 379


>gi|2764983|emb|CAA69022.1| (Y07740) cell wall hydrolase Ply187
           [Staphylococcus phage 187]
           Length = 628

 Score = 76.9 bits (186), Expect = 2e-13
 Identities = 50/144 (34%), Positives = 68/144 (46%), Gaps = 18/144 (12%)

Query: 5   QQAKEWIYKHEGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMW-----GNAKDAINNDF 59
           +Q  +W     G+GVD DG YG QC DL   Y++          R W     GNA+D    +
Sbjct: 12  KQVVDWAINLIGSGVDVDGYYGRQCWDLP-NYIFN------RYWNFKTPGNARDMAWYRY 64

Query: 60  KGLATVYKNTPSFKPQLGDVAVYTNGQY-----GHIQCVLS-GNLDYYTCLEQNWLGGGF 113
                V++NT   F P+ GD+AV+T G Y      GH  V+      Y+  ++QNW
Sbjct: 65  PEGFKVFRNTSDFVPKPGDIAVWTGGNYNWNTWGHTGIVVGPSTKSYFYSVDQNWNNSNS 124

Query: 114 DGWEKATIRTHYYDGVTHFIRPKF 137
             A   H Y GVTHF+RP +
Sbjct: 125 YVGSPAAKIKHSYFGVTHFVRPAY 148
```

```
>gi|3287732|sp|O05156|ALE1_STACP GLYCYL-GLYCINE ENDOPEPTIDASE ALE-1
          PRECURSOR >gi|1890068|dbj|BAA13069| (D86328) ALE-1
          [Staphylococcus capitis]
          Length = 362

 Score = 73.4 bits (177), Expect = 2e-12
 Identities = 47/117 (40%), Positives = 61/117 (51%), Gaps = 10/117 (8%)

Query: 132 FIRPKFSGSNSKALETSKVNTFGKWKRNQYGTYYRNENGTFTCGFLPIFARVGSPKLSEP 191
           F++    GSNS    TS  N  G +K N+YGT Y++E+  +FT     I  R+  P  S P
Sbjct: 252 FLKSAGYGSNS----TSSSNNNG-YKTNKYGTLYKSESASFTAN-TDIITRLTGPFRSMP 305

Query: 192 NGYWFQPNGYTPYNEVCLSDGYVWIGYNW-QGTRYYLPVRQWNGKTGNSYSVGIPWG 247
                +        Y+EV   DG+VW+GYN   G R YLPVR WN  TG     +G  WG
Sbjct: 306 QSGVLRKGLTIKYDEVMKQDGHVWVGYNTNSGKRVYLPVRTWNESTG---ELGPLWG 359


>gi|79926|pir||A25881 lysostaphin precursor - Staphylococcus
          simulans >gi|153047 (M15686) lysostaphin (ttg start
          codon) [Staphylococcus simulans]
          Length = 389

 Score = 69.5 bits (167), Expect = 3e-11
 Identities = 48/133 (36%), Positives = 62/133 (46%), Gaps = 20/133 (15%)

Query: 131 HFIRPKFSGSNSKALETS---KVNTFGK------------WKRNQYGTYYRNENGTFTCG 175
           HF R    S SNS A +       K    +GK            WK N+YGT Y++E+ +FT
Sbjct: 258 HFQRMVNSFSNSTAQDPMPFLKSAGYGKAGGTVTPTPNTGWKTNKYGTLYKSESASFTPN 317

Query: 176 FLPIFARVGSPKLSEPNGYWFQPNGYTPYNEVCLSDGYVWIGYNW-QGTRYYLPVRQWNG 234
                I   R   P   S P       +         Y+EV   DG+VW+GY    G R YLPVR WN
Sbjct: 318 -TDIITRTTGPFRSMPQSGVLKAGQTIHYDEVMKQDGHVWVGYTGNSGQRIYLPVRTWNK 376

Query: 235 KTGNSYSVGIPWG 247
            T    ++G+ WG
Sbjct: 377 STN---TLGVLWG 386


>gi|126496|sp|P10548|LSTP_STAST LYSOSTAPHIN PRECURSOR
          (GLYCYL-GLYCINE ENDOPEPTIDASE) >gi|79927|pir||S01079
          lysostaphin precursor - Staphylococcus simulans bv.
          staphylolyticus >gi|581744|emb|CAA29494| (X06121)
          lysostaphin (AA 1-480) [Staphylococcus simulans bv.
          staphylolyticus]
          Length = 480

 Score = 69.5 bits (167), Expect = 3e-11
 Identities = 48/133 (36%), Positives = 62/133 (46%), Gaps = 20/133 (15%)

Query: 131 HFIRPKFSGSNSKALETS---KVNTFGK------------WKRNQYGTYYRNENGTFTCG 175
           HF R    S SNS A +       K    +GK            WK N+YGT Y++E+ +FT
Sbjct: 349 HFQRMVNSFSNSTAQDPMPFLKSAGYGKAGGTVTPTPNTGWKTNKYGTLYKSESASFTPN 408

Query: 176 FLPIFARVGSPKLSEPNGYWFQPNGYTPYNEVCLSDGYVWIGYNW-QGTRYYLPVRQWNG 234
                I   R   P   S P       +         Y+EV   DG+VW+GY    G R YLPVR WN
Sbjct: 409 -TDIITRTTGPFRSMPQSGVLKAGQTIHYDEVMKQDGHVWVGYTGNSGQRIYLPVRTWNK 467

Query: 235 KTGNSYSVGIPWG 247
            T    ++G+ WG
Sbjct: 468 STN---TLGVLWG 477


>gi|3287967|sp|P10547|LSTP_STASI LYSOSTAPHIN PRECURSOR
          (GLYCYL-GLYCINE ENDOPEPTIDASE) >gi|2072411 (U66883)
          lysostaphin [Staphylococcus simulans]
          Length = 493

 Score = 69.5 bits (167), Expect = 3e-11
 Identities = 48/133 (36%), Positives = 62/133 (46%), Gaps = 20/133 (15%)

Query: 131 HFIRPKFSGSNSKALETS---KVNTFGK------------WKRNQYGTYYRNENGTFTCG 175
           HF R    S SNS A +       K    +GK            WK N+YGT Y++E+ +FT
Sbjct: 362 HFQRMVNSFSNSTAQDPMPFLKSAGYGKAGGTVTPTPNTGWKTNKYGTLYKSESASFTPN 421

Query: 176 FLPIFARVGSPKLSEPNGYWFQPNGYTPYNEVCLSDGYVWIGYNW-QGTRYYLPVRQWNG 234
```

```
              I  R   P  S P      +       Y+EV    DG+VW+GY    G R YLPVR WN
Sbjct: 422 -TDIITRTTGPFRSMPQSGVLKAGQTIHYDEVMKQDGHVWVGYTGNSGQRIYLPVRTWNK 480

Query: 235 KTGNSYSVGIPWG 247
           T    ++G+ WG
Sbjct: 481 STN---TLGVLWG 490
```

>gi|3341932|dbj|BAA31898.1| (AB009866) amidase (peptidoglycan hydrolase) [bacteriophage phi PVL]
Length = 484

Score = 68.3 bits (164), Expect = 6e-11
Identities = 52/150 (34%), Positives = 71/150 (46%), Gaps = 17/150 (11%)

```
Query: 3    SQQQAKEWIYKHEGAGVDFDGAYGFQCMDLSVAYVYYITDGKVRMWGNAKDAINNDFKGL 62
            ++ QA++W     G    + D  YGFQC D +   + + I  G+ R+ G     I  D K
Sbjct: 4    TKNQAEKWFDNSLGKQFNPDLFYGFQCYDYASMF-FMIATGE-RLQGLYAYNIPFDNKAR 61

Query: 63   ATVY----KNTPSFKPQLGDVAVYTN---GQYGHIQCVLSGNLDYYTCLEQNWLGGGF-- 113
              Y     KN  SF PQ  D+ V+ +    G  GH++ V S NL+ +T    QNW G G+
Sbjct: 62   IEKYGQIIKNYDSFLPQKLDIVVFPSKYGGGAGHVEIVESANLNTFTSFGQNWNGKGWTN 121

Query: 114  ----DGW--EKATIRTHYYDGVTHFIRPKF 137
             GW  E  T    HYYD    +FIR  F
Sbjct: 122  GVAQPGWGPETVTRHVHYYDDPMYFIRLNF 151
```

Query= pt|110882 44AHJDORF012 Phage 44AHJD ORF |8391-8813|3 1
(140 letters)

>gi|140528|sp|P24811|YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION (ORF2)
>gi|322189|pir||B44816 orf2 5'of autolytic amidase - Bacillus subtilis >gi|142801 (M59232) open reading frame 2 [Bacillus subtilis] >gi|1217874|dbj|BAA06959| (D32216) ORF121 [Bacillus subtilis] >gi|1303767|dbj|BAA12423| (D84432) YqdD [Bacillus subtilis]
>gi|2635036|emb|CAB14532| (Z99117) alternate gene name: yqdD; similar to holin [Bacillus subtilis]
Length = 140

Score = 80.4 bits (195), Expect = 6e-15
Identities = 45/130 (34%), Positives = 67/130 (50%), Gaps = 3/130 (2%)

```
Query: 4    VKFRFTDSEAFHMFIYAGDLKLLYFLFVLMFVDIITGISKAIKNNNLWSKKSMRGFSKKX 63
            + F   D    ++F   G +K L  L VL  +D++TG+ KA K    L S+ +  G+ +K
Sbjct: 8    INFETLDLARVYLF---GGVKYLDLLLVLSIIDVLTGVIKAWKFKKLRSRSAWFGYVRKL 64

Query: 64   XXXXXXXXXXXXXXXXXXXKGGLLMITIFYYIANEGLSIVENCAEMDVLVPEQIKDKLRVI 123
                                 G L    T+ +YIANEGLSI EN A++ V +P  I D+L+ I
Sbjct: 65   LNFFAVILANVIDTVLNLNGVLTFGTVLFYIANEGLSITENLAQIGVKIPSSITDRLQTI 124

Query: 124 KNDTEKSDNN 133
           +N+ E+S NN
Sbjct: 125 ENEKEQSKNN 134
```

>gi|4126631|dbj|BAA36651.1| (AB016282) ORF45 [bacteriophage phi-105]
Length = 135

Score = 76.1 bits (184), Expect = 1e-13
Identities = 44/115 (38%), Positives = 61/115 (52%), Gaps = 4/115 (3%)

```
Query: 21   GDLKLLYFLFVLMFVDIITGISKAIKNNNLWSKKSMRGFSKKXXXXXXXXXXXXXXXXXXX 80
            G++K L   + VL  +DIITG+ KA K    L S+ +  G+ +K
Sbjct: 17   GEVKYLDLMLVLNIIDIITGVIKAWKFKELRSRSAWFGYVRKMLSFLVVIVANAIDTIMD 76

Query: 81   XKGGLLMITIFYYIANEGLSIVENCAEMDVLVPEQIKDKLRVIKND----TEKSD 131
              G L    T+ +YIANEGLSI EN A++ V +P  I D+L VI+++D     TEK D
Sbjct: 77   LNGVLTFATVLFYIANEGLSITENLAQIGVKIPAVITDRLHVIESDNDQKTEKDD 131
```

>gi|141088|sp|P26835|YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN NAGH 3'REGION (ORFD) >gi|1075967|pir||S43905 hypothetical protein D - Clostridium perfringens >gi|455154 (M81878)

```
          ORF D [Clostridium perfringens]
          Length = 132

 Score = 60.9 bits (145), Expect = 4e-09
 Identities = 38/127 (29%), Positives = 63/127 (48%), Gaps = 3/127 (2%)

Query: 1   MNEVKFRFTDSEAFHMFIY-AGDLKLLYFLFVLMFVDIITGISKAIKNNNLWSKKSMRGF 59
            +N +K+            +I+ A D+ L+  L V +F+D +TG+ K  K+  L S   +RG
Sbjct: 5   INYIKWGIVSLGTLFTWIFGAWDIPLITLL-VFIFLDYLTGVIKGCKSKELCSNIGLRGI 63

Query: 60  SKXXXXXXXXXXXXXXXXXXXXKGGLLMITI-FYYIANEGLSIVENCAEMDVLVPEQIKD 118
            +KK                       +     I ++YI NEG+SI+ENCA + V +PE++K
Sbjct: 64  TKKGLILVVLLVAVMLDRLLDNGTWMFRTLIAYFYIMNEGISILENCAALGVPIPEKLKQ 123

Query: 119 KLRVIKN 125
             L+ + N
Sbjct: 124 ALKQLNN 130


>gi|2293160 (AF008220) YtkC [Bacillus subtilis]
          >gi|2635548|emb|CAB15042| (Z99119) similar to autolytic
          amidase [Bacillus subtilis]
          Length = 134

 Score = 36.4 bits (82), Expect = 0.099
 Identities = 25/109 (22%), Positives = 41/109 (36%)

Query: 17  FIYAGDLKLLYFLFVLMFVDIITGISKAIKNNNLWSKKSMRGFSKXXXXXXXXXXXXXXXX 76
            F + G        L  LM ++ I+    K     + L  KK       KK
Sbjct: 20  FFFGGFQYSFLILLSLMAIEFISTTLKETIIHKLSFKKVFARLVKKLVTLALISVCHFFD 79

Query: 77  XXXXXKGGLLMITIFYYIANEGLSIVENCAEMDVLVPEQIKDKLRVIKN 125
                 +G +   + I +YI  E + IV   + + + VP+ + D L  +KN
Sbjct: 80  QLLNTQGSIRDLAIMFYILYESVQIVVTASSLGIPVPQMLVDLLETLKN 128


>gi|1181973|emb|CAA87743.1| (Z47794) holin protein [Bacteriophage
          CP-1]
          Length = 134

 Score = 31.3 bits (69), Expect = 3.3
 Identities = 27/88 (30%), Positives = 36/88 (40%), Gaps = 5/88 (5%)

Query: 29  LFVLMFVDIITGISKAIKNNNLWSKKSMRGFSKXXXXXXXXXXXXXXXXXXXXXK--GGLL 86
            LF L+  D ITG  KA K      S    ++G  K                        G +L
Sbjct: 18  LFALILFDFITGFLKAWKWKVTDSWTGLKGVIKHTLTFIFYYFVAVFLTYIHAMAVGQIL 77

Query: 87  MITIFYYIANEGLSIVENCAEMDVLVPE 114
            ++ I  Y A   LSI+EN A M V +P+
Sbjct: 78  LVIINLYYA---LSIMENLAVMGVFIPK 102
```

Table 21

Phage 182 complete genome sequence. 17833 nucleotides.

```
1      tagaatattg tcataaaaca caaacataat aatgcatatt attgtttaca aatatgtaat ttcgtgatat
71     aatatatttg taagttaaag gaggtgacaa aagaacaaat cataaatgct ttagaaattg caaaaactat
141    tggaggaaaa ataatgaaat attcactaca acaaatagat gaaattaaat caacaatttt cagaattaga
211    ttaaaaaggc atgaactaga ggaattggtg gacgaagtaa acgatattgc taaagatccg gaggaaagat
281    atctttatc gttttattac acagaagaag aacgtttgtt tgaaattccc tctgcaagat taatagatta
351    ttacaacgaa aagatcacaa atctgaaatc ggaaatcata tcactcgaaa aaagattaca aaaactagta
421    aaataattac acaaaaagct ttacaaatat aacacatcat gttatactaa aagagtagta agggaacgga
491    aaatacctta cttcacacct caatcattct tatcaaaata caaaaggagg gaaaataatg ggtcgaaaac
561    taatgcaacg aaacgtaaca tcaactaaag tagaattctc agaagttatc gtacaagatg gagcgccaac
631    aattgtacca tgcgaaccag ttgtcttaac aggaaaactt tcagaagaaa aagctttatc agcgatcaaa
701    cgtaaaaacc ctgataaaaa cgtagttgta acaaatgttt cacatgaaac agcgctttac acaatgccag
771    tcgataaatt tatcgagtta gcagacaaat caacacaagc ctaataaaaa caaaactaaa acaaaacaga
841    ggagattata atcatggaaa tcgtaaaaag cacatttgac acacaaacac cagaaggaat gttacaagta
911    ttcaatgcca caaacggggc ttcaattccg ttacgtaacg caattggcga agtactagaa ttgaaagata
981    ttctagttta ctcagacgaa gtttctggtt ttggtggagc cgaaccatca caagcagaac tagtcgcttt
1051   cttcacagaa gatggtaaaa cttatgcggg tgtatcagca gtagcaacaa aatcagctaa aaacctaatt
1121   gatatgatga ctgctaaccc tgacatcaaa ccaaaaattt cttttgtcga aggaaaatca aacggtggac
1191   aaaaatttgt aaatctacaa gtggtttcac tgtagcataa aaatacagga atctagtaag ccacttagcg
1261   aatctcgcta ggtggttttt attatgtttc tacattgagg tgtgtagaat tgaccgtaag aatatcaaag
1331   aatgatagag ccaagttaga gaaaatctac ggtaaatcta acaaagctcg taaaaaatac aatcgtttaa
1401   gacaaaaagg agttgaggaa aggcaacttc caactgttcc aacatcaaag aaaagactta ttgactacgt
1471   aaaatcaaca aatatgagtc gtagtgattt taacaagatg ttagacgagt tggtagattt tgcacaacct
1541   tacaacgaga attacatttt tgagatcaac aagcgaaatg ttgcaatctc aagagcgcaa atcaaagaag
1611   cgcaaattaa aacagagcaa gctcaaaaag cgaaagaaga acactacaaa gagcttaaca aagttgaagt
1681   taagaagccc acagaaaaca caattgtcac accaactatt ttaacagagt taggtgctga cttacctttt
1751   caagcaatac cagattttaa tattgacgct ttcacttctc cagaaggagt tcagtcttat ttagaaaata
1821   taggaaaaca agacgaacaa tattttgacg aaagagacca actttattac gacaatttca gacaagcgat
1891   gtttactatt ttcaattcag acgctgacga tattgttcgt ttacttgact caatggggct tgatctattt
1961   atgaaaacat atgttagtaa cttcttagac atgaaccttg actacattta tgacgaagca gaagtacaac
2031   agaaaaaaga acaagtttac agtaagattg caaaagtgat cgagtctgaa acaggtggag aagtcccctc
2101   atataacccc acgaagaaca tcacaattaa ttcagaaaca ggagaagaat tatgattaag aaatatactg
2171   gcgactttga aacaacaact gatctcaacg attgtcgtgt atggtcgtgg ggcgtatgcg atatagacaa
2241   cgttgacaat atgacgttcg gtttagaaat cgattctttt tttgagtggt gtaaaatgca aggcagcaca
2311   gacatttatt tccacaacga aaaatttgac ggagagttta tgctttcatg gttattcaaa aatggtttca
2381   aatggtgtaa agaagcaaaa gaagatcgaa cattctccac actcatatca aatatgggtc aatggtatgc
2451   tttggaaatt tgttgggaag ttaattacac aacaacaaaa tcaggtaaaa cgaaaaaaga gaaatctcga
2521   acaataattt atgatagcct taaaaaatat ccttttccag tgaaacaaat tgcagaagct tttaattttc
2591   ctataaaaaa aggcgaaata gattatacaa aagaaagacc tattggttac aaaccaacaa aagatgaatg
2661   ggagtattta aagaacgaca ttcagattat ggcgatggca ttaaaaattc aattcgatca aggactaact
2731   cgaatgacta gaggaagcga cgctttaggc gattacaaag attggctaaa agctacacat ggaaaatcaa
2801   ctttcaaaca atggtttcct attttgtctt tagggtttga taaagactta cgtaaagcat acaaaggcgg
2871   cttcacttgg gtaaacaaag tttttcaagg gaaagaaata ggtgacggca ttgtctttga tgtcaactct
2941   ttgtatccct ctcaaatgta cgtaagacct ttaccatatg gaacacctct attctacgaa ggagaataca
3011   aaccgaacaa cgactatccg ctgtacattc aaaatatcaa agtaagattc cgtttaaagg agggttatat
3081   tccaaccatt caagttaagc aaagttcatt attcattcaa aacgaatatc ttgaatcaag tgtaaacaag
3151   ttaggagttg acgaattaat cgatcttact cttacaaatg ttgacctaga attatttttt gaacactacg
3221   atattttaga gatacattac acttacggat atatgttcaa agcttcttgt gatatgttca aaggctggat
3291   cgataaatgg atcgaagtaa agaacaccac cgaaggggct agaaaagcta acgccaaagg tatgttaaat
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17221 tcaataagat aatgtttatt gttttcggta tctatgatat gataattcat atcccactca ttaaaggggt
17291 gaagtagaga tacctctcct ttttcagcta ttaatgattt attgttcata tgaaacactc cttttatatt
17361 aatttgatat tgataccacc aatcaaatgt gattggtagc attgtattaa attaatattc tggataattt
17431 attgagaaag tccagttatc atcaaatgaa attgttttat tttcaagtaa ctttttagcc tcatccacct
17501 caaattctaa atagaggaat ttactaagtt tatcctcatc tctaaaaatt ttcatacata ccacgttatt
17571 tgaataaatt tctgtgtata cgatcggttc attcatgttt atcatccttt ctttattaca tatatagtat
17641 atcatgtatt tacatatatg tcaatcattt aattcattta ttttaatgat ttatttgatt gttttttttat
17711 gatcctttct ttattacatc tatattatat catgtatgat tgtatttgtc aacaattaaa ttcatataaa
17781 tgtagtttgg ggtcagttac atttgtgtta tcaaaaaaag ataatattct att

Table 22

Phage 182 ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	182ORF001	2	5966..7780	604	Tail protein;
2	182ORF002	1	2152..3873	573	DNA polymerase;
3	182ORF003	1	11305..12639	444	
4	182ORF004	3	4626..5954	442	Major head protein;
5	182ORF005	3	12651..13700	349	Glycyl-Glycine endopeptidase; Lysostaphin precursor;
6	182ORF006	1	14995..16026	343	Encapsidation protein; ATG/GTP-binding site motif A;
7	182ORF007	1	7795..8775	326	Upper collar protein;
8	182ORF008	2	14105..14983	292	Lysozyme; Muramidase;
9	182ORF010	2	1310..2155	281	Terminal protein;
10	182ORF009	2	8765..9601	278	Lower collar protein;
11	182ORF011	1	9607..10158	183	Pre-neck appendage protein;
12	182ORF012	3	10872..11294	140	
13	182ORF013	1	10456..10860	134	
14	182ORF014	3	13716..14108	130	Lysis protein;
15	182ORF015	2	854..1225	123	Early protein;
16	182ORF018	-2	16429..16737	102	
17	182ORF020	3	10158..10454	98	Leucine-zipper motif;
18	182ORF019	3	4323..4613	96	Head protein;
19	182ORF016	-3	16749..17033	94	
20	182ORF022	1	12868..13149	93	
21	182ORF023	-2	11914..12189	91	
22	182ORF017	1	154..426	90	
23	182ORF024	3	6174..6446	90	
24	182ORF025	2	548..814	88	Early protein;
25	182ORF026	-3	12999..13259	86	
26	182ORF027	-1	14642..14896	84	
27	182ORF028	3	14430..14672	80	
28	182ORF021	-3	17106..17339	77	
29	182ORF030	-1	16199..16429	76	
30	182ORF031	-3	8379..8603	74	
31	182ORF032	-1	11195..11413	72	
32	182ORF033	-1	4727..4942	71	
33	182ORF034	-1	5951..6160	69	
34	182ORF029	-3	17412..17606	64	
35	182ORF035	-3	15570..15758	62	
36	182ORF036	-3	2127..2315	62	
37	182ORF037	-1	12095..12280	61	
38	182ORF038	3	14769..14951	60	
39	182ORF039	2	9992..10171	59	
40	182ORF040	-3	16029..16202	57	
41	182ORF041	1	3886..4056	56	Early protein;
42	182ORF042	-3	10671..10832	53	
43	182ORF043	-3	10491..10652	53	
44	182ORF044	-1	6299..6457	52	
45	182ORF045	-2	6571..6729	52	
46	182ORF046	2	2372..2527	51	
47	182ORF047	-2	13201..13353	50	
48	182ORF048	-3	3243..3395	50	
49	182ORF049	3	1578..1724	48	
50	182ORF050	2	8012..8155	47	
51	182ORF051	3	9390..9530	46	
52	182ORF052	1	4096..4233	45	
53	182ORF053	2	15656..15793	45	
54	182ORF054	-2	8002..8136	44	
55	182ORF055	2	8324..8455	43	
56	182ORF056	3	6549..6680	43	
57	182ORF057	-3	8133..8264	43	
58	182ORF058	-1	5048..5176	42	
59	182ORF059	-2	15748..15876	42	
60	182ORF060	-3	15276..15404	42	
61	182ORF061	-3	1974..2102	42	
62	182ORF062	-2	1867..1992	41	
63	182ORF063	-3	14181..14306	41	
64	182ORF064	-2	7234..7356	40	

65	182ORF065	-2	3460..3582	40	
66	182ORF066	1	4234..4353	39	
67	182ORF067	-1	13763..13882	39	
68	182ORF068	-1	7148..7267	39	
69	182ORF069	-3	4908..5027	39	
70	182ORF070	-3	912..1031	39	
71	182ORF071	2	11741..11857	38	
72	182ORF072	-3	11610..11723	37	
73	182ORF073	-3	2763..2876	37	
74	182ORF074	-1	8813..8923	36	
75	182ORF075	-3	7353..7463	36	
76	182ORF076	-3	2316..2426	36	
77	182ORF077	2	11858..11965	35	
78	182ORF078	-2	7564..7671	35	
79	182ORF079	-2	7381..7488	35	
80	182ORF080	-2	4372..4473	33	

Table 23

Predicted amino acid sequences of ORFs from phage 182

182ORF001	
5966	atggcaagaaggtatacaaatgtaaaattgttggctaacgtgccttttgataacacctatacacacacaagatggtttaaaact
1	M A R R Y T N V K L L A N V P F D N T Y T H T R W F K T
6050	caacaggaacaggaatcgtactttaattcgtttcctgttcttaacgagaatagagattgttcttatcaaagggatacacaactc
29	Q Q E Q E S Y F N S F P V L N E N R D C S Y Q R D T Q L
6134	gggggagttttagagtagataaacacaaagacgccttatatgcttgtaactatctcatctttaaaaacgaagaaacttatcct
57	G G V F R V D K H K D A L Y A C N Y L I F K N E E T Y P
6218	agtaaatggcagtatgcctttgttactgatattgaatataagaatgacaacacaagtttcgttacctttgaaattgatgtttta
85	S K W Q Y A F V T D I E Y K N D N T S F V T F E I D V L
6302	caaacttatcgtttcgatattggtatacgagaaagtttcattgcaaaagaacaccctcaactttattattcgaatggaatacct
113	Q T Y R F D I G I R E S F I A K E H P Q L Y Y S N G I P
6386	ttcattaatacaattgaagagtcgcttgattacggtagagaatacacaacaacaaatgtaacaacttttcatcctaacgatgga
141	F I N T I E E S L D Y G R E Y T T T N V T T F H P N D G
6470	gtcaatttcttgttattctaacaagtgaagcaatgccagttggagataaggaagataaatcaggaggatcaatagtaggtggc
169	V N F L V I L T S E A M P V G D K E D K S G G S I V G G
6554	ccatctcctttttcctattatttacttcctatcaattcaagtggggaggtatacaaaccaaatggggcaggcaatgctaatttt
197	P S P F S Y Y L L P I N S S G E V Y K P N G A G N A N F
6638	ggagagtacatggcgtttcttacaacgaaagaacctttttaaataagatagtcgggatgtatgtaacgtcgtatacaggtata
225	G E Y M A F L T T K E P F L N K I V G M Y V T S Y T G I
6722	ccattcattgtggatcacgcgaacaaaacggtaaggtataatgcaggaggttcttataagatcatgcttccaacctacgctagt
253	P F I V D H A N K.T V R Y N A G G S Y K I M L P T Y A S
6806	gatccaacaggaacaatgaaaacattcgctttcttttgtgtaaaagaagcaagaacattcgtacctaaaagaattgatcttgta
281	D P T G T M K T F A F F C V K E A R T F V P K R I D L V
6890	gggaacgtgtataactactttagagaagcttttccgtttaatgttaaggaatcaaaactatttatgtatccctattgtttaata
309	G N V Y N Y F R E A F P F N V K E S K L F M Y P Y C L I
6974	gaaattacagatacaaaaggacatgtaatgactttaagacctgaatatcttacaggtggtaaattgagtgtatatgtaaaaggt
337	E I T D T K G H V M T L R P E Y L T G G K L S V Y V K G
7058	tcgttaggaatttctaataaagtgatgatcgagccgattgattatgatgtaagtaactcaaccattattaccaatttaagtgac
365	S L G I S N K V M I E P I D Y D V S N S T I I T N L S D
7142	aagatgttaatcgataatgatcctaacgatgtaggagttaaatctgactatgcttctgcattcatgcaaggaaacaaaaactcc
393	K M L I D N D P N D V G V K S D Y A S A F M Q G N K N S
7226	ttgattgctcaagagcaaaacattcgcaatactttcagacatggtatgggaaacagtgcaatgagtacaggaggagcgatcttt
421	L I A Q E Q N I R N T F R H G M G N S A M S T G G A I F
7310	tcagccttagcaagtaacaaccctttgttggtttgactaacatcatgggagcaggacaacaagtaaacaactatgtttctgaa
449	S A L A S N N P F V G L T N I M G A G Q Q V N N Y V S E
7394	aaagaaaacggtttgaacctcttggcaggtaaagtggcagatatcgaaaatattccagataatgtaacacagcttggatcaaac
477	K E N G L N L L A G K V A D I E N I P D N V T Q L G S N
7478	ttatctttcacaacaggaaactttcaaaactattatcaattgcgcttcaaacaaattaaatatgagtatgcaacaagacttgat
505	L S F T T G N F Q N Y Y Q L R F K Q I K Y E Y A T R L D
7562	cgttacttctcaatgtatggcacaaagagcaatcgagtagctacaccaaacttacaaacaagaaaagcatggaatttcattaaa
533	R Y F S M Y G T K S N R V A T P N L Q T R K A W N F I K
7646	ttaaaagaaccaaatattgtaggcacaatgagtaacgatgtattaacacgtgtgaaacaaattttagtgcaggcgttacgctt
561	L K E P N I V G T M S N D V L T R V K Q I F S A G V T L
7730	tggcatacgaatgatgttttgaattataaccaagacaacggagatgtatag 7780
589	W H T N D V L N Y N Q D N G D V *
182ORF002	
2152	atgattaagaaatatactggcgactttgaaacaacaactgatctcaacgattgtcgtgtatggtcgtggggcgtatgcgatata
1	M I K K Y T G D F E T T T D L N D C R V W S W G V C D I
2236	gacaacgttgacaatatgacgttcggtttagaaatcgattctttttttgagtggtgtaaaatgcaaggcagcacagacatttat
29	D N V D N M T F G L E I D S F F E W C K M Q G S T D I Y
2320	ttccacaacgaaaaatttgacggagagtttatgctttcatggttattcaaaaatggtttcaaatggtgtaaagaagcaaaagaa
57	F H N E K F D G E F M L S W L F K N G F K W C K E A K E
2404	gatcgaacattctccacactcatatcaaatatgggtcaatggtatgctttggaaatttgttgggaagttaattacacaacaaca
85	D R T F S T L I S N M G Q W Y A L E I C W E V N Y T T T
2488	aaatcaggtaaaacgaaaaaagagaaatctcgaacaataatttatgatagccttaaaaaatatccttttccagtgaaacaaatt
113	K S G K T K K E K S R T I I Y D S L K K Y P F P V K Q I
2572	gcagaagcttttaatttttcctataaaaaaaggcgaaatagattatacaaaagaaagacctattggttacaaaccaacaaaagat
141	A E A F N F P I K K G E I D Y T K E R P I G Y K P T K D
2656	gaatgggagtatttaaagaacgacattcagattatggcgatggcattaaaaattcaattcgatcaaggactaactcgaatgact
169	E W E Y L K N D I Q I M A M A L K I Q F D Q G L T R M T
2740	agaggaagcgacgctttaggcgattacaaagattggctaaaagctacacatggaaaatcaactttcaaacaatggtttcctatt
197	R G S D A L G D Y K D W L K A T H G K S T F K Q W F P I
2824	ttgtctttagggtttgataaagacttacgtaaagcatacaaaggcggcttcacttgggtaaacaaagttttcaagggaaagaa
225	L S L G F D K D L R K A Y K G G F T W V N K V F Q G K E
2908	ataggtgacggcattgtctttgatgtcaactctttgtatccctctcaaatgtacgtaagacctttaccatatggaacacctcta
253	I G D G I V F D V N S L Y P S Q M Y V R P L P Y G T P L
2992	ttctacgaaggagaatacaaaccgaacaacgactatccgctgtacattcaaaatatcaaagtaagattccgtttaaaggagggt
281	F Y E G E Y K P N N D Y P L Y I Q N I K V R F R L K E G
3076	tatattccaaccattcaagttaagcaaagttcattattcattcaaaacgaatatcttgaatcaagtgtaaacaagttaggagtt

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309      Y  I  P  T  I  Q  V  K  Q  S  S  L  F  I  Q  N  E  Y  L  E  S  S  V  N  K  L  G  V

3160     gacgaattaatcgatcttactcttacaaatgttgacctagaattatttttgaacactacgatattttagagatacattacact
337      D  E  L  I  D  L  T  L  T  N  V  D  L  E  L  F  F  E  H  Y  D  I  L  E  I  H  Y  T
3244     tacggatatatgttcaaagcttcttgtgatatgttcaaaggctggatcgataaatggatcgaagtaaagaacaccaccgaaggg
365      Y  G  Y  M  F  K  A  S  C  D  M  F  K  G  W  I  D  K  W  I  E  V  K  N  T  T  E  G
3328     gctagaaaagctaacgccaaaggtatgttaaatagcttgtatggaaagttcggaacaaaccctgacattacaggaaaagtgcct
393      A  R  K  A  N  A  K  G  M  L  N  S  L  Y  G  K  F  G  T  N  P  D  I  T  G  K  V  P
3412     tacatgggcgaggacggcattgttcgattgacactaggagaagaagaattaagagatcctgtttatgttccgcttgctagtttt
421      Y  M  G  E  D  G  I  V  R  L  T  L  G  E  E  E  L  R  D  P  V  Y  V  P  L  A  S  F
3496     gtgacggcttggggtagatatactaccattacaaccgctcaaaaatgtttgatcgcattatttattgtgatacagatagcatt
449      V  T  A  W  G  R  Y  T  T  I  T  T  A  Q  K  C  F  D  R  I  I  Y  C  D  T  D  S  I
3580     catctagtaggaacagaagttccagaagcaatcgatcacttggttgatcctaaaaaacttggttattggggcatgaaagcaca
477      H  L  V  G  T  E  V  P  E  A  I  D  H  L  V  D  P  K  K  L  G  Y  W  G  H  E  S  T
3664     tttcaacgagcaaaattcattcggcagaaaacatacgtagaagaaattgatggcgaattaaatgtaaagtgtgctggtatgcca
505      F  Q  R  A  K  F  I  R  Q  K  T  Y  V  E  E  I  D  G  E  L  N  V  K  C  A  G  M  P
3748     gatcgaataaaagagattgtaactttgacaatttgaagttggtttttcaagctatggaaagttgctacctaaaagaacacaa
533      D  R  I  K  E  I  V  T  F  D  N  F  E  V  G  F  S  S  Y  G  K  L  L  P  K  R  T  Q
3832     ggtggcgtggtattagtagacacaatgtttacaatcaaataa 3873
561      G  G  V  V  L  V  D  T  M  F  T  I  K  *
182ORF003
11305    atggaagaacgaattgatattcaaatgaacaagatgaaagaagaaaatcaaaagaattacctattgcaccctgaaacgaacccg
1        M  E  E  R  I  D  I  Q  M  N  K  M  K  E  E  N  Q  K  N  Y  L  L  H  P  E  T  N  P
11389    aaacaagttgtttttgatgaaacattgcatggaaatgaaaatcaggagagtttcaacaatttttgttgacacaagaaaaatgaca
29       K  Q  V  V  F  D  E  T  L  H  G  N  E  N  Q  E  S  F  N  N  F  V  D  T  R  K  M  T
11473    actacaattgatgtaagtgcttatggggttatcgctgacggtgtaacagattgtacaccaatattaaataaattacttgaagaa
57       T  T  I  D  V  S  A  Y  G  V  I  A  D  G  V  T  D  C  T  P  I  L  N  K  L  L  E  E
11557    aaaagcgaaatgggtatcacttttttatttcctccttgtgaacgtgattcatattatcgctttgctaacaccattgaattgaaa
85       K  S  E  M  G  I  T  F  Y  F  P  P  C  E  R  D  S  Y  Y  R  F  A  N  T  I  E  L  K
11641    cgtgatgtacctgtagttactttcttaggatcgggagaaacgacattaaagtttgaaacaatgacggcatttaatgtaaacatc
113      R  D  V  P  V  V  T  F  L  G  S  G  E  T  T  L  K  F  E  T  M  T  A  F  N  V  N  I
11725    gaaagtttcaatattgatggttttgcattatggttgccacaaggcgctcaaagtggtaaaggaatttttctttaatgatactcgc
141      E  S  F  N  I  D  G  F  A  L  W  L  P  Q  G  A  Q  S  G  K  G  I  F  F  N  D  T  R
11809    aattacaatcgttttgactttgatttgtttgttcgtaactgtactttaaatgaaggaacgtatgttgttgttgctagaggtaga
169      N  Y  N  R  F  D  F  D  L  F  V  R  N  C  T  L  N  E  G  T  Y  V  V  V  A  R  G  R
11893    ggggttacatttgaaaattgtctattctctaatatctctcaagcaattatcaaaacagcttttcccgatgtaaatggtatgtgg
197      G  V  T  F  E  N  C  L  F  S  N  I  S  Q  A  I  I  K  T  A  F  P  D  V  N  G  M  W
11977    caagggaacgatatcaatactaggggtacaggtttagaggtttctttgtgaaaaacaaccgtattcatttttgtacagcgatc
225      Q  G  N  D  I  N  T  R  G  T  G  F  R  G  F  F  V  K  N  N  R  I  H  F  C  T  A  I
12061    attatcgacaatgacgatgattatcagaatgtaattaatttctgtgaaatttctggtaacacaatcgaaggtggcgtaagttat
253      I  I  D  N  D  D  D  Y  Q  N  V  I  N  F  C  E  I  S  G  N  T  I  E  G  G  V  S  Y
12145    tatcgaggatatgcgcataacttgcatgtccaaaacaacaaccatttttctagcatacggaaatagaaacgctttgtttgagttt
281      Y  R  G  Y  A  H  N  L  H  V  Q  N  N  N  H  F  L  A  Y  G  N  R  N  A  L  F  E  F
12229    caagatgtggatcaagcttatattgatgtagatgtttattgtcgtaactcacaagtcgagggaatgaatagtacagctatttca
309      Q  D  V  D  Q  A  Y  I  D  V  D  V  Y  C  R  N  S  Q  V  E  G  M  N  S  T  A  I  S
12313    cgtttaattgttgtttacggacattaccgaaacttaaagattacaggtaaattatatcgttgtcaaggacatgttatcacgttg
337      R  L  I  V  V  Y  G  H  Y  R  N  L  K  I  T  G  K  L  Y  R  C  Q  G  H  V  I  T  L
12397    tatggcggtggcgttaatttctattgtgacttgatggcacaagaagcacctttgacggacggttaccggtttattcaaacggct
365      Y  G  G  G  V  N  F  Y  C  D  L  M  A  Q  E  A  P  L  T  D  G  Y  R  F  I  Q  T  A
12481    gacaatcgagttaactatgatgggtttgttgttcgtggtttgtctaattcaacaaaagtaaatacaccaatgatctataaagca
393      D  N  R  V  N  Y  D  G  F  V  V  R  G  L  S  N  S  T  K  V  N  T  P  M  I  Y  K  A
12565    cctcagactgttttctataatcgtagaatcgatcatgtgctaacaggtccaaatgcaagtaatgtatataactag 12639
421      P  Q  T  V  F  Y  N  R  R  I  D  H  V  L  T  G  P  N  A  S  N  V  Y  N  *
182ORF004
4626     atggctgacaaaatcacagaacaagatgttcttcgtgccacaaatgtagaaacaccagtacaattaatgactgctatttataat
1        M  A  D  K  I  T  E  Q  D  V  L  R  A  T  N  V  E  T  P  V  Q  L  M  T  A  I  Y  N
4710     agttcatcatctctttttcaggcgaacgtacctatgccaaatgcagataacatcgaagcggttggtgcagggatcacacgttta
29       S  S  S  S  L  F  Q  A  N  V  P  M  P  N  A  D  N  I  E  A  V  G  A  G  I  T  R  L
4794     gacgtagtaaaaaacgaatttatttcaactttagttgaccgtattggtaaagtagttatccgatacaaatcttggcgtaaccct
57       D  V  V  K  N  E  F  I  S  T  L  V  D  R  I  G  K  V  V  I  R  Y  K  S  W  R  N  P
4878     ttgaaaatgtttaaaaaaggaaacatgcctttaggtcgaacgattgaagaaattttttgttgacattgcacaggaacataagttc
85       L  K  M  F  K  K  G  N  M  P  L  G  R  T  I  E  E  I  F  V  D  I  A  Q  E  H  K  F
4962     aaccctgacgagtctgttacaggggtatttaaacaggaagttcccgatgtaaaaacattgttccacgaaattaatcgtgaaggt
113      N  P  D  E  S  V  T  G  V  F  K  Q  E  V  P  D  V  K  T  L  F  H  E  I  N  R  E  G
5046     tactacaaacaaacgatccaagaagcatggttagaaaaagcatttacttcatgggataatttcaatagtttcgttgctggtgta
141      Y  Y  K  Q  T  I  Q  E  A  W  L  E  K  A  F  T  S  W  D  N  F  N  S  F  V  A  G  V
5130     atgaacgctttatacacaggtgacgaagtaagcgaatttgaatacacgaaattattaatagcaaactaccaagaaaaagagcta
169      M  N  A  L  Y  T  G  D  E  V  S  E  F  E  Y  T  K  L  L  I  A  N  Y  Q  E  K  E  L
5214     ttcaaagagatcgaaattggcgaaattactgaatcaaatgcaaaagaatttatccgtaagatcaaatcaacctctaacaaatta
197      F  K  E  I  E  I  G  E  I  T  E  S  N  A  K  E  F  I  R  K  I  K  S  T  S  N  K  L
5298     gaatttatgagttccgcttacaacgctcaaggagttaaaacatctacctcaaaatctgatcaatacgttatcattgacgccgac
225      E  F  M  S  S  A  Y  N  A  Q  G  V  K  T  S  T  S  K  S  D  Q  Y  V  I  I  D  A  D

5382     acagacgcaaccattgacgttgacgttttagcagcggcattcaatatgagtaaaactgactttgtaggacacaaaatcgttatt
253      T  D  A  T  I  D  V  D  V  L  A  A  A  F  N  M  S  K  T  D  F  V  G  H  K  I  V  I
5466     gatgagtttcctaaaaaagaaggcgaagaatcgtcaaatattgtggcagttattgtagatagtgaatggtttatgatctacgac
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281     D E F P K K E G E E S S N I V A V I V D S E W F M I Y D
5550    aaattgtacaaaacaacaagtctatacaaccctgaagggttatattggaattattggttgcaccaccaccaactatattctact
309     K L Y K T T S L Y N P E G L Y W N Y W L H H H Q L Y S T
5634    tctcaattcgggaacgctgttgcttttgttaaatcagcaacaaaacctgtcacaaaagttgcttttgcaagtgcaacaactagt
337     S Q F G N A V A F V K S A T K P V T K V A F A S A T T S
5718    gttgttaaaggatcatctaaagatatcgcattgacatttacaccagtagaagcaacaaaccaacaaggagaagttgtttcatca
365     V V K G S S K D I A L T F T P V E A T N Q Q G E V V S S
5802    gcaccagcattggttaaggcaaccgtaaaacaaacagcaggtaaagcgactgccgtaaccgtagaaggcttagaagtcggtcaa
393     A P A L V K A T V K Q T A G K A T A V T V E G L E V G Q
5886    tcattagtaacattcacagctatcggaggtcaacaagcaacggttcttgttacggttacttctgactaa 5954
421     S L V T F T A I G G Q Q A T V L V T V T S D *
182ORF005
12651   atggcaactcttacaaatgaacaaatagctagaggacaaacaatcgctaaaatactttcaaaatatggctataataaaaattca
1       M A T L T N E Q I A R G Q T I A K I L S K Y G Y N K N S
12735   caagtaggagttgtcgccaatctccattgggaatcggctggtttgaacccgaacagcaatgaatatggtggaggcggatatggg
29      Q V G V V A N L H W E S A G L N P N S N E Y G G G G Y G
12819   ttaggtcaatggacgcctaaaagcaatctttatcgccaagcacaaatttgtgggttgtctaatgctaaagctgaaacgttggaa
57      L G Q W T P K S N L Y R Q A Q I C G L S N A K A E T L E
12903   ggtcaagcagagatcatcgctcaaggggataaaacaggtcaatggatggataatacacctgtttcttctgcaggttatactaac
85      G Q A E I I A Q G D K T G Q W M D N T P V S S A G Y T N
12987   cctcagaccctttcagcatttaaacaatctgcaaatattgatgttgctacaattaattttatgtgtcactgggaacgccctggt
113     P Q T L S A F K Q S A N I D V A T I N F M C H W E R P G
13071   aaacttcatatcgaagaaagacttgatcttgcacaagcttatagtaagcatattgacggtagcggtggcggtggcgtaaaacgt
141     K L H I E E R L D L A Q A Y S K H I D G S G G G G V K R
13155   tgctatggaaccccaatcaagaatacaaatcttgatcctaaaagtttcatgagtggacaacttttggcacgcatgcaggaaac
169     C Y G T P I K N T N L D P K S F M S G Q L F G T H A G N
13239   ggcagaccaaataatttccatgatggtttggactttggttcaattgatcaccctggcaatgaaatgattgcatgttgcgatgga
197     G R P N N F H D G L D F G S I D H P G N E M I A C C D G
13323   acagtaacacatgttggaacaatgggagcattaagagcgtattttgtgataaatgatggtacttacaatatcgtttatcaagaa
225     T V T H V G T M G A L R A Y F V I N D G T Y N I V Y Q E
13407   tttagttataaccagtcaaatataaaggtaaaagttggcgacaaagttaagaacggacaagtttgcgcaatacgtgacgcggat
253     F S Y N Q S N I K V K V G D K V K N G Q V C A I R D A D
13491   catttacatttaggttttactaaaaaagatttcatgactgcgttaggatcttctttcatagatgatggaacatgggaagaccct
281     H L H L G F T K K D F M T A L G S S F I D D G T W E D P
13575   ttgaagttttagggcaatgttttggagatggagatactggcggagataatgacgataacaataaggataaaaatgatcttatt
309     L K F L G Q C F G D G D T G G D N D D N N K D K N D L I
13659   tatctattgctatccgatgccttgaatggttggaaatttaa 13700
337     Y L L L S D A L N G W K F *
182ORF006
14995   atgacaaatagcttaggcgttaaacttgaagagaaaaacttatactataaccctaacaatgctttaggttttaattgcctaatg
1       M T N S L G V K L E E K N L Y Y N P N N A L G F N C L M
15079   ttgtttgtaataggcgcacgtggtataggtaaaacttatggttataaaaaatttgttgttaatcgctttattaaacacggcgaa
29      L F V I G A R G I G K T Y G Y K K F V V N R F I K H G E
15163   caatttatttatttaagaagattcaaaacagaacttaaaaagattcctcaatttttcaaaacaatggcgaaagaatttcctgat
57      Q F I Y L R R F K T E L K K I P Q F F K T M A K E F P D
15247   cataaacttgaagtaaaaggaaaagaattctattgtgatgataaattaatgggttgggctgttccacttagtacgtggggaatt
85      H K L E V K G K E F Y C D D K L M G W A V P L S T W G I
15331   gaaaaatctaatgaatatcccgaagttcgtacaattttgtttgatgagtttttaattgagaaatcaaaaatcacttatttacca
113     E K S N E Y P E V R T I L F D E F L I E K S K I T Y L P
15415   aacgaagctgaagccttattgaacatgatggaaacggttttccgaagacgtacaaatacaagatgtgttatgttgagtaatgca
141     N E A E A L L N M M E T V F R R R T N T R C V M L S N A
15499   actagtgtagtgaacccttatttcttgtatttcaatctgcagccagatttgaataagcgttttaatctatatcaagatcgaggt
169     T S V V N P Y F L Y F N L Q P D L N K R F N L Y Q D R G
15583   atattgattgaattgtgtgattcaaaagactttgcagaagtgaagagagaaacacctttggtagattgattcgtggaacagaa
197     I L I E L C D S K D F A E V K R E T P F G R L I R G T E
15667   tacgaagatttagtatcaacaatgagtttgtcaatgatagtgatacgtttattgaaaagagaagtaaaaatagtagtttctta
225     Y E D F S I N N E F V N D S D T F I E K R S K N S S F L
15751   tgcgccattgcttttgaagggaaaatctttgggtattggatagacgctgaaacaggttgtgtctatgtgagttatgattatcaa
253     C A I A F E G K I F G Y W I D A E T G C V Y V S Y D Y Q
15835   ccaaatacaaatcattttatgcaatgactacgaaagaccatgaagaaaatagattgctgatgaaaaattggcgaaataattat
281     P N T N H F Y A M T T K D H E E N R L L M K N W R N N Y
15919   tatctttcaacagtggcgaaagcattcaagaatagttatctgcggtttgataacattgttattaagaatttacattatgatttg
309     Y L S T V A K A F K N S Y L R F D N I V I K N L H Y D L
16003   tttaataagatgaaaatctggtaa 16026
337     F N K M K I W *


182ORF007
7795    atgagtagacgaaaaggtgcaggacttgctagaaataaccgttatacagcaaaaagcagaccttatccaaatgaacccattca
1       M S R R K G A G L A R N N R Y T A K S R P Y P N E P Y S
7879    agtgatgtagaagaaatcagctactatgaacattatcgtagacaactcacgctccttacgtttcagttgtttgaatgggaaaat
29      S D V E E I S Y Y E H Y R R Q L T L L T F Q L F E W E N
7963    ttgccaaaatcaattgaccctcgttatttagaaattgctttacacactaatggttatcttggtttctttaaagaccctacactt
57      L P K S I D P R Y L E I A L H T N G Y L G F F K D P T L
8047    gggttcatggtttgcgcaggggcagaagatggtcaaatcgatcattatcacaaccctatttctttacagcaaacgaagcaatg
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85 G F M V C A G A E D G Q I D H Y H N P I F F T A N E A M
8131 tatcacaagagatatcctgttttaagatatgatgatgatgatgataaatcaaaatgtatcatgttgtataataatgacttgaaa
113 Y H K R Y P V L R Y D D D D D K S K C I M L Y N N D L K
8215 gttcctacgttaccaagtttacatcgttttgctttagatatggcggacataaaccagatatcacgagtgaatcgaagagcgcaa
141 V P T L P S L H R F A L D M A D I N Q I S R V N R R A Q
8299 aaaacacctgtaattattcaaactgatgaaaagaaatacttctcattgctacaagcttataaccaaattgacgaaaataatcag
169 K T P V I I Q T D E K K Y F S L L Q A Y N Q I D E N N Q
8383 gctgttttgtggataaagatatggagtttgacgaatcttttaatgtatggcaaacaaatgctccatatgtagtagataaacta
197 A V F V D K D M E F D E S F N V W Q T N A P Y V V D K L
8467 cgatcagaattgaacgaagtatggaatgaagtgttaacttttctaggtatcaacaatgctaacgtagataagactgcacgtgta
225 R S E L N E V W N E V L T F L G I N N A N V D K T A R V
8551 caaacatcagaagtcttatctaacaatgaacagattgaaagttcaggtaacatcttgttaaaatcaagaaaagagttttgcgat
253 Q T S E V L S N N E Q I E S S G N I L L K S R K E F C D
8635 cgtgtaaatcgtgtctttggcgatgaacttgacggaaagattgacgtgaagtttagaacagacgccgttcgacaattacaactg
281 R V N R V F G D E L D G K I D V K F R T D A V R Q L Q L
8719 gcggcaggtcaatcaaaaaaagaccagatgagtggagggttgccaagtgctacttaa 8775
309 A A G Q S K K D Q M S G G L P S A T *

182ORF008
14105 atgatgaatggtattgatatctctagttatcaaacaggaattgatctttcaaaagttccatgcgattttgtaaatattaaagca
1 M M N G I D I S S Y Q T G I D L S K V P C D F V N I K A
14189 acaggcggaacaggttatgtaaaccctgattgtgaccgagcatttcaacaagctttgtctttaggtaaaaagattggtgtgtat
29 T G G T G Y V N P D C D R A F Q Q A L S L G K K I G V Y
14273 cattttgcgcatgagaggggtttagaaggtacacctcaacaagaagcgcaattctttttagataatattaagggttacattggt
57 H F A H E R G L E G T P Q Q E A Q F F L D N I K G Y I G
14357 aaagctgttcttattcttgactttgaagggtcaaatcagaaagatgtaaattgggcgaaagcatttcttgattatgtttataat
85 K A V L I L D F E G S N Q K D V N W A K A F L D Y V Y N
14441 aaaacaggcgttaaagcatggttttatacgtatacagcaaacctcaatacaactgatttttctagtattgcaaaaggcgattat
113 K T G V K A W F Y T Y T A N L N T T D F S S I A K G D Y
14525 ggtttatgggttgctgaatatggatcaaatcaaccacaaggctactctcaaccagcgccacctaaaacaaataatttcccaatt
141 G L W V A E Y G S N Q P Q G Y S Q P A P P K T N N F P I
14609 gttgcctgttttcagtttacaagtaaaggacgtttaccaggatacaacggcaatcttgatttgaatgttttctatggcgatggt
169 V A C F Q F T S K G R L P G Y N G N L D L N V F Y G D G
14693 aatacatgggatctgtatgtaggtaaaaaacaggatcaaattgttcctcctgaaaataaaatatttgacgccacaagtgatgag
197 N T W D L Y V G K K Q D Q I V P P E N K I F D A T S D E
14777 tttattttcactcttacaacaggtagcacaagcgtgttttattttgacggagaaacgatctttgaattgtctgatccaacacaa
225 F I F T L T T G S T S V F Y F D G E T I F E L S D P T Q
14861 ctcgatcatattagaggaacatacaatcatgttcatggaaaagaaatcccatcaatggtgtggacacctgaacaatttgatatt
253 L D H I R G T Y N H V H G K E I P S M V W T P E Q F D I
14945 tacttaaaaatgtatgaaaagaaaccagtatataaatag 14983
281 Y L K M Y E K K P V Y K *

182ORF009
8765 gtgctacttaaacgttatattgaaagtttcacttattaccaacctgaattatctcgaaaagaacgtattgaagttggccgaaaa
1 V L L K R Y I E S F T Y Y Q P E L S R K E R I E V G R K
8849 caattgtttgattttgattatccgttttatgacgaaacaaaacgagcagaatttgaaacaaaatttatcaatcacttttacttg
29 Q L F D F D Y P F Y D E T K R A E F E T K F I N H F Y L
8933 agagagataggctcagaaacgatgggatcatttaagtttaatcttgacgaatatttaaatctaaacatgccctattggaataaa
57 R E I G S E T M G S F K F N L D E Y L N L N M P Y W N K
9017 atgttcctatcaaatcttgaagagtttccgatttttgatgacatggactacaccattgatgagaaacagaaattgttaaatgag
85 M F L S N L E E F P I F D D M D Y T I D E K Q K L L N E
9101 attgatacaaacatcaaagcgaatcgtgatgaatcgaagaaccaaacgaagcaagtagatcaaacagacaacagaaacaaaaat
113 I D T N I K A N R D E S K N Q T K Q V D Q T D N R N K N
9185 acacgtgacacaggaacaaccgattctttctcaaggaacacttatacagacacccctcaaaaagatttgagaattgccagcaat
141 T R D T G T T D S F S R N T Y T D T P Q K D L R I A S N
9269 ggagatggaacaggtgtaatcaattatgcaacaaatatcacagaagatttgagtaaagaaacaacaagctccacaggcgttgaa
169 G D G T G V I N Y A T N I T E D L S K E T T S S T G V E
9353 acaaacaacgacaaaacaaatcaaaatacacgaagcaatgcttctgaaaaagaaacaaagaacacagacattaataaagatcaa
197 T N N D K T N Q N T R S N A S E K E T K N T D I N K D Q
9437 aatcaaaccaaagatacgattacacgatataaaggtaaaaagggaaacactgattatgctgacttactcgaaaaatatcgtaga
225 N Q T K D T I T R Y K G K K G N T D Y A D L L E K Y R R
9521 agtgttttgagaattgagaaaatgatctttagagaaatgaacaaggaaggcttatttctccttgtttatggagggaggtag
9601
253 S V L R I E K M I F R E M N K E G L F L L V Y G G R *

182ORF010
1310 ttgaccgtaagaatatcaaagaatgatagagccaagttagagaaaatctacggtaaatctaacaaagctcgtaaaaaatacaat
1 L T V R I S K N D R A K L E K I Y G K S N K A R K K Y N
1394 cgtttaagacaaaaaggagttgaggaaaggcaacttccaactgttccaacatcaaagaaaagacttattgactacgtaaaatca
29 R L R Q K G V E E R Q L P T V P T S K K R L I D Y V K S
1478 acaaatatgagtcgtagtgattttaacaagatgttagacgagttggtagatttgcacaaccttacaacgagaattacatttt
57 T N M S R S D F N K M L D E L V D F A Q P Y N E N Y I F
1562 gagatcaacaagcgaaatgttgcaatctcaagagcgcaaatcaaagaagcgcaaattaaaacagagcaagctcaaaaagcgaaa
85 E I N K R N V A I S R A Q I K E A Q I K T E Q A Q K A K
1646 gaagaacactacaaagagcttaacaaagttgaagttaagaagcccacagaaaacacaattgtcacaccaactatttaacagag
113 E E H Y K E L N K V E V K K P T E N T I V T P T I L T E
1730 ttaggtgctgacttacctttcaagcaataccagatttaatattgacgctttcacttctccagaaggagttcagtcttattta

141 L G A D L P F Q A I P D F N I D A F T S P E G V Q S Y L
1814 gaaaatataggaaaacaagacgaacaatatttgacgaaagagaccaacttttattacgacaatttcagacaagcgatgtttact
169 E N I G K Q D E Q Y F D E R D Q L Y Y D N F R Q A M F T
1898 atttcaattcagacgctgacgatattgttcgtttacttgactcaatggggcttgatctatttatgaaaacatatgttagtaac
197 I F N S D A D D I V R L L D S M G L D L F M K T Y V S N
1982 ttcttagacatgaaccttgactacatttatgacgaagcagaagtacaacagaaaaaagaacaagtttacagtaagattgcaaaa
225 F L D M N L D Y I Y D E A E V Q Q K K E Q V Y S K I A K
2066 gtgatcgagtctgaaacaggtggagaagtcccctcatataaccccacgaagaacatcacaattaattcagaaacaggagaagaa
253 V I E S E T G G E V P S Y N P T K N I T I N S E T G E E
2150 ttatga 2155
281 L *
182ORF011
9607 atggtagatttaaccccgacaagcggtttgacggtttacccgctgtattcaaagaacgctttagcaaatatcctcatactgaa
1 M V D F N P D K R F D G L P A V F K E R F S K Y P H T E
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9775 agtggttatttaaattactttatcgaacatttgttgagaagttagaagagatcacaaatgacacactcaaaaaatggttgtct
57 S G Y L N Y F I E H F V E K L E E I T N D T L K K W L S
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169 A T G D I Y L N I K G T E G V *
182ORF012
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11292 taa 11294
141 *
182ORF013
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113 A T D L A V R V S S L E D T A I Q Y T V L P *
182ORF014
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1 M I E Y I T Q W L A D D N H L V Y G L I I W L M V A M I
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29 I D F V L G F T I A K F N K E I D F S S F K A K A G I I
13884 gttaaggtggcagaaatggttttagtggtttactttattcctgtagcagtaaaattcggtgcagtaggtattacaatgtatata
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14052 gattatgttaagaagtttttagacggaacactcaacagaaaggacgatattaaatga 14108
113 D Y V K K F L D G T L N R K D D I K *
182ORF015
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1 M E I V K S T F D T Q T P E G M L Q V F N A T N G A S I
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29 P L R N A I G E V L E L K D I L V Y S D E V S G F G G A
1022 gaaccatcacaagcagaactagtcgctttcttcacagaagatggtaaaacttatgcgggtgtatcagcagtagcaacaaaatca
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85 A K N L I D M M T A N P D I K P K I S F V E G K S N G G
1190 caaaaatttgtaaatctacaagtggtttcactgtag 1225
113 Q K F V N L Q V V S L *
182ORF016
17033 atgattaacaatttatcattaatttagagggtttaaatcaactaactaaagatgacaacgatagtttagcgtctatcaagtca
1 M I N N L S L I L E G L N Q L T K D D N D S L A S I K S
16949 gaaataacacaaggaggaaaacaattaattttatacattgattacgttacaaaagagttcgtgttaacacatgatacatataac

29 E I T Q G G K Q L I L Y I D Y V T K E F V L T H D K Y N
16865 tatgtttatcttgatagccattgcattaatatcgcaataacgaaatcaatgaaaagcgttgaacactatgcggaacaattgaaa
57 Y V Y L D S H C I N I A I T K S M K S V E H Y A E Q L K
16781 catgacggatataaacaaattacggacaaatag 16749
85 H D G Y K Q I T D K *
182ORF017
154 atgaaatattcactacaacaaatagatgaaattaaatcaacaattttcagaattagattaaaaaggcatgaactagaggaattg
1 M K Y S L Q Q I D E I K S T I F R I R L K R H E L E E L
238 gtggacgaagtaaacgatattgctaaagatccggaggaaagatatcttttatcgttttattacacagaagaagaacgtttgttt
29 V D E V N D I A K D P E E R Y L L S F Y Y T E E E R L F
322 gaaattccctctgcaagattaatagattattacaacgaaaagatcacaaatctgaaatcggaaatcatatcactcgaaaaaaga
57 E I P S A R L I D Y Y N E K I T N L K S E I I S L E K R
406 ttacaaaaactagtaaaataa 426
85 L Q K L V K *
182ORF018
16737 atgattgcacgaacattcaaagaacaccgcgaactaattgaatggttacgtttctactgtaaacgtaacctttcagacaatgaa
1 M I A R T F K E H R E L I E W L R F Y C K R N L S D N E
16653 aaaatagagatcatagaggggactttacaagatttcgacgttccggaaataaatatcaccgaacttttgttaactcattcaacg
29 K I E I I E G T L Q D F D V P E I N I T E L L L T H S T
16569 ctattacccgaatcgagtcaatttaacattcttgaaaagtattgtcaggcaatgaaattagtaacttcatacgtaaaagttggt
57 L L P E S S Q F N I L E K Y C Q A M K L V T S Y V K V G
16485 tctcgctatcagttagcgttacaaataccaaaaggctatttaaaggaggtggaataa 16429
85 S R Y Q L A L Q I P K G Y L K E V E *
182ORF019
4323 atggaaattaaagaacatgaatcaattttaaatggtattcttgaaagtgtcacagacggtgaagcaagatcaaagattgtagaa
1 M E I K E H E S I L N G I L E S V T D G E A R S K I V E
4407 catcttgaagcattgcgagaagactacggagcaacaactgaagctttgacatcagcaaatagcacacttgaaaagttaaagaaa
29 H L E A L R E D Y G A T T E A L T S A N S T L E K L K K
4491 gataacgaagcgttggttatttcaaactcaaaattgttccgagaacgagcgatcgtagaaccagcagaaaataacgaaccagaa
57 D N E A L V I S N S K L F R E R A I V E P A E N N E P E
4575 acagaccagaatattacactagacgatttaggaatttaa 4613
85 T D Q N I T L D D L G I *
182ORF020
10158 atggcagacattagaacacaactaacaagtgaagatggatcagacaatttatttccaatttcaaaagccgttaatattatgact
1 M A D I R T Q L T S E D G S D N L F P I S K A V N I M T
10242 aatagcggtacgaatgtagaaggagaattgggtacactcaaacaaaatgacgaaacaatgaatacctcagttcaaaatgctgta
29 N S G T N V E G E L G T L K Q N D E T M N T S V Q N A V
10326 gttactgccaatcaagcaaaagattctgtagctgaattaaatgtaaatgttggtaaactaaccaatcgaataacaacattagag
57 V T A N Q A K D S V A E L N V N V G K L T N R I T T L E
10410 agtacagtggctaatcttgatggtattcgttatgtagaggtgtaa 10454
85 S T V A N L D G I R Y V E V *
182ORF021
17339 atgaacaataaatcattaatagctgaaaaaggagaggtatctctacttcacccctttaatgagtgggatatgaattatcatatc
1 M N N K S L I A E K G E V S L L H P F N E W D M N Y H I
17255 atagataccgaaaacaataaacattatcttattgatattgatgaggtaggcgatgaggaatattgtttgttatctttgaagaa
29 I D T E N N K H Y L I D I D E V G D E E Y C L L S F E E
17171 ctaaaggaattagatatggatcttatttccgagtattcatggaaaactacagaaataacatattaa 17106
57 L K E L D M D L I S E Y S W K T T E I T Y *
182ORF022
12868 gtgggttgtctaatgctaaagctgaaacgttggaaggtcaagcagagatcatcgctcaaggggataaaacaggtcaatggatgg
1 V G C L M L K L K R W K V K Q R S S L K G I K Q V N G W
12952 ataatacacctgtttcttctgcaggttatactaaccctcagaccctttcagcatttaaacaatctgcaaatattgatgttgcta
29 I I H L F L L Q V I L T L R P F Q H L N N L Q I L M L L

13036 caattaattttatgtgtcactgggaacgccctggtaaacttcatatcgaagaaagacttgatcttgcacaagcttatagtaagc
57 Q L I L C V T G N A L V N F I S K K D L I L H K L I V S
13120 atattgacggtagcggtggcggtggcgtaa 13149
85 I L T V A V A V A *
182ORF023
12189 atggttgttgttttggacatgcaagttatgcgcatatcctcgataataacttacgccaccttcgattgtgttaccagaaatttc
1 M V V V L D M Q V M R I S S I I T Y A T F D C V T R N F
12105 acagaaattaattacattctgataatcatcgtcattgtcgataatgatcgctgtacaaaaatgaatacggttgtttttcacaaa
29 T E I N Y I L I I I V I V D N D R C T K M N T V V F H K
12021 gaaacctctaaaacctgtacccctagtattgatatcgttcccttgccacataccatttacatcgggaaaagctgttttgataat
57 E T S K T C T P S I D I V P L P H T I Y I G K S C F D N
11937 tgcttgagagatattagagaatag 11914
85 C L R D I R E *
182ORF024
6174 atgcttgtaactatctcatctttaaaaacgaagaaacttatcctagtaaatggcagtatgcctttgttactgatattgaatata
1 M L V T I S S L K T K K L I L V N G S M P L L L I L N I
6258 agaatgacaacacaagtttcgttacctttgaaattgatgttttacaaacttatcgtttcgatattggtatacgagaaagtttca
29 R M T T Q V S L P L K L M F Y K L I V S I L V Y E K V S
6342 ttgcaaaagaacaccctcaactttattattcgaatggaataccttttcattaatacaattgaagagtcgcttgattacggtagag
57 L Q K N T L N F I I R M E Y L S L I Q L K S R L I T V E
6426 aatacacaacaacaaatgtaa 6446
85 N T Q Q Q M *

182ORF025
548 atgggtcgaaaactaatgcaacgaaacgtaacatcaactaaagtagaattctcagaagttatcgtacaagatggagcgccaaca
1 M G R K L M Q R N V T S T K V E F S E V I V Q D G A P T
632 attgtaccatgcgaaccagttgtcttaacaggaaaactttcagaagaaaaagctttatcagcgatcaaacgtaaaaaccctgat
29 I V P C E P V V L T G K L S E E K A L S A I K R K N P D
716 aaaaacgtagttgtaacaaatgtttcacatgaaacagcgctttacacaatgccagtcgataaatttatcgagttagcagacaaa
57 K N V V V T N V S H E T A L Y T M P V D K F I E L A D K
800 tcaacacaagcctaa 814
85 S T Q A *
182ORF026
13259 atggaaattatttggtctgccgtttcctgcatgcgtgccaaaaagttgtccactcatgaaacttttaggatcaagatttgtatt
1 M E I I W S A V S C M R A K K L S T H E T F R I K I C I
13175 cttgattggggttccatagcaacgttttacgccaccgccaccgctaccgtcaatatgcttactataagcttgtgcaagatcaag
29 L D W G S I A T F Y A T A T A T V N M L T I S L C K I K
13091 tctttcttcgatatgaagtttaccagggcgttcccagtgacacataaaattaattgtagcaacatcaatatttgcagattgttt
57 S F F D M K F T R A F P V T H K I N C S N I N I C R L F
13007 aaatgctga 12999
85 K C *
182ORF027
14896 atgaacatgattgtatgttcctctaatatgatcgagttgtgttggatcagacaattcaaagatcgtttctccgtcaaaataaaa
1 M N M I V C S S N M I E L C W I R Q F K D R F S V K I K
14812 cacgcttgtgctacctgttgtaagagtgaaaataaactcatcacttgtggcgtcaaatatttttatttcaggaggaacaatttg
29 H A C A T C C K S E N K L I T C G V K Y F I F R R N N L
14728 atcctgtttttacctacatacagatcccatgtattaccatcgccatagaaaacattcaaatcaagattgccgttgtatcctgg
57 I L F F T Y I Q I P C I T I A I E N I Q I K I A V V S W
14644 taa 14642
85 *
182ORF028
14430 atgtttataataaaacaggcgttaaagcatggttttatacgtatacagcaaacctcaatacaactgatttttctagtattgcaa
1 M F I I K Q A L K H G F I R I Q Q T S I Q L I F L V L Q
14514 aaggcgattatggtttatgggttgctgaatatggatcaaatcaaccacaaggctactctcaaccagcgccacctaaaacaaata
29 K A I M V Y G L L N M D Q I N H K A T L N Q R H L K Q I
14598 atttttccaattgttgcctgttttcagtttacaagtaaaggacgtttaccaggatacaacggcaatcttgatttga 14672
57 I F Q L L P V F S L Q V K D V Y Q D T T A I L I *
182ORF029
17606 atgaatgaaccgatcgtatacacagaaatttattcaaataacgtggtatgtatgaaaatttttagagatgaggataaacttagt
1 M N E P I V Y T E I Y S N N V V C M K I F R D E D K L S
17522 aaattcctctatttagaatttgaggtggatgaggctaaaaagttacttgaaaataaaacaatttcatttgatgataactggact
29 K F L Y L E F E V D E A K K L L E N K T I S F D D N W T
17438 ttctcaataaattatccagaatattaa 17412
57 F S I N Y P E Y *
182ORF030
16429 atggctacattctacaaggaaccaatatacgatatcacagtattttatatagatggttgggaggttttgatacacaaaaccgaa
1 M A T F Y K E P I Y D I T V F Y I D G W E V L I H K T E
16345 cctctcaccttaacaaaagcattaaaatatagccgtatatacctagaaatggatatagtgaattgcgttagaatagaaagaaat
29 P L T L T K A L K Y S R I Y L E M D I V N C V R I E R N
16261 ggacgtcctatagctacatttacagggaattattaaaactgtataaggagaaagaactatga 16199
57 G R P I A T F Y R E L L K L Y K E K E L *

182ORF031
8603 atgttacctgaactttcaatctgttcattgttagataagacttctgatgtttgtacacgtgcagtcttatctacgttagcattg
1 M L P E L S I C S L L D K T S D V C T R A V L S T L A L
8519 ttgatacctagaaaagttaacacttcattccatacttcgttcaattctgatcgtagtttatctactacatatggagcatttgtt
29 L I P R K V N T S F H T S F N S D R S L S T T Y G A F V
8435 tgccatacattaaaagattcgtcaaactccatatctttatccacaaaaacagcctga 8379
57 C H T L K D S S N S I S L S T K T A *
182ORF032
11413 atgtttcatcaaaaacaacttgtttcgggttcgtttcagggtgcaataggtaattcttttgatttcttctttcatcttgttca
1 M F H Q K Q L V S G S F Q G A I G N S F D F L L S S C S
11329 tttgaatatcaattcgttcttccatatgaacctccttatttagagggaaaacgcaattatctagggatagatattcgattta
29 F E Y Q F V L P Y E P P Y F R G K T Q L S R D R Y S I L
11245 cctacattgtcatttacagttactttgccatcaggtgtgattgatacataa 11195
57 P T L S F T V T L P S G V I D T *
182ORF033
4942 atgtcaacaaaaatttcttcaatcgttcgacctaaaggcatgttcctttttaaacattttcaaagggttacgccaagatttg
1 M S T K I S S I V R P K G M F P F L N I F K G L R Q D L
4858 tatcggataactactttaccaatacggtcaactaaagttgaaataaattcgtttttactacgtctaaacgtgtgatccctgca
29 Y R I T T L P I R S T K V E I N S F F T T S K R V I P A
4774 ccaaccgcttcgatgttatctgcatttggcataggtacgttcgcctga 4727
57 P T A S M L S A F G I G T F A *
182ORF034
6160 gtgtttatctactctaaaaactcccccgagttgtgtatccctttgataagaacaatctctattctcgttaagaacaggaaacga
1 V F I Y S K N S P E L C I P L I R T I S I L V K N R K R
6076 attaaagtacgattcctgttcctgttgagttttaaaccatcttgtgtgtgtataggtgttatcaaaaggcacgttagccaacaa
29 I K V R F L F L L S F K P S C V C I G V I K R H V S Q Q
5992 ttttacatttgtataccttcttgccataattgtcctccttag 5951

57 F Y I C I P S C H N C P P *
182ORF035
15758 atggcgcataagaaactactattttacttctcttttcaataaacgtatcactatcattgacaaactcattgttgatactaaaa
1 M A H K K L L F L L L F S I N V S L S L T N S L L I L K
15674 tcttcgtattctgttccacgaatcaatctaccaaaaggtgtttctctcttcacttctgcaaagtctttgaatcacacaattca
29 S S Y S V P R I N L P K G V S L F T S A K S F E S H N S
15590 atcaatatacctcgatcttga 15570
57 I N I P R S *
182ORF036
2315 atgtctgtgctgccttgcatttacaccactcaaaaaagaatcgatttctaaaccgaacgtcatattgtcaacgttgtctata
1 M S V L P C I L H H S K K E S I S K P N V I L S T L S I
2231 tcgcatacgccccacgaccatacacgacaatcgttgagatcagttgttgtttcaaagtcgccagtatatttcttaatcataatt
29 S H T P H D H T R Q S L R S V V V S K S P V Y F L I I I
2147 cttctcctgtttctgaattaa 2127
57 L L L F L N *
182ORF037
12280 gtgagttacgacaataaacatctacatcaatataagcttgatccacatcttgaaactcaaacaaagcgtttctatttccgtatg
1 V S Y D N K H L H Q Y K L D P H L E T Q T K R F Y F R M
12196 ctagaaaatggttgttgttttggacatgcaagttatgcgcatatcctcgataataacttacgccaccttcgattgtgttaccag
29 L E N G C C F G H A S Y A H I L D N N L R H L R L C Y Q
12112 aaatttcacagaaattaa 12095
57 K F H R N *
182ORF038
14769 gtgatgagtttattttcactcttacaacaggtagcacaagcgtgttttatttgacggagaaacgatctttgaattgtctgatc
1 V M S L F S L L Q Q V A Q A C F I L T E K R S L N C L I
14853 caacacaactcgatcatattagaggaacatacaatcatgttcatggaaaagaaatcccatcaatggtgtggacacctgaacaat
29 Q H N S I I L E E H T I M F M E K K S H Q W C G H L N N
14937 ttgatatttacttaa 14951
57 L I F T *
182ORF039
9992 atgttgctgatgatcgaacatttggtataagattcaacgcgacaatactgattatggagccgatcctattgacacgttacgta
1 M L L M I E H F G I R F N A T I L I M E P I L L T R Y V
10076 ttgttgcaatcaataaagttagtggctggaataccgctacaggagatatttatcttaacattaaaggaacggagggtgtataat
29 L L Q S I K L V A G I P L Q E I F I L T L K E R R V Y N
10160 ggcagacattag 10171
57 G R H *
182ORF040
16202 atgagaaaagatttcgtctacattaacacacccgatccaaaagcaaacaaaaaggcgttagcaaaaatcactaacgccaaagaa
1 M R K D F V Y I N T P D P K A N K K A L A K I T N A K E
16118 ccaaaacaaaactatcgcagactacaattactatgttatctactattcatcattgtaatagaactaatcgtggtagctctacta
29 P K Q N Y R R L Q L L C Y L L F I I V I E L I V V A L L
16034 aaatag 16029
57 K *

182ORF041
3886 atggaactatataaagcaatgtttatcgtacgtgatgaaggtactattgacggttacgatactgaacactatgtagatatttct
1 M E L Y K A M F I V R D E G T I D G Y D T E H Y V D I S
3970 ttacatgactttgaagaaatatatggaaaagaaacacgtgaaattgaagcagtaacattagtaaaaacaggaaatttaaaaaaa
29 L H D F E E I Y G K E T R E I E A V T L V K T G N L K K
4054 taa 4056
57 *
182ORF042
10832 gtgtcctctaaactgcttactcgaacagctagatcagttgcactttttgtgctgaatcagctgtgtttttagctgccgttgca
1 V S S K L L T R T A R S V A L F C A E S A V F L A A V A
10748 actgcgctgatactgtttgctgttgttttcgcttgttctgcggtttgttgtgctgtaccagccttcgtcaacgcttga 10671
29 T A L I L F A V V F A C S A V C C A V P A F V N A *
182ORF043
10652 gtgtcaatttctgttgacaaaccagcagcagtttctttagcttgttgtgcaagtgttttagcttcactagcgttacctcttatt
1 V S I S V D K P A A V S L A C C A S V L A S L A L P L I
10568 tcagcattaactaattcaagattagagtcgcctgttagaacatttttagcaattgtaacaggcattaaacgattatga 10491
29 S A L T N S R L E S P V R T F L A I V T G I K R L *
182ORF044
6457 atgaaaagttgttacatttgttgttgtgtattctctaccgtaatcaagcgactcttcaattgtattaatgaaaggtattccatt
1 M K S C Y I C C C V F S T V I K R L F N C I N E R Y S I
6373 cgaataataaagttgagggtgttcttttgcaatgaaactttctcgtataccaatatcgaaacgataagtttgtaa 6299
29 R I I K L R V F F C N E T F S Y T N I E T I S L *
182ORF045
6729 atgaatggtatacctgtatacgacgttacatacatcccgactatcttatttaaaaaaggttctttcgttgtaagaaacgccatg
1 M N G I P V Y D V T Y I P T I L F K K G S F V V R N A M
6645 tactctccaaaattagcattgcctgccccatttggtttgtatacctccccacttgaattgataggaagtaaataa 6571
29 Y S P K L A L P A P F G L Y T S P L E L I G S K *
182ORF046
2372 atggtttcaaatggtgtaaagaagcaaaagaagatcgaacattctccacactcatatcaaatatgggtcaatggtatgctttgg
1 M V S N G V K K Q K K I E H S P H S Y Q I W V N G M L W
2456 aaatttgttgggaagttaattacacaacaacaaaatcaggtaaaacgaaaaaagagaaatctcgaacaataa 2527
29 K F V G K L I T Q Q Q N Q V K R K K R N L E Q *

182ORF047
13353 atgctcccattgttccaacatgtgttactgttccatcgcaacatgcaatcatttcattgccagggtgatcaattgaaccaaagt
1 M L P L F Q H V L L F H R N M Q S F H C Q G D Q L N Q S
13269 ccaaaccatcatggaaattatttggtctgccgtttcctgcatgcgtgccaaaaagttgtccactcatga 13201
29 P N H H G N Y L V C R F L H A C Q K V V H S *
182ORF048
3395 atgtcagggtttgttccgaactttccatacaagctatttaacataccttggcgttagctttctagccccttcggtggtgttc
1 M S G F V P N F P Y K L F N I P L A L A F L A P S V V F
3311 tttacttcgatccatttatcgatccagcctttgaacatatcacaagaagctttgaacatatatccgtaa 3243
29 F T S I H L S I Q P L N I S Q E A L N I Y P *
182ORF049
1578 atgttgcaatctcaagagcgcaaatcaaagaagcgcaaattaaaacagagcaagctcaaaaagcgaaagaagaacactacaaag
1 M L Q S Q E R K S K K R K L K Q S K L K K R K K N T T K
1662 agcttaacaaagttgaagttaagaagcccacagaaaacacaattgtcacaccaactattttaa 1724
29 S L T K L K L R S P Q K T Q L S H Q L F *
182ORF050
8012 atggttatcttggtttctttaaagaccctacacttgggttcatggtttgcgcaggggcagaagatggtcaaatcgatcattatc
1 M V I L V S L K T L H L G S W F A Q G Q K M V K S I I I
8096 acaaccctatttctttacagcaaacgaagcaatgtatcacaagagatatcctgttttaa 8155
29 T T L F S L Q Q T K Q C I T R D I L F *
182ORF051
9390 atgcttctgaaaaagaaacaaagaacacagacattaataaagatcaaaatcaaaccaaagatacgattacacgatataaaggta
1 M L L K K K Q R T Q T L I K I K I K P K I R L H D I K V
9474 aaaagggaaacactgattatgctgacttactcgaaaaatatcgtagaagtgttttga 9530
29 K R E T L I M L T Y S K N I V E V F *
182ORF052
4096 gtgatagttgacaagagtcaaatttggcgagattgggcgaatgtacacgtgaaatatcgtgcgctcccgttaagttatggacac
1 V I V D K S Q I W R D W A N V H V K Y R A L P L S Y G H
4180 ataaacgttttgaccgtcaaccaatcgcaaaaacctttaggagtagccctaa 4233
29 I N V L T V N Q S Q K P F R S S P *
182ORF053
15656 gtggaacagaatacgaagattttagtatcaacaatgagtttgtcaatgatagtgatacgtttattgaaaagagaagtaaaaata
1 V E Q N T K I L V S T M S L S M I V I R L L K R E V K I
15740 gtagtttcttatgcgccattgcttttgaagggaaaatctttgggtattggatag 15793
29 V V S Y A P L L L K G K S L G I G *

182ORF054
8136 gtgatacattgcttcgtttgctgtaaagaaaatagggttgtgataatgatcgatttgaccatcttctgcccctgcgcaaaccat
1 V I H C F V C C K E N R V V I M I D L T I F C P C A N H
8052 gaacccaagtgtagggtctttaaagaaaccaagataaccattagtgtgtaa 8002
29 E P K C R V F K E T K I T I S V *
182ORF055
8324 atgaaaagaaatacttctcattgctacaagcttataaccaaattgacgaaaataatcaggctgtttttgtggataaagatatgg
1 M K R N T S H C Y K L I T K L T K I I R L F L W I K I W
8408 agtttgacgaatcttttaatgtatggcaaacaaatgctccatatgtag 8455
29 S L T N L L M Y G K Q M L H M *
182ORF056
6549 gtggcccatctcctttttcctattatttacttcctatcaattcaagtggggaggtatacaaaccaaatggggcaggcaatgcta
1 V A H L L F P I I Y F L S I Q V G R Y T N Q M G Q A M L
6633 atttggagagtacatggcgtttcttacaacgaaagaacctttttaa 6680
29 I L E S T W R F L Q R K N L F *
182ORF057
8264 atgtccgccatatctaaagcaaaacgatgtaaacttggtaacgtaggaactttcaagtcattattatacaacatgatacatttt
1 M S A I S K A K R C K L G N V G T F K S L L Y N M I H F
8180 gatttatcatcatcatcatcatatcttaaaacaggatatctcttgtga 8133
29 D L S S S S S Y L K T G Y L L *
182ORF058
5176 gtgtattcaaattcgcttacttcgtcacctgtgtataaagcgttcattacaccagcaacgaaactattgaaattatcccatgaa
1 V Y S N S L T S S P V Y K A F I T P A T K L L K L S H E
5092 gtaaatgctttttctaaccatgcttcttggatcgtttgtttgtag 5048
29 V N A F S N H A S W I V C L *
182ORF059
15876 atggtctttcgtagtcattgcataaaaatgatttgtatttggttgataatcataactcacatagacacaacctgtttcagcgtc
1 M V F R S H C I K M I C I W L I I I T H I D T T C F S V
15792 tatccaatacccaaagatttcccttcaaaagcaatggcgcataa 15748
29 Y P I P K D F P F K S N G A *
182ORF060
15404 gtgattttgatttctcaattaaaaactcatcaaacaaaattgtacgaacttcgggatattcattagattttcaattccccac
1 V I F D F S I K N S S N K I V R T S G Y S L D F S I P H
15320 gtactaagtggaacagcccaacccattaatttatcatcacaatag 15276
29 V L S G T A Q P I N L S S Q *
182ORF061
2102 atgaggggacttctccacctgtttcagactcgatcacttttgcaatcttactgtaaacttgttctttttctgttgtacttctg

1 M R G L L H L F Q T R S L L Q S Y C K L V L F S V V L L
2018 cttcgtcataaatgtagtcaaggttcatgtcctaagaagttactaa 1974
29 L R H K C S Q G S C L R S Y *
182ORF062
1992 atgtctaagaagttactaacatatgttttcataaatagatcaagccccattgagtcaagtaaacgaacaatatcgtcagcgtct
1 M S K K L L T Y V F I N R S S P I E S S K R T I S S A S
1908 gaattgaaaatagtaaacatcgcttgtctgaaattgtcgtaa 1867
29 E L K I V N I A C L K L S *
182ORF063
14306 gtgtaccttctaaacccctctcatgcgcaaaatgatacacaccaatctttttacctaaagacaaagcttgttgaaatgctcggt
1 V Y L L N P S H A Q N D T H Q S F Y L K T K L V E M L G
14222 cacaatcagggtttacataacctgttccgcctgttgctttaa 14181
29 H N Q G L H N L F R L L L *
182ORF064
7356 atgatgttagtcaaaccaacaaaagggttgttacttgctaaggctgaaaagatcgctcctcctgtactcattgcactgtttccc
1 M M L V K P T K G L L L A K A E K I A P P V L I A L F P
7272 ataccatgtctgaaagtattgcgaatgttttgctcttga 7234
29 I P C L K V L R M F C S *
182ORF065
3582 atgaatgctatctgtatcacaataaataatgcgatcaaaacatttttgagcggttgtaatggtagtatatctaccccaagccgt
1 M N A I C I T I N N A I K T F L S G C N G S I S T P S R
3498 cacaaaactagcaagcggaacataaacaggatctcttaa 3460
29 H K T S K R N I N R I S *
182ORF066
4234 atgtggctactctttttgtgtttcacagaattatgtttcacgtgaaacagtttttatggtataatagaatcaaaaggaggtgg
1 M W L L F F V F H R I M F H V K Q F L W Y N R I K R R W
4318 agattatggaaattaaagaacatgaatcaattttaa 4353
29 R L W K L K N M N Q F *
182ORF067
13882 atgatacctgctttagctttaaaactactaaagtcgatttccttgttaaatttggcaattgtaaaacctaacacaaaatcgata
1 M I P A L A L K L L K S I S L L N L A I V K P N T K S I
13798 atcattgcaaccattaaccatataatcaaaccataa 13763
29 I I A T I N H I I K P *

182ORF068
7267 atgtctgaaagtattgcgaatgttttgctcttgagcaatcaaggagtttttgtttccttgcatgaatgcagaagcatagtcaga
1 M S E S I A N V L L L S N Q G V F V S L H E C R S I V R
7183 tttaactcctacatcgttaggatcattatcgattaa 7148
29 F N S Y I V R I I I D *
182ORF069
5027 gtggaacaatgttttacatcgggaacttcctgtttaaatacccctgtaacagactcgtcagggttgaacttatgttcctgtgc
1 V E Q C F Y I G N F L F K Y P C N R L V R V E L M F L C
4943 aatgtcaacaaaaatttcttcaatcgttcgacctaa 4908
29 N V N K N F F N R S T *
182ORF070
1031 gtgatggttcggctccaccaaaaccagaaacttcgtctgagtaaactagaatatctttcaattctagtacttcgccaattgcgt
1 V M V R L H Q N Q K L R L S K L E Y L S I L V L R Q L R
947 tacgtaacggaattgaagccccgtttgtggcattga 912
29 Y V T E L K P R L W H *
182ORF071
11741 atggttttgcattatggttgccacaaggcgctcaaagtggtaaaggaatttctctttaatgatactcgcaattacaatcgttttg
1 M V L H Y G C H K A L K V V K E F S L M I L A I T I V L
11825 actttgatttgtttgttcgtaactgtactttaa 11857
29 T L I C L F V T V L *
182ORF072
11723 atgtttacattaaatgccgtcattgtttcaaactttaatgtcgtttctcccgatcctaagaaagtaactacaggtacatcacgt
1 M F T L N A V I V S N F N V V S P D P K K V T T G T S R
11639 ttcaattcaatggtgttagcaaagcgataa 11610
29 F N S M V L A K R *
182ORF073
2876 gtgaagccgcctttgtatgctttacgtaagtctttatcaaaccctaaagacaaaataggaaaccattgtttgaaagttgatttt
1 V K P P L Y A L R K S L S N P K D K I G N H C L K V D F
2792 ccatgtgtagcttttagccaatctttgtaa 2763
29 P C V A F S Q S L *
182ORF074
8923 gtgattgataaattttgtttcaaattctgctcgttttgtttcgtcataaaacggataatcaaaatcaaacaattgttttcggcc
1 V I D K F C F K F C S F C F V I K R I I K I K Q L F S A
8839 aacttcaatacgttcttttcgagataa 8813
29 N F N T F F S R *
182ORF075
7463 gtgttacattatctggaatatttcgatatctgccactttacctgccaagaggttcaaaccgtttcttttttcagaaacatagt
1 V L H Y L E Y F R Y L P L Y L P R G S N R F L F Q K H S
7379 tgtttacttgttgtcctgctcccatga 7353
29 C L L V V L L P *
182ORF076
2426 atgagtgtggagaatgttcgatcttcttttgcttctttacaccatttgaaaccatttttgaataaccatgaaagcataaactct

1 M S V E N V R S S F A S L H H L K P F L N N H E S I N S
2342 ccgtcaaattttcgttgtggaaataa 2316
29 P S N F S L W K *
18ORF077
11858 atgaaggaacgtatgttgttgttgctagaggtagaggggttacatttgaaaattgtctattctctaatatctctcaagcaatta
1 M K E R M L L L L E V E G L H L K I V Y S L I S L K Q L
11942 tcaaaacagcttttcccgatgtaa 11965
29 S K Q L F P M *
18ORF078
7671 gtgcctacaatatttggttcttttaatttaatgaaattccatgcttttcttgtttgtaagtttggtgtagctactcgattgctc
1 V P T I F G S F N L M K F H A F L V C K F G V A T R L L
7587 tttgtgccatacattgagaagtaa 7564
29 F V P Y I E K *
18ORF079
7488 gtgaaagataagtttgatccaagctgtgttacattatctggaatattttcgatatctgccactttacctgccaagaggttcaaa
1 V K D K F D P S C V T L S G I F S I S A T L P A K R F K
7404 ccgtttttctttttcagaaacatag 7381
29 P F S F S E T *
18ORF080
4473 gtgtgctatttgctgatgtcaaagcttcagttgttgctccgtagtcttctcgcaatgcttcaagatgttctacaatctttgatc
1 V C Y L L M S K L Q L L L R S L L A M L Q D V L Q S L I
4389 ttgcttcaccgtctgtga 4372
29 L L H R L *

Table 24

Sequence similarities phage 182 and public databases

Phage: 182

Database: nr

Query= sid|110156|lan|182ORF001 Phage 182 ORF|5966-7780|2
(604 letters)

gi|138124|sp|P07534|VG9_BPPZA TAIL PROTEIN (LATE PROTEIN GP9) >...	384	e-105
gi|138123|sp|P04331|VG9_BPPH2 TAIL PROTEIN (LATE PROTEIN GP9) >...	374	e-103
gi|1429238|gnl|PID|e1173412 (X99260) tail protein [Bacteriophag...	346	3e-94
gi|215339 (M12456) p9 tail protein [Bacteriophage phi-29] >gi|2...	208	8e-53
gi|1181970|gnl|PID|e221269 (Z47794) tail protein [Bacteriophage...	62	8e-09
gi|1181968|gnl|PID|e221267 (Z47794) tail protein [Bacteriophage...	56	6e-07
gi|2500030|sp|Q59968|CARA_SULSO CARBAMOYL-PHOSPHATE SYNTHASE SM...	49	8e-05

Query= sid|110157|lan|182ORF002 Phage 182 ORF|2152-3873|1
(573 letters)

gi|118848|sp|P19894|DPOL_BPM2 DNA POLYMERASE >gi|76896|pir||JQ0...	665	0.0
gi|1429230|gnl|PID|e1173404 (X99260) DNA polymerase [Bacterioph...	657	0.0
gi|118849|sp|P03680|DPOL_BPPH2 DNA POLYMERASE (EARLY PROTEIN GP...	654	0.0
gi|118851|sp|P06950|DPOL_BPPZA DNA POLYMERASE (EARLY PROTEIN GP...	654	0.0
gi|15732 (X53371) DNA polymerase (AA 1-575) [Bacteriophage phi-29]	651	0.0
gi|15734 (X53370) DNA polymerase (AA 1-575) [Bacteriophage phi-29]	651	0.0
gi|1572479|gnl|PID|e242301 (X96987) DNA polymerase [Bacteriopha...	565	e-160
gi|1072656|pir||S51275 DNA polymerase - phage CP-1 >gi|836593|g...	301	1e-80
gi|118847|sp|P22374|DPOM_ASCIM PROBABLE DNA POLYMERASE >gi|8385...	71	3e-11
gi|461962|sp|P33537|DPOM_NEUCR PROBABLE DNA POLYMERASE >gi|2833...	65	1e-09
gi|461963|sp|P33538|DPOM_NEUIN PROBABLE DNA POLYMERASE >gi|1018...	62	1e-08
gi|1084487|pir||S41618 DNA polymerase - slime mold (Physarum po...	61	3e-08
gi|2435429 (AF012250) unassigned reading frame (possible DNA po...	61	3e-08
gi|578157|gnl|PID|e246743 (X52106) DNA polymerase [Neurospora i...	59	1e-07
gi|2147969|pir||S72369 probable DNA-polymerase - Gelasinospora ...	58	2e-07
gi|2147968|pir||S62752 probable DNA-polymerase - Gelasinospora ...	58	2e-07
gi|3511140 (AF061244) B type DNA polymerase [Agrocybe aegerita]	57	3e-07
gi|118850|sp|P10479|DPOL_BPPRD DNA POLYMERASE (PROTEIN P1) >gi|...	56	6e-07
gi|578144 (X63909) putative DNA-polymerase, B-type [Morchella c...	47	3e-04
gi|232013|sp|P30322|DPOM_AGABT PROBABLE DNA POLYMERASE >gi|3208...	46	6e-04

Query= sid|110159|lan|182ORF004 Phage 182 ORF|4626-5954|3
(442 letters)

gi|138117|sp|P13849|VG8_BPPH2 MAJOR HEAD PROTEIN (LATE PROTEIN ...	309	2e-83
gi|138118|sp|P07531|VG8_BPPZA MAJOR HEAD PROTEIN (LATE PROTEIN ...	305	3e-82
gi|1429236|gnl|PID|e1173410 (X99260) major head protein [Bacter...	300	1e-80
gi|1181958|gnl|PID|e221257 (Z47794) major head protein [Bacteri...	152	6e-36

Query= sid|110160|lan|182ORF005 Phage 182 ORF|12651-13700|3
(349 letters)

gi|137932|sp|P15132|VG13_BPPH2 MORPHOGENESIS PROTEIN 1 (LATE PR...	52	8e-06
gi|1429242|gnl|PID|e1173416 (X99260) morphogenesis protein [Bac...	48	7e-05
gi|137933|sp|P07538|VG13_BPPZA MORPHOGENESIS PROTEIN 1 (LATE PR...	47	2e-04

Query= sid|110161|lan|182ORF006 Phage 182 ORF|14995-16026|1
(343 letters)

gi|137944|sp|P11014|VG16_BPPH2 ENCAPSIDATION PROTEIN (LATE PROT...	402	e-111
gi|137945|sp|P07541|VG16_BPPZA ENCAPSIDATION PROTEIN (LATE PROT...	402	e-111
gi|1429245|gnl|PID|e1173419 (X99260) encapsidation protein [Bac...	381	e-105
gi|1181972|gnl|PID|e221271 (Z47794) encapsidation protein [Bact...	159	2e-38

Query= sid|110162|lan|182ORF007 Phage 182 ORF|7795-8775|1
(326 letters)

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gi|1429239|gnl|PID|e1173413 (X99260) upper collar protein [Bact...  271  5e-72
gi|137915|sp|P07535|VG10_BPPZA UPPER COLLAR PROTEIN (CONNECTOR ...  256  1e-67
gi|137914|sp|P04332|VG10_BPPH2 UPPER COLLAR PROTEIN (CONNECTOR ...  256  2e-67
gi|1181960|gnl|PID|e221259 (Z47794) connector protein [Bacterio...  148  6e-35

Query= sid|110163|lan|182ORF008 Phage 182 ORF|14105-14983|2
        (292 letters)

gi|4210750|gnl|PID|e1374037 (AJ132604) LysL protein [Lactococcu...  139  2e-32
gi|462559|sp|P34020|LYC_CLOAB AUTOLYTIC LYSOZYME (1,4-BETA-N-AC...   75  8e-13
gi|2327014 (U82823) putative lysozyme [Saccharopolyspora erythr...   64  2e-09
gi|126652|sp|P25310|LYCM_STRGL LYSOZYME M1 PRECURSOR (1,4-BETA-...   60  2e-08
gi|127789|sp|P19386|LYCA_BPCP9 LYSOZYME (ENDOLYSIN) (MURAMIDASE...   60  2e-08
gi|67761|pir||MUBPCP N-acetylmuramoyl-L-alanine amidase (EC 3.5...   59  3e-08
gi|4105636 (AF049087) lys [Leuconostoc oenos bacteriophage 10MC]     59  3e-08
gi|623084 (L02496) muramidase; muramidase [Bacteriophage LL-H]       57  1e-07
gi|127787|sp|P15057|LYCA_BPCP1 LYSOZYME (ENDOLYSIN) (MURAMIDASE...   57  2e-07
gi|126597|sp|P00721|LYCH_CHASP N,O-DIACETYLMURAMIDASE (LYSOZYME...   57  2e-07
gi|127788|sp|P19385|LYCA_BPCP7 LYSOZYME (ENDOLYSIN) (MURAMIDASE...   57  2e-07
gi|67762|pir||MUBPC7 N-acetylmuramoyl-L-alanine amidase (EC 3.5...   56  3e-07
gi|3025168|sp|P76421|YEGX_ECOLI HYPOTHETICAL 32.0 KD PROTEIN IN...   53  2e-06
gi|4204413 (AF047001) Lys44 [Oenococcus oeni temperate bacterio...   53  3e-06
gi|2116978|gnl|PID|d1020940 (D88151) cortical fragment-lytic en...   52  5e-06
gi|2392844 (AF011378) lysin [Bacteriophage sk1]                      48  8e-05

Query= sid|110164|lan|182ORF009 Phage 182 ORF|8765-9601|2
        (278 letters)

gi|1429240|gnl|PID|e1173414 (X99260) lower collar protein [Bact...  180  1e-44
gi|137921|sp|P04333|VG11_BPPH2 LOWER COLLAR PROTEIN (LATE PROTE...  171  5e-42
gi|215341 (M12456) p11 lower collar protein [Bacteriophage phi-29]   98  9e-20
gi|224162|prf||1011232B protein p11,lower collar [Bacteriophage...   97  1e-19
gi|535260 (Z30339) STARP antigen [Plasmodium reichenowi]             50  1e-05
gi|4049753 (AF063866) ORF MSV230 hypothetical protein [Melanopl...   49  4e-05
gi|2131557|pir||S70306 hypothetical protein YEL077c - yeast (Sa...   48  5e-05
gi|131782|sp|P12753|RA50_YEAST DNA REPAIR PROTEIN RAD50 (153 KD...   48  7e-05
gi|2131309|pir||S70305 hypothetical protein YBL113c - yeast (Sa...   47  2e-04
gi|499325 (Z26314) STARP antigen [Plasmodium falciparum]             46  3e-04
gi|3845171 (AE001391) ribosome releasing factor (OO, TP) [Plasm...   46  3e-04
gi|731903|sp|P40434|YIR7_YEAST HYPOTHETICAL 197.5 KD PROTEIN IN...   45  5e-04
gi|1632829|gnl|PID|e276379 (Y08924) AARP2 protein [Plasmodium f...   45  5e-04
gi|1176490|sp|P40889|YJW5_YEAST HYPOTHETICAL 197.6 KD PROTEIN I...   45  5e-04
gi|1077300|pir||S51848 hypothetical protein HRD1054 - yeast (Sa...   45  5e-04
gi|2425143 (AF020407) WimA [Dictyostelium discoideum]                45  6e-04
gi|1181961|gnl|PID|e221260 (Z47794) collar protein [Bacteriopha...   45  6e-04
gi|2132657|pir||S64819 probable membrane protein YLL067c - yeas...   45  8e-04
gi|2133041|pir||S65341 probable membrane protein YPR204w - yeas...   45  8e-04
gi|730275|sp|P39793|PBPA_BACSU PENICILLIN-BINDING PROTEINS 1A/1...   45  8e-04

Query= sid|110165|lan|182ORF010 Phage 182 ORF|1310-2155|2
        (281 letters)

gi|135604|sp|P06812|TERM_BPNF DNA TERMINAL PROTEIN >gi|75815|pi...   69  3e-11
gi|1572478|gnl|PID|e242334 (X96987) terminal protein [Bacteriop...   65  3e-10
gi|1429231|gnl|PID|e1173405 (X99260) terminal protein [Bacterio...   64  1e-09

Query= sid|110166|lan|182ORF011 Phage 182 ORF|9607-10158|1
        (183 letters)

gi|137928|sp|P07537|VG12_BPPZA PRE-NECK APPENDAGE PROTEIN (LATE...   51  6e-06
gi|1429241|gnl|PID|e1173415 (X99260) pre-neck appendage protein...   51  6e-06
gi|137927|sp|P20345|VG12_BPPH2 PRE-NECK APPENDAGE PROTEIN (LATE...   50  1e-05


Query= sid|110169|lan|182ORF014 Phage 182 ORF|13716-14108|3
        (130 letters)

gi|137936|sp|P11188|VG14_BPPH2 LYSIS PROTEIN (LATE PROTEIN GP14...   97  6e-20
gi|137938|sp|P07539|VG14_BPPZA LYSIS PROTEIN (LATE PROTEIN GP14...   96  8e-20
gi|1429243|gnl|PID|e1173417 (X99260) lysis protein [Bacteriopha...   96  8e-20
gi|215332 (M14782) lysis protein [Bacteriophage phi-29]              94  5e-19

Query= sid|110170|lan|182ORF015 Phage 182 ORF|854-1225|2
        (123 letters)
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gi|15670 (V01155) reading frame 10 (may be gene 4) [Bacteriopha...     70  5e-12
gi|138072|sp|P06953|VG5A_BPPZA EARLY PROTEIN GP5A >gi|75836|pir...    69  7e-12

Query= sid|110174|lan|182ORF019 Phage 182 ORF|4323-4613|3
         (96 letters)

gi|1429235|gnl|PID|e1173409 (X99260) head morphogenesis protein...    61  2e-09
gi|138111|sp|P13848|VG7_BPPH2 HEAD MORPHOGENESIS PROTEIN (LATE ...    57  3e-08
gi|138112|sp|P07533|VG7_BPPZA HEAD MORPHOGENESIS PROTEIN (LATE ...    54  1e-07

Query= sid|110180|lan|182ORF025 Phage 182 ORF|548-814|2
         (88 letters)

gi|138099|sp|P06955|VG6_BPPZA EARLY PROTEIN GP6 >gi|75841|pir||...    55  7e-08
gi|138098|sp|P03685|VG6_BPPH2 EARLY PROTEIN GP6 >gi|75840|pir||...    54  2e-07
gi|1429234|gnl|PID|e1173408 (X99260) gene 6 product [Bacterioph...    54  2e-07
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Table 25

Homologies between 182 ORFs and proteins in public databases

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Phage: 182

Database: Swissprot

Query= sid|110156|lan|182ORF001 Phage 182 ORF|5966-7780|2
        (604 letters)

gi|138124|sp|P07534|VG9_BPPZA TAIL PROTEIN (LATE PROTEIN GP9)          384  e-106
gi|138123|sp|P04331|VG9_BPPH2 TAIL PROTEIN (LATE PROTEIN GP9)          374  e-103
gi|2500030|sp|Q59968|CARA_SULSO CARBAMOYL-PHOSPHATE SYNTHASE SM...      49  2e-05

Query= sid|110157|lan|182ORF002 Phage 182 ORF|2152-3873|1
        (573 letters)

gi|118848|sp|P19894|DPOL_BPM2 DNA POLYMERASE                           665  0.0
gi|118849|sp|P03680|DPOL_BPPH2 DNA POLYMERASE (EARLY PROTEIN GP2)      654  0.0
gi|118851|sp|P06950|DPOL_BPPZA DNA POLYMERASE (EARLY PROTEIN GP2)      654  0.0
gi|118847|sp|P22374|DPOM_ASCIM PROBABLE DNA POLYMERASE                  71  7e-12
gi|461962|sp|P33537|DPOM_NEUCR PROBABLE DNA POLYMERASE                  65  3e-10
gi|461963|sp|P33538|DPOM_NEUIN PROBABLE DNA POLYMERASE                  62  3e-09
gi|118850|sp|P10479|DPOL_BPPRD DNA POLYMERASE (PROTEIN P1)              56  2e-07
gi|232013|sp|P30322|DPOM_AGABT PROBABLE DNA POLYMERASE                  46  2e-04
gi|118887|sp|P10582|DPOM_MAIZE DNA POLYMERASE (S-1 DNA ORF 3)           46  2e-04

Query= sid|110159|lan|182ORF004 Phage 182 ORF|4626-5954|3
        (442 letters)

gi|138117|sp|P13849|VG8_BPPH2 MAJOR HEAD PROTEIN (LATE PROTEIN ...     309  6e-84
gi|138118|sp|P07531|VG8_BPPZA MAJOR HEAD PROTEIN (LATE PROTEIN ...     305  7e-83

Query= sid|110160|lan|182ORF005 Phage 182 ORF|12651-13700|3
        (349 letters)

gi|137932|sp|P15132|VG13_BPPH2 MORPHOGENESIS PROTEIN 1 (LATE PR...      52  2e-06
gi|137933|sp|P07538|VG13_BPPZA MORPHOGENESIS PROTEIN 1 (LATE PR...      47  6e-05

Query= sid|110161|lan|182ORF006 Phage 182 ORF|14995-16026|1
        (343 letters)

gi|137945|sp|P07541|VG16_BPPZA ENCAPSIDATION PROTEIN (LATE PROT...     402  e-112
gi|137944|sp|P11014|VG16_BPPH2 ENCAPSIDATION PROTEIN (LATE PROT...     402  e-112

Query= sid|110162|lan|182ORF007 Phage 182 ORF|7795-8775|1
        (326 letters)

gi|137915|sp|P07535|VG10_BPPZA UPPER COLLAR PROTEIN (CONNECTOR ...     256  3e-68
gi|137914|sp|P04332|VG10_BPPH2 UPPER COLLAR PROTEIN (CONNECTOR ...     256  5e-68

Query= sid|110163|lan|182ORF008 Phage 182 ORF|14105-14983|2
        (292 letters)

gi|462559|sp|P34020|LYC_CLOAB AUTOLYTIC LYSOZYME (1,4-BETA-N-AC...      75  2e-13
gi|126652|sp|P25310|LYCM_STRGL LYSOZYME M1 PRECURSOR (1,4-BETA-...      60  5e-09
gi|127789|sp|P19386|LYCA_BPCP9 LYSOZYME (ENDOLYSIN) (MURAMIDASE...      60  5e-09
gi|127787|sp|P15057|LYCA_BPCP1 LYSOZYME (ENDOLYSIN) (MURAMIDASE...      57  4e-08
gi|126597|sp|P00721|LYCH_CHASP N,O-DIACETYLMURAMIDASE (LYSOZYME...      57  4e-08
gi|127788|sp|P19385|LYCA_BPCP7 LYSOZYME (ENDOLYSIN) (MURAMIDASE...      57  5e-08
gi|3025168|sp|P76421|YEGX_ECOLI HYPOTHETICAL 32.0 KD PROTEIN IN...      53  5e-07

Query= sid|110164|lan|182ORF009 Phage 182 ORF|8765-9601|2
        (278 letters)

gi|137921|sp|P04333|VG11_BPPH2 LOWER COLLAR PROTEIN (LATE PROTE...     171  1e-42
gi|131782|sp|P12753|RA50_YEAST DNA REPAIR PROTEIN RAD50 (153 KD...      48  2e-05
gi|1176490|sp|P40889|YJW5_YEAST HYPOTHETICAL 197.6 KD PROTEIN I...      45  1e-04
gi|731903|sp|P40434|YIR7_YEAST HYPOTHETICAL 197.5 KD PROTEIN IN...      45  1e-04
gi|730275|sp|P39793|PBPA_BACSU PENICILLIN-BINDING PROTEINS 1A/1...      45  2e-04
gi|1168610|sp|P41696|AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PRO...      44  3e-04
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gi|731587|sp|P38900|YH19_YEAST HYPOTHETICAL 70.1 KD PROTEIN IN ...    44  3e-04

Query= sid|110165|lan|182ORF010 Phage 182 ORF|1310-2155|2
        (281 letters)

gi|135604|sp|P06812|TERM_BPNF DNA TERMINAL PROTEIN                    69  8e-12

Query= sid|110166|lan|182ORF011 Phage 182 ORF|9607-10158|1
        (183 letters)

gi|137928|sp|P07537|VG12_BPPZA PRE-NECK APPENDAGE PROTEIN (LATE...    51  2e-06
gi|137927|sp|P20345|VG12_BPPH2 PRE-NECK APPENDAGE PROTEIN (LATE...    50  3e-06

Query= sid|110169|lan|182ORF014 Phage 182 ORF|13716-14108|3
        (130 letters)

gi|137936|sp|P11188|VG14_BPPH2 LYSIS PROTEIN (LATE PROTEIN GP14)      97  2e-20
gi|137938|sp|P07539|VG14_BPPZA LYSIS PROTEIN (LATE PROTEIN GP14)      96  2e-20

Query= sid|110170|lan|182ORF015 Phage 182 ORF|854-1225|2
        (123 letters)

gi|138072|sp|P06953|VG5A_BPPZA EARLY PROTEIN GP5A                     69  2e-12

Query= sid|110174|lan|182ORF019 Phage 182 ORF|4323-4613|3
        (96 letters)

gi|138111|sp|P13848|VG7_BPPH2 HEAD MORPHOGENESIS PROTEIN (LATE ...    57  9e-09
gi|138112|sp|P07533|VG7_BPPZA HEAD MORPHOGENESIS PROTEIN (LATE ...    54  4e-08

Query= sid|110180|lan|182ORF025 Phage 182 ORF|548-814|2
        (88 letters)

gi|138099|sp|P06955|VG6_BPPZA EARLY PROTEIN GP6                       55  2e-08
gi|138098|sp|P03685|VG6_BPPH2 EARLY PROTEIN GP6                       54  5e-08
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BLASTP 2.0.8 [Jan-05-1999]

Query= sid|110156|lan|182ORF001 Phage 182 ORF|5966-7780|2
        (604 letters)

>gi|138124|sp|P07534|VG9_BPPZA TAIL PROTEIN (LATE PROTEIN GP9)
           >gi|75849|pir||WMBP9Z gene 9 protein - phage PZA
           >gi|216058 (M11813) tail protein [Bacteriophage PZA]
           Length = 599

 Score =  384 bits (975), Expect = e-105
 Identities = 231/610 (37%), Positives = 344/610 (55%), Gaps = 36/610 (5%)

Query: 6   TNVKLLANVPFDNTYTHTRWFKTQQEQESYFNSFPVLNENRDCSYQRDTQLGGVFRVDKH 65
            TNV++LA+VPF N Y +TRWF +   Q ++FNS   + E    ++Q   +      V
Sbjct: 9   TNVRILADVPFSNDYKNTRWFTSSSNQYNWFNSKTRVYEMSKVTFQGFRENKSYISVSLR 68

Query: 66  KDALYACNYLIFKNEETYPSKWQYAFVTDIEYKNDNTSFVTFEIDVLQTYRFDIGIRESF 125
             D LY  +Y++F+N + Y +KW YAFVT++EYKN  T++V FEIDVLQT+ F+I  +ESF
Sbjct: 69  LDLLYNASYIMFQNAD-YGNKWFYAFVTELEYKNVGTTYVHFEIDVLQTWMFNIKFQESF 127

Query: 126 IAKEHPQLYYSNGIPFINTIEESLDYGREYTTTNVTTFHPNDGVNFLVILTSEAM--PVG 183
            I +EH +L+  +G P INTI+E L+YG EY   +V    P D + FLV+++   M   G
Sbjct: 128 IVREHVKLWNDDGTPTINTIDEGLNYGSEYDIVSVENHRPYDDMMFLVVISKSIMHGTAG 187

Query: 184 DKEDKSG---GSIVGGPSPFSYYLLPINSSGEVYKPN-GAGNANFGEYMAFLT---TKEP 236
            + E +      S+ G P P  YY+ P    G+V K   G  NAN     + LT   +++
Sbjct: 188 EAESRLNDINASLNGMPQPLCYYIHPFYKDGKVPKTFIGDNNANLSPIVNMLTNIFSQKS 247

Query: 237 FLNKIVGMYVTSYTGIPFIVDHANKTVRYNAGGSYKIMLPTYASDPTGTMKTFAFFCVKE 296
            +N IV MYVT Y G+      + +K ++ +        +  +  A D  G + T     VK+
Sbjct: 248 AVNNIVNMYVTDYIGLKLDYKNGDKELKLDKDMFEQAGI---ADDKHGNVDTIF---VKK 301

Query: 297 ARTFVPKRIDLVGNVYNYFREAFPFNVKESKLFMYPYCLIEITDTKGHVMTLRPEYLTGG 356
                +     ID  G+ +  F +·     +ESKL MYPYC+ E+TD KG+ M L+ EY+
Sbjct: 302 IPDYETLEID-TGDKWGGFTKD-----QESKLMMYPYCVTEVTDFKGNHMNLKTEYIDNN 355

Query: 357 KLSVYVKGSLGISNKVMIEPIDYDVSNSTI----ITNLSDKMLIDNDPNDVGVKSDYASA 412
            KL + V+GSLG+SNKV     DY+   S        +T   D  LI+N+PND+ + +DY SA
Sbjct: 356 KLKIQVRGSLGVSNKVAYSIQDYNAGGSLSGGDRLTASLDTSLINNNPNDIAIINDYLSA 415

Query: 413 FMQGNKNSLIAQEQNIRNTFRHGMGNSAMSTGGAIFSALASNNPFVGLTNIMGAGQQVNN 472
            ++QGNKNSL  Q+ +I       GM    +S G    ++    +PF    +++ G       N
Sbjct: 416 YLQGNKNSLENQKSSILFNGIVGMLGGGVSAG----ASAVGRSPFGLASSVTGMTSTAGN 471

Query: 473 YVSEKENGLNLLAGKVADIENIPDNVTQLGSNLSFTTGN-FQNYYQLRFKQIKYEYATRL 531
            V +     +  L  K ADI NIP  +T++G N +F  GN ++  Y ++ KQ+K EY     L
Sbjct: 472 AVLD----MQALQAKQADIANIPPQLTKMGGNTAFDYGNGYRGVYVIK-KQLKAEYRRSL 526

Query: 532 DRYFSMYGTKSNRVATPNLQTRKAWNFIKLKEPNIVGTMSNDVLTRVKQIFSAGVTLWHT 591
              +F  YG K NRV  PNL+TRKA+N+I+ K+  I G ++N+ L  ++ IF  G+TLWHT
Sbjct: 527 SSFFHKYGYKINRVKKPNLRTRKAYNYIQTKDCFISGDINNNDLQEIRTIFDNGITLWHT 586

Query: 592 NDVLNYNQDN 601
            +D+ NY+ +N
Sbjct: 587 DDIGNYSVEN 596


Query= sid|110157|lan|182ORF002 Phage 182 ORF|2152-3873|1
        (573 letters)

>gi|118848|sp|P19894|DPOL_BPM2 DNA POLYMERASE >gi|76896|pir||JQ0161
           DNA-directed DNA polymerase (EC 2.7.7.7) - phage M2
           >gi|215509 (M33144) DNA polymerase [Bacteriophage M2]
           Length = 572

 Score =  665 bits (1697), Expect = 0.0
 Identities = 327/589 (55%), Positives = 420/589 (70%), Gaps = 38/589 (6%)

Query: 3   KKYTGDFETTTDLNDCRVWSWGVCDIDNVDNMTFGLEIDSFFEWCKMQGSTDIYFHNEKF 62
            K ++ DFETTT L+DCRVW++G  +I N+DN   G  +D F +W  M+   D+YFHN KF
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Sbjct: 4   KMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWV-MEIQADLYFHNLKF 62

Query: 63  DGEFMLSWLFKNGFKWCKEAKEDRTFSTLISNMGQWYALEICWEVNYXXXXXXXXXXXXX 122
            DG F+++WL ++GFKW  E   + T++T+IS MGQWY ++IC+
Sbjct: 63  DGAFIVNWLEQHGFKWSNEGLPN-TYNTIISKMGQWYMIDICFGYK---------GKRKL 112

Query: 123 XXIIYDSLKKYPFPVKQIAEAFNFPIKKGEIDYTKERPIGYKPTKDEWEYLKNDIQIMAM 182
              +IYDSLKK PFPVK+IA+ F  P+ KG+IDY  ERP+G++ T +E+EY+KNDI+I+A
Sbjct: 113 HTVIYDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIAR 172

Query: 183 ALKIQFDQGLTRMTRGSDALGDYKDWLKATHGKSTFKQWFPILSLGFDKDLRKAYKGGFT 242
            AL IQF QGL RMT GSD+L  +KD L        F +  FP LSL  DK++RKAY+GGFT
Sbjct: 173 ALDIQFKQGLDRMTAGSDSLKGFKDILST----KKFNKVFPKLSLPMDKEIRKAYRGGFT 228

Query: 243 WVNKVFQGKEIGDGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKPNNDYPLYIQNIKVR 302
            W+N  ++ KEIG+G+VFDVNSLYPSQMY RPLPYG P+ ++G+Y+ +  YPLYIQ I+
Sbjct: 229 WLNDKYKEKEIGEGMVFDVNSLYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFE 288

Query: 303 FRLKEGYIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLELFFEHYDILEIH 362
            F LKEGYIPTIQ+K++  F  NEYL++S    GV E ++L LTNVDLEL  EHY++  +
Sbjct: 289 FELKEGYIPTIQIKKNPFFKGNEYLKNS----GV-EPVELYLTNVDLELIQEHYELYNVE 343

Query: 363 YTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYM 422
            Y  G+ F+    +FK +IDKW  VK   EGA+K  AK MLNSLYGKF +NPD+TGKVPY+
Sbjct: 344 YIDGFKFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKLMLNSLYGKFASNPDVTGKVPYL 403

Query: 423 GEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQKCFDRIIYCDTDSIHLVGTE 482
             +DG +   +G+EE +DPVY P+  F+TAW R+TTIT AQ C+DRIIYCDTDSIHL GTE
Sbjct: 404 KDDGSLGFRVGDEEYKDPVYTPMGVFITAWARFTTITAAQACYDRIIYCDTDSIHLTGTE 463

Query: 483 VPEAIDHLVDPKKLGYWGHESTFQRAKFIRQKT-----YVEEIDGEL------------ 524
            VPE I  +VDPKKLGYW HESTF+RAK++RQKT     YV+E+DG+L
Sbjct: 464 VPEIIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATTTKF 523

Query: 525 NVKCAGMPDRIKEIVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK 573
            +VKCAGM D IK+ VTFDNF VGFSS GK  P +  GGVVLVD++FTIK
Sbjct: 524 SVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQVNGGVVLVDSVFTIK 572


Query= sid|110159|lan|182ORF004 Phage 182 ORF|4626-5954|3
         (442 letters)

>gi|138117|sp|P13849|VG8_BPPH2 MAJOR HEAD PROTEIN (LATE PROTEIN GP8)
            >gi|75845|pir||WMBP89 gene 8 protein - phage phi-29
            >gi|215325 (M14782) major head protein [Bacteriophage
            phi-29] >gi|225362|prf||1301270B gene 8 [Bacillus sp.]
            Length = 448

 Score =  309 bits (783), Expect = 2e-83
 Identities = 176/440 (40%), Positives = 250/440 (56%), Gaps = 27/440 (6%)

Query: 4   KITEQDVLRATNVETPVQLMTAIYNSSSSLFQANVPMPNADNIEAVGAGITRLDVVKNEF 63
            +IT  DV  +  +      ++ AI NS    F++ VP+  A+N+  VGAGI      V+N+F
Sbjct: 2   RITFNDVKTSLGITESYDIVNAIRNSQGDNFKSYVPLATANNVAEVGAGILINQTVQNDF 61

Query: 64  ISTLVDRIGKVVIRYKSWRNPLKMFKKGNMPLGRTIEEIFVDIAQEHKFNPDESVTGVFK 123
            I++LVDRIG VVIR  S  NPLK FKKG +PLGRTIEEI+ DI +E +++ +E+   VF+
Sbjct: 62  ITSLVDRIGLVVIRQVSLNNPLKKFKKGQIPLGRTIEEIYTDITKEKQYDAEEAEQKVFE 121

Query: 124 QEVPDVKTLFHEINREGYYKQTIQEAWLEKAFTSWDNFNSFVAGVMNALYTGDEVSEFEY 183
            +E+P+VKTLFHE NR+G+Y QTIQ+  L+ AF SW NF SFV+ ++NA+Y   EV E+EY
Sbjct: 122 REMPNVKTLFHERNRQGFYHQTIQDDSLKTAFVSWGNFESFVSSIINAIYNSAEVDEYEY 181

Query: 184 TKLLIANYQEKELFKEIEIGEITESNA--KEFIRKIKSTSNKLEFM--SSAYNAQGVKTS 239
             KLL+ NY  K LF  ++I E T S     EF++K+++T+ KL      S  +N+  V+T
Sbjct: 182 MKLLVDNYYSKGLFTTVKIDEPTSSTGALTEFVKKMRATARKLTLPQGSRDWNSMAVRTR 241

Query: 240 TSKSDQYXXXXXXXXXXXXXXXXXXXFNMSKTDFVGHKIVIDEFPKKEGEESSNIVAVIV 299
            +   D +                    FNM++TDF+G+  VID F       S+ + AV+V
Sbjct: 242 SYMEDLHLIIDADLEAELDVDVLAKAFNMNRTDFLGNVTVIDGF------ASTGLEAVLV 295

Query: 300 DSEWFMIYDKLYKTTSLYNPEGLYWNYWLHHHQLYSTSQFGNAVAFVKSATKPVTKVAFA 359
            D +WFM+YD L+K  ++ NP GLYWNY+ H  Q  S S+F NAVAFV         VT+V  +
Sbjct: 296 DKDWFMVYDNLHKMETVRNPRGLYWNYYYHVWQTLSVSRFANAVAFVSGDVPAVTQVIVS 355

Query: 360 SATTSVVKGSSKDIALTFTPVEATNQQGEVVSSAPALVKATVKQTAGKATAVTVEGLEVG 419
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               +V +G  +        V ATN +   V           V   G +T   +    G
Sbjct: 356 PNIAAVKQGGQQQFT---AYVRATNAKDHKV----------VWSVEGGSTGTAI----TG 398

Query: 420 QSLVTFTAIGGQQATVLVTV 439
              L++ +     Q TV  TV
Sbjct: 399 DGLLSVSGNEDNQLTVKATV 418


Query= sid|110160|lan|182ORF005 Phage 182 ORF|12651-13700|3
         (349 letters)

>gi|137932|sp|P15132|VG13_BPPH2 MORPHOGENESIS PROTEIN 1 (LATE
           PROTEIN GP13) >gi|75858|pir||WMBP23 gene 13 protein -
           phage phi-29 >gi|215331 (M14782) morphogenesis protein
           [Bacteriophage phi-29] >gi|225368|prf||1301270H gene 13
           [Bacteriophage phi-29]
           Length = 365

 Score = 51.5 bits (121), Expect = 8e-06
 Identities = 44/166 (26%), Positives = 70/166 (41%), Gaps = 14/166 (8%)

Query: 6    NEQIARGQTIAKILSKYGYNKNSQVGVVANLHWESA---GLNPNSNEXXXXXXXXX-QWT 61
             +E     Q I    LS  G+ K +  G++ N+  ES     GL  N +E          QWT
Sbjct: 12   SEMKVNAQYILNYLSSNGWTKQAICGMLGNMQSESTINPGLWQNLDEGNTSLGFGLVQWT 71

Query: 62   PKSNLYRQAQICGLSNAKAETLEGQAEIIAQGDKTGQWMDNTPVSSAGYTNPQTLSAFKQ 121
             P SN     A   GL       ++        II + +    QW++     ++     Y           K
Sbjct: 72   PASNYINWANSQGLPYKDMDS--ELKRIIWEVNNNAQWINLRDMTFKEY--------IKS 121

Query: 122  SANIDVATINFMCHWERPGKLHIEERLDLAQAYSKHIDGSGGGGVK 167
             +          + F+   +ERP     +   ER D A+ + K++ G GGGG++
Sbjct: 122  TKTPRELAMIFLASYERPANPNQPERGDQAEYWYKNLSGGGGGGLQ 167


Query= sid|110161|lan|182ORF006 Phage 182 ORF|14995-16026|1
         (343 letters)

>gi|137945|sp|P07541|VG16_BPPZA ENCAPSIDATION PROTEIN (LATE PROTEIN
           GP16) >gi|75861|pir||WMBP16 gene 16 protein - phage PZA
           >gi|216065 (M11813) morphogenesis protein C
           [Bacteriophage PZA]
           Length = 332

 Score =  402 bits (1023), Expect = e-111
 Identities = 186/332 (56%), Positives = 244/332 (73%), Gaps = 2/332 (0%)

Query: 11   EKNLYYNPNNALGFNCLMLFVIGARGIGKTYGYKKFVVNRFIKHGEQFIYLRRFKTELKK 70
             +K+L+YNP     L ++ ++ FVIGARGIGK+Y   K + +NRFIK+GEQFIY+RR+K EL K
Sbjct: 2    DKSLFYNPQKMLSYDRILNFVIGARGIGKSYAMKVYPINRFIKYGEQFIYVRRYKPELAK 61

Query: 71   IPQFFKTMAKEFPDHKLEVKGKEFYCDDKLMGWAVPLSTWGIEKSNEYPEVRTILFDEFL 130
             +  +F  +A+EFPDH+L VKG+  FY D KL GWA+PLS W  EKSN YP V TI+FDEF+
Sbjct: 62   VSNYFNDVAQEFPDHELVVKGRRFYIDGKLAGWAIPLSVWQSEKSNAYPNVSTIVFDEFI 121

Query: 131  IEKSKITYLPNEAEALLNMMETVFRRRTNTRCVMLSNATSVVNPYFLYFNLQPDLNKRFN 190
              EK     Y+PNE  ALLN+M+TVFR R    RC+ LSNA SVVNPYFL+FNL PD+NKRFN
Sbjct: 122  REKDNSNYIPNEVSALLNLMDTVFRNRERVRCICLSNAVSVVNPYFLFFNLVPDVNKRFN 181

Query: 191  LYQDRGILIELCDSKDFAEVKRETPFGRLIRGTEYEDFSINNEFVNDSDTFIEKRSKNSS 250
             +Y D    LIE+ DS DF+   +R+T FGRLI GTEY + S++N+F+ DS   FIEKRSK+S
Sbjct: 182  VYDD--ALIEIPDSLDFSSERRKTRFGRLIDGTEYGEMSLDNQFIGDSHVFIEKRSKDSK 239

Query: 251  FLCAIAFEGKIFGYWIDAETGCVYVSYDYQPNTNHFYAMTTKDHEENRLLMKNWRNNYYL 310
             F+ +I + G    G W+D    G +YV    + P+T + Y +TT D  EN +L+ N++NNY+L
Sbjct: 240  FVFSIVYNGFTLGVWVDVNQGLMYVDTAHDPSTKNVYTLTTDDLNENMMLITNYKNNYHL 299

Query: 311  STVAKAFKNSYLRFDNIVIKNLHYDLFNKMKI 342
              +A AF N YLRFDN VI+N+  Y+LF KM+I
Sbjct: 300  RKLASAFMNGYLRFDNQVIRNIAYELFRKMRI 331


Query= sid|110162|lan|182ORF007 Phage 182 ORF|7795-8775|1
         (326 letters)

>gi|1429239|emb|CAA67658| (X99260) upper collar protein
           [Bacteriophage B103]
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          Length = 308

 Score =  271 bits (685), Expect = 6e-72
 Identities = 131/275 (47%), Positives = 187/275 (67%), Gaps = 5/275 (1%)

Query: 36  YYEHYRRQLTLLTFQLFEWENLPKSIDPRYLEIALHTNGYLGFFKDPTLGFMVCAGAEDG 95
            +Y HY + L  L +QLFEWE LP S+DP YLE ++H  GY+GF+KDP +G++ C GA  G
Sbjct: 22  WYYHYYQYLCSLAYQLFEWERLPPSVDPSYLEKSIHQFGYVGFYKDPRIGYIACQGALSG 81

Query: 96  QIDHYHNPIFFTANEAMYHKRYPVLRYDDDDDKSKCIMLYNNDLKVPTLPSLHRFALDMA 155
             +DHY+ P  F A+     Y    + +  Y D  +K+  + +YNNDLK  TLP+L  FA D+A
Sbjct: 82  TVDHYNLPDRFHASSVGYQNTFKLYNYSDMKEKNMGVAIYNNDLKCSTLPALEMFAQDLA 141

Query: 156 DINQISRVNRRAQKTPVIIQTDEKKYFSLLQAYNQIDENNQAVFVDKDMEFDESFNVWQT 215
            ++ +I  VN+ AQKTPV+I  ++     SL   YNQ + N    +FV + ++ D +  V++T
Sbjct: 142 ELKEIIAVNQNAQKTPVLIAANDNNQLSLKNIYNQYEGNAPVIFVHESLDLD-NLKVFKT 200

Query: 216 NAPYVVDKLRSELNEVWNEVLTFLGINNANVDKTARVQTSEVLSNNEQIESSGNILLKSR 275
            +APYVVDKL ++ N VWNEV+T+LGI NAN++K  R+ TSEV SN+EQIESSGNI LK+R
Sbjct: 201 DAPYVVDKLNAQKNAVWNEVMTYLGIKNANLEKKERMVTSEVDSNDEQIESSGNIYLKAR 260

Query: 276 KEFCDRVNRVFGDELDGKIDVKFRTDAVRQLQLAA 310
            +E C++++ ++G  L      VKFR D V Q++L A
Sbjct: 261 QEACNKISELYGLNL----KVKFRYDIVEQMRLNA 291


Query= sid|110163|lan|182ORF008 Phage 182 ORF|14105-14983|2
        (292 letters)

>gi|4210750|emb|CAA10710| (AJ132604) LysL protein [Lactococcus
          lactis]
          Length = 235

 Score =  139 bits (347), Expect = 2e-32
 Identities = 85/210 (40%), Positives = 114/210 (53%), Gaps = 14/210 (6%)

Query: 2   MNGIDISSYQTGIDLSKVPCDFVNIKATGGTGYVNPDCDRAFQQALSLGKKIGVYHFAHE 61
            MNGIDISSYQ  ++    VP DFV IKAT GT Y+NP  +     Q +    K +G YHFA
Sbjct: 1   MNGIDISSYQAELNAGIVPSDFVIIKATEGTNYINPTWEEQAGQVIQTNKLLGFYHFAS- 59

Query: 62  RGLEGTPQQEAQFFLDNIKGYIGKAVLILDFEGS--NQKDVNWAKAFLDYVYNKTGVKAW 119
               G P  EA FF+  +K YIGKAVL+LDFE     N      A+ FL+ V  KTG+
Sbjct: 60  ---VGNPIAEADFFISVVKNYIGKAVLVLDFEAGAINAWGNVGARQFLNRVKEKTGINPM 116

Query: 120 FYTYTANLNTTDFSSIAKGDYGLWVAEYGSNQPQGYSQPAPPKTNN-----FPIVACFQF 174
            Y  +      ++S+I+  +  LWVA+Y S  P GY    + P T+      +  A  Q+
Sbjct: 117 IYMSSDVTRQFNWSTISSTN-PLWVAQYASMNPTGYQ--SEPWTDGKGYGAWSSAAIHQY 173

Query: 175 TSKGRLPGYNGNLDLNVFYGDGNTWDLYVG 204
            +S G L  ++GNLD+N+ Y + N W    G
Sbjct: 174 SSAGSLSNWSGNLDINLAYINANQWKSLAG 203



Query= sid|110164|lan|182ORF009 Phage 182 ORF|8765-9601|2
        (278 letters)

>gi|1429240|emb|CAA67659| (X99260) lower collar protein
          [Bacteriophage B103]
          Length = 293

 Score =  180 bits (451), Expect = 1e-44
 Identities = 115/296 (38%), Positives = 161/296 (53%), Gaps = 33/296 (11%)

Query: 3   LKRYIESFTYYQPELSRKERIEVGRKQLFDFDYPFYDETKRAEFETKFINHFYLREIGSE 62
            L  YIE ++ Y+  LS  E+IE GR +LFDF YP +DE+ R  FET FI +FY+REIG E
Sbjct: 8   LSTYIEMWSQYETGLSMAEKIEKGRPKLFDFQYPIFDESYRKVFETHFIRNFYMREIGFE 67

Query: 63  TMGSFKFNLDEYLNLNMPYWNKMFLSNLEEF-PIFDDMDYTIDEKQKLLNEIDTNIKANR 121
            T G FKFNL+ +L +NMPY+NK+F S L ++ P+ +      T    K+       DT   NR
Sbjct: 68  TEGLFKFNLETWLIINMPYFNKLFESELIKYDPLENTRLNTTGNKKN-----DTERNDNR 122

Query: 122 D-------ESKNQTKQVDQTDNRNKNTRDTGTT-----DSFSRNTYTDTPQKDLRIASNG 169
            D       + K+ TK  D+T+     +  D  TT     D+F+R  +D P    L + +N
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```
Sbjct: 123 DTTGSMKADGKSNTKTSDKTNATGSSKEDGKTTGSVTDDNFNRKIDSDQPDSRLNLTTN- 181

Query: 170 DGTGVINYATNITEDLSKETTSSTGVETNNDKTNQNTRSNAS----------EKETKNTD 219
           DG G + YA+ I E+ +     ++TG  TNN  ++  + S  S          T N
Sbjct: 182 DGQGTLEYASAIEENNTNNKRNTTG--TNNVTSSAESESTGSGTSDTVTTDNANTTTNDK 239

Query: 220 INKDQNQTKDTITRYKGKKGNTDYADLLEKYRRSVLRIEKMIFREMNKEGLFLLVY 275
           +N   N  +D I    GK G    YA L++ YR ++LRIEK IF EM +   LF+LVY
Sbjct: 240 LNSQINNVEDYIESKIGKSGTQSYASLVQDYRAALLRIEKRIFDEMQE--LFMLVY 293


Query= sid|110165|lan|182ORF010 Phage 182 ORF|1310-2155|2
        (281 letters)

>gi|135604|sp|P06812|TERM_BPNF DNA TERMINAL PROTEIN
           >gi|75815|pir||ERBPNP terminal protein - phage NF
           >gi|579177|emb|CAA68440| (Y00363) gene E product (AA
           1-267) [Bacteriophage NF]
           Length = 266

 Score = 74.9 bits (181), Expect = 6e-13
 Identities = 73/275 (26%), Positives = 129/275 (46%), Gaps = 37/275 (13%)

Query: 3   VRISKNDRAKLEKIYGKSNKARKKYNRLRQK-GVE---ERQLPTVPTSKKRLIDYVKSTN 58
           +RI+ ND+A   K+  K+ KA  K +R ++K G++    E +LP + + +
Sbjct: 7   IRITNNDKALYAKLV-KNTKA--KISRTKKKYGIDLSNEIELPPLESFQ----------- 52

Query: 59  MSRSDFNKMLDELVDFAQPYNENYIFEINKRNVAISRAQIKEAQIKTEQAQKAKEEHYKE 118
            +R +FNK    +   F    N+NY F  NK  +  S+A+I E    T++AQ+  +E  +E
Sbjct: 53  -TREEFNKWKQKQESFTNRANQNYQFVKNKYGIVASKAKINEIAKNTKEAQRIVDEQREE 111

Query: 119 L--------NKVEVKKPTENTIVTPTILTELGADLPFQAIPDFNIDAFTSPEGVQSYLEN 170
           +          K +          I++P+ +T  G   P     DFN D   S  +++  E
Sbjct: 112 IEDKPFISGGKQQGTVGQRMQILSPSQVT--GISRP----SDFNFDDVRSYARLRTLEEG 165

Query: 171 IG-KQDEQYFDERDQLYYDNFRQAMFTIFNSD--ADDIVRLLDSMGLDLFMKTYVSNFLD 227
           +  K    Y+D R     + NF + +   FNSD  +D++V  L  +  D F + Y+  F +
Sbjct: 166 MAEKASPDYYDRRMTQMHQNFIEIVEKSFNSDWLSDELVERLKKIPPDDFFELYLM-FDE 224

Query: 228 MNLDYIYDEAEVQQKKEQVYSKIAKVIESETGGEV 262
           ++ +Y    E E  +  E + +KI    ++    G+V
Sbjct: 225 ISFEYFDSEGEDVEASEAMLNKIHSYLDRYERGDV 259




Query= sid|110166|lan|182ORF011 Phage 182 ORF|9607-10158|1
        (183 letters)

>gi|1429241|emb|CAA67660| (X99260) pre-neck appendage protein
           [Bacteriophage B103]
           Length = 860

 Score = 50.8 bits (119), Expect = 6e-06
 Identities = 29/105 (27%), Positives = 56/105 (52%), Gaps = 6/105 (5%)

Query: 8   KRFDGLPAVFKERFSKYPHTEYRYELLLDEEVSALIAYLNEVGALVNDMSGYLNYFIEHF 67
           +RF+ L   +  + + +Y  T +    + L E+++ +I YLN++G L ND+      N  +E
Sbjct: 7   RRFEKLGEMMVQVYERYLPTAFDESMTLLEKMNKIIEYLNQIGRLTNDVVEEWNKVMEWI 66

Query: 68  V-EKLEEITNDTLKKWLSDGTLENLINDTVFANYIKEIKRLQILV 111
           + + LE+   +TL+KW  +G   +L+          I E+K+  + V
Sbjct: 67  LNDGLEDYVKETLEKWYEEGKFADLV------IQVIDELKQFGVSV 106


Query= sid|110169|lan|182ORF014 Phage 182 ORF|13716-14108|3
        (130 letters)

>gi|137936|sp|P11188|VG14_BPPH2 LYSIS PROTEIN (LATE PROTEIN GP14)
           >gi|75860|pir||WMBP29 gene 14 protein - phage phi-29
           >gi|15678|emb|CAA28631| (X04962) gene 14 product (AA
```

```
          1-393) [Bacteriophage phi-29] >gi|225369|prf||1301270J
          gene 14 [Bacteriophage phi-29]
          Length = 131

 Score = 96.7 bits (237), Expect = 6e-20
 Identities = 53/131 (40%), Positives = 81/131 (61%), Gaps = 3/131 (2%)

Query: 1   MIEYITQWL-ADDNHLVYGLIIWLMVAMIIDFVLGFTIAKFNKEIDFSSFKAKAGIIVKV 59
            MI ++  +L  D+  L+Y L  +LMV M++D VLG   AK N  I FSSFK K G+++KV
Sbjct: 3   MIAWMQHFLETDETKLIYWLT-FLMVCMVVDTVLGVLFAKLNPNIKFSSFKIKTGVLIKV 61

Query: 60  AEMVLVVYFIPVAVKFGAVGITMYITMLVGLILSEIYSILGHISDIDDDNNWTDYVKKFL 119
            +EM+L +   IP AV F A G+ +   T+    L +SEIYSI GH+  +DD +++ + ++ F
Sbjct: 62  SEMILALLAIPFAVPFPA-GLPLLYTVYTALCVSEIYSIFGHLRLVDDKSDFLEILENFF 120

Query: 120 DGTLNRKDDIK 130
             T  +  + K
Sbjct: 121 KRTSGKNKEEK 131


Query= sid|110170|lan|182ORF015 Phage 182 ORF|854-1225|2
        (123 letters)

>gi|15670|emb|CAA24483| (V01155) reading frame 10 (may be gene 4)
          [Bacteriophage phi-29]
          Length = 124

 Score = 69.9 bits (168), Expect = 6e-12
 Identities = 39/119 (32%), Positives = 64/119 (53%), Gaps = 3/119 (2%)

Query: 3   IVKSTFDTQTPEGMLQVFNATNGASIPLRNAI-GEVLELKDILVYSDEVSGFGGAEPSQA 61
            IVK+TFDT+T EG +++FNA  G      +N   G ++E   I  Y       +G A+  +
Sbjct: 6   IVKATFDTETLEGQIKIFNAQTGGGQSFKNLPDGTIIEANAIAQYKQVSDTYGDAK--EE 63

Query: 62  ELVAFFTEDGKTYAGVSAVATKSAKNLIDMMTANPDIKPKISFVEGKSNGGQKFVNLQV 120
             +   F  DG  Y+ +S     ++A +LID++T +     K+  V+G S+ G  F +LQ+
Sbjct: 64  TVTTIFAADGSLYSAISKTVAEAASDLIDLVTRHKLETFKVKVVQGTSSKGNVFFSLQL 122


Query= sid|110174|lan|182ORF019 Phage 182 ORF|4323-4613|3
        (96 letters)

>gi|1429235|emb|CAA67654| (X99260) head morphogenesis protein
          [Bacteriophage B103]
          Length = 101

 Score = 60.9 bits (145), Expect = 1e-09
 Identities = 34/96 (35%), Positives = 53/96 (54%), Gaps = 5/96 (5%)

Query: 1   MEIKEHESILNGILESVTDGEARSKIVEHLEALREDYGATTEALTSANSTLEKLKKDNEA 60
            ME   HE ILN + +     +   R+++    L+ LR DYG+       +   S   EKL+ +N
Sbjct: 3   MERDSHEEILNKLNDPELEHSERTEL---LQQLRADYGSVLSEFSELTSATEKLRAENSD 59

Query: 61  LVISNSKLFRERAIVEPAEN--NEPETDQNITLDDL 94
            L++SNSKLFR+  I +  E   + E  + IT++DL
Sbjct: 60  LIVSNSKLFRQVGITKEKEEEIKQEELSETITIEDL 95


Query= sid|110180|lan|182ORF025 Phage 182 ORF|548-814|2
        (88 letters)

>gi|138099|sp|P06955|VG6_BPPZA EARLY PROTEIN GP6
          >gi|75841|pir||ERBP6Z gene 6 protein - phage PZA
          >gi|216047 (M11813) gene 6 product [Bacteriophage PZA]
          >gi|224746|prf||1112171K ORF 6 [Bacteriophage PZA]
          Length = 96

 Score = 55.0 bits (130), Expect = 8e-08
 Identities = 28/79 (35%), Positives = 45/79 (56%)
```

```
Query: 4  KLMQRNVTSTKVEFSEVIVQDGAPTIVPCEPVVLTGKLSEEKALSAIKRKNPDKNVVVTN 63
          K+MQR +T T V  +++++ DG    +            G LS E+A    +KRK    + V V +
Sbjct: 3  KMMQREITKTTVNVAKMVMVDGEVQVEQLPSETFVGNLSMEQAQWRMKRKYKGEPVQVVS 62

Query: 64 VSHETALYTMPVDKFIELA 82
           V    T +Y +PV+KF+E+A
Sbjct: 63 VEPNTEVYELPVEKFLEVA 81
```

Table 26

Secondary structure prediction for ORF 182ORF008

```
1    MMNGIDISSY QTGIDLSKVP CDFVNIKATG GTGYVNPDCD RAFQQALSLG KKIGVYHFAH
     CCCCCCCCCC CCCCCCCCCC CCEEEEEECC CCCCCCCCCC HHHHHHHHHC CCCCEEEEEE
61   ERGLEGTPQQ EAQFFLDNIK GYIGKAVLIL DFEGSNQKDV NWAKAFLDYV YNKTGVKAWF
     CCCCCCCCHH HHHHHHHHHC CCCCEEEEEE CCCCCCCHHH HHHHHHHHHH HCCCCCEEEE
121  YTYTANLNTT DFSSIAKGDY GLWVAEYGSN QPQGYSQPAP PKTNNFPIVA CFQFTSKGRL
     EEECCCCCCC CCCEECCCCC CEEEEECCCC CCCCCCCCCC CCCCCCCEEE EEEECCCCCC
181  PGYNGNLDLN VFYGDGNTWD LYVGKKQDQI VPPENKIFDA TSDEFIFTLT TGSTSVFYFD
     CCCCCCCCEE EEECCCCCCE EEECCCCCCC CCCCCCCCCC CCCEEEEEEC CCCCEEEECC
241  GETIFELSDP TQLDHIRGTY NHVHGKEIPS MVWTPEQFDI YLKMYEKKPV YK
     CCEEEECCCC CCHHHHCCEE CCCCCCEECC CCCCCCCHHH HHHHHCCCCE EC
```

Secondary structure prediction for ORF 182ORF014

```
  1  MIEYITQWLA DDNHLVYGLI IWLMVAMIID FVLGFTIAKF NKEIDFSSFK AKAGIIVKVA
     CCCCEECCCC CCCCHHHHHH HHHHHHHHHH HHHHHHHHHC CCCCCHHHHH HHHCEEEEEE
 61  EMVLVVYFIP VAVKFGAVGI TMYITMLVGL ILSEIYSILG HISDIDDDNN WTDYVKKFLD
     EEEEEEEECC CEEECCCEEE EEEEEEEEEE EEEEEEEECC CCCCCCCCCC CEEEEEEECC
121  GTLNRKDDIK
     CCCCCCCEEC
```

Table 27

Enterococcus accession numbers 242/242

gi|2895751|gb|AF044978.1|AF044978 [2895751]

gi|4803755|dbj|AB026843.1|AB026843 [4803755]

gi|4769001|gb|AF140549.1|AF140549 [4769001]

gi|4760901|gb|AF099088.1|AF099088 [4760901]

gi|4704705|gb|AF121254.1|AF121254 [4704705]

gi|3342117|gb|AF076604.1|AF076604 [3342117]

gi|4688824|emb|AJ132470.1|ESP132470 [4688824]

gi|4732085|gb|AF125553.1|AF125553 [4732085]

gi|4732082|gb|AF125552.1|AF125552 [4732082]

gi|4732079|gb|AF125551.1|AF125551 [4732079]

gi|4732076|gb|AF125550.1|AF125550 [4732076]

gi|4732073|gb|AF125548.1|AF125548 [4732073]

gi|4732070|gb|AF125547.1|AF125547 [4732070]

gi|4732067|gb|AF125546.1|AF125546 [4732067]

gi|4732064|gb|AF125545.1|AF125545 [4732064]

gi|4732061|gb|AF125544.1|AF125544 [4732061]

gi|4704653|gb|AF114715.1|AF114715 [4704653]

gi|4704564|gb|AF102550.1|AF102550 [4704564]

gi|4688827|emb|AJ238249.1|EFA238249 [4688827]

gi|4680606|gb|AF125198.1|AF125198 [4680606]

gi|4633279|gb|AF117609.1|AF117609 [4633279]

gi|4633124|gb|AF110130.1|AF110130 [4633124]

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gi|4545122|gb|AF077816.1|AF077816 [4545122]

gi|4433610|gb|AF106614.1|AF106614 [4433610]

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gi|4158179|emb|AL035206.1|SC9B5 [4158179]

gi|4165458|emb|X79343.1|EF16SSPA [4165458]

gi|4165457|emb|X79342.1|EFTRNALA [4165457]

gi|4165456|emb|X79341.1|EF23SRNA [4165456]

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gi|4127803|emb|AJ223161.1|EFAJ3161 [4127803]

gi|2956685|emb|Y16413.1|EFENTIJO [2956685]

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gi|3757810|gb|AF042288.1|AF042288 [3757810]
gi|3747039|gb|AF093509.1|AF093509 [3747039]
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gi|2353762|gb|AF016233.1|AF016233 [2353762]
gi|2149899|gb|U94707.1|EFU94707 [2149899]
gi|2149149|gb|U82366.1|LSU82366 [2149149]
gi|1469463|gb|U49512.1|EFU49512 [1469463]
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gi|460079|gb|U00457.1|U00457 [460079]
gi|460077|gb|U00456.1|U00456 [460077]
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gi|431124|gb|L15633.1|TRN916ENT [431124]
gi|388106|gb|L23802.1|ENEEBSA [388106]
gi|3608387|gb|AF071085.1|AF071085 [3608387]
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gi|2765268|emb|Y12917.1|ECY12917 [2765268]
gi|2765267|emb|Y12916.1|EPY12916 [2765267]
gi|2765266|emb|Y12915.1|ESY12915 [2765266]
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gi|2765264|emb|Y12913.1|EMY12913 [2765264]
gi|2765263|emb|Y12912.1|EHY12912 [2765263]
gi|2765262|emb|Y12911.1|EMY12911 [2765262]
gi|2765261|emb|Y12910.1|EGY12910 [2765261]
gi|2765260|emb|Y12909.1|EDY12909 [2765260]
gi|2765259|emb|Y12908.1|ECY12908 [2765259]
gi|2765258|emb|Y12907.1|EAY12907 [2765258]
gi|2765257|emb|Y12906.1|EFY12906 [2765257]
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gi|3108058|gb|AF060881.1|AF060881 [3108058]
gi|3087776|emb|AJ223633.1|EFAJ3633 [3087776]
gi|3080754|gb|AF016483.1|AF016483 [3080754]
gi|2197119|gb|AF003921.1|AF003921 [2197119]
gi|2982722|dbj|AB012213.1|AB012213 [2982722]
gi|2982721|dbj|AB012212.1|AB012212 [2982721]
gi|2058780|gb|B07890.1|B07890 [2058780]
gi|2058779|gb|B07889.1|B07889 [2058779]
gi|2058778|gb|B07888.1|B07888 [2058778]
gi|2058777|gb|B07887.1|B07887 [2058777]
gi|2058776|gb|B07886.1|B07886 [2058776]
gi|2058775|gb|B07885.1|B07885 [2058775]
gi|2058774|gb|B07884.1|B07884 [2058774]
gi|2058773|gb|B07873.1|B07873 [2058773]
gi|2058772|gb|B07872.1|B07872 [2058772]
gi|2058771|gb|B07871.1|B07871 [2058771]
gi|2058770|gb|B07870.1|B07870 [2058770]
gi|2058769|gb|B07869.1|B07869 [2058769]
gi|2058768|gb|B07868.1|B07868 [2058768]
gi|2058767|gb|B07867.1|B07867 [2058767]
gi|2058766|gb|B07866.1|B07866 [2058766]
gi|2058765|gb|B07865.1|B07865 [2058765]
gi|2058764|gb|B07864.1|B07864 [2058764]
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gi|47047|emb|X17214.1|SFPASA1 [47047]
gi|47044|emb|X68847.1|SFNOXAA [47044]
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Table 28

Phage Dp1 complete genome sequence. 56506 nucleotides.

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631	tcttggacga	gctattcgat	aggaggctgg	aatgaaatca	gtagttttat	tatccggcgg	agtcgactca
701	gccacttgtt	tagcaattga	agttgacaag	tggggttcta	aaaatgttca	tgctatagca	ttcaattacg
771	gacaaaagca	tgaagcagaa	cttgaaaatg	ctgctaatgt	tgcaatgttc	tacggagtca	agttcaccat
841	tcttgaaatt	gactcgaaaa	tctactcaag	ctctagctct	tccttattac	aaggaaaagg	cgaaatttca
911	catggaaaat	cttacgctga	aatcctagca	gagaaggaag	tagttgacac	ctatgttcca	tttagaaatg
981	gactaatgct	ttcacaggct	gcggcttatg	cttattcggt	tggagcttct	tacgtcgtat	atggtgctca
1051	cgcagacgat	gcggctggag	gtgcttaccc	tgattgcact	cctgagttct	ataattcaat	gtcaaatgca
1121	atggaatatg	gaactggagg	caaggtaacc	cttgtcgctc	ctctacttac	tctaaccaag	gcgcaagtcg
1191	ttaaatgggg	aattgattta	gatgttcctt	atttcttgac	tcgttcatgt	tatgaaagtg	acgctgaaag
1261	ttgtggaact	tgcgcaactt	gtatcgaccg	caaaaaggca	ttcgaagaaa	atggaatgac	tgaccctatt
1331	cattataagg	agaattgata	tgagagtttc	taaaacctta	acattcgacg	cagctcatca	actagttgga
1401	cattttggaa	aatgcgcaaa	tttgcacggg	catacttaca	aagtcgaaat	ttcattagca	ggcggaactt
1471	atgaccacgg	ttcgagtcaa	gggatggttg	ttgactttta	tcacgtcaag	aaaatcgcag	gtacattcat
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1681	agcttatgtg	gaagcatgct	cgtatcgact	ctatcaaact	atgggaaact	cctacaggtt	gcgcagaatg
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2171	gaggaaatcc	tgccttaatc	aacgagccta	tggctaagat	gatttcgatt	ctaaaagaac	atggattcaa
2241	gtttggtctc	gaaactcaag	gaactcgatt	ccaagaatgg	ttcaaagaag	taagcgatat	cactattagt
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43401 tgaggtggaa taatgggagt cgatattgaa aaaggcgttg cgtggatgca ggcccgaaag ggtcgagtat
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43541 ctcagccgga gcttcaagtg ctggatgggc agtcaatact gagtacatgc acgcatggct tattgaaaac
43611 ggttatgaac taattagtga aaatgctccg tgggatgcta aacgaggcga catcttcatc tggggacgca
43681 aaggtgctag cgcaggcgct ggaggtcata cagggatgtt cattgacagt gataacatca ttcactgcaa
43751 ctacgcctac gacggaattt ccgtcaacga ccacgatgag cgttggtact atgcaggtca accttactac
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43891 ctggtttctg gtacgctcga gcaaacggaa cttatccaaa agatgagttc gagtatatcg aagaaaacaa
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45711 ttagcaggaa ggcaagtttc aaacattgtt taatcgtatg ttgcatatca gggctcaaat ggaattgggc
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56491 attcattcat tattat

Table 29

Phage dp1 ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	dp1ORF001	2	36698..40390	1230	Putative tail;
2	dp1ORF002	1	32386..35835	1149	Tail;
3	dp1ORF003	3	53538..55877	779	DNA polymerase I;
4	dp1ORF004	3	40401..42440	679	Minor structural;
5	dp1ORF005	1	23674..25434	586	
6	dp1ORF006	2	45296..46987	563	SWI/SNF Helicase;
7	dp1ORF007	3	22230..23621	463	Terminase;
8	dp1ORF008	1	49624..50961	445	DNAb Helicase;
9	dp1ORF009	2	13160..14404	414	
10	dp1ORF010	2	8699..9859	386	RecA;
11	dp1ORF011	3	28017..29096	359	Major head;
12	dp1ORF012	3	5346..6419	357	DNA pol. III beta;
13	dp1ORF013	3	10215..11240	341	DNA pol. III gamma and tau;
14	dp1ORF014	3	50961..51974	337	DNA primase;
15	dp1ORF015	1	3793..4728	311	
16	dp1ORF016	3	43413..44303	296	Amidase;
17	dp1ORF017	1	11242..12081	279	
18	dp1ORF018	3	35847..36686	279	
19	dp1ORF019	2	12161..12967	268	
20	dp1ORF020	1	1864..2658	264	exsD; Coenzyme PQQ;
21	dp1ORF021	2	2504..3295	263	GTP cyclohydrolase;
22	dp1ORF022	2	30896..31675	259	
23	dp1ORF023	2	6419..7195	258	
24	dp1ORF025	-1	18026..18778	250	
25	dp1ORF024	3	25992..26738	248	
26	dp1ORF026	2	21512..22252	246	
27	dp1ORF027	1	52762..53490	242	
28	dp1ORF028	3	44595..45299	234	
29	dp1ORF029	2	662..1348	228	exsB;
30	dp1ORF031	3	26943..27611	222	
31	dp1ORF030	-2	19423..20088	221	
32	dp1ORF032	1	52033..52647	204	
33	dp1ORF033	2	7670..8239	189	
34	dp1ORF035	-1	16859..17425	188	
35	dp1ORF036	1	48808..49362	184	DNAc replication;
36	dp1ORF037	1	55855..56388	177	
37	dp1ORF034	2	131..652	173	
38	dp1ORF038	3	1350..1871	173	exsC; 6-pyruvoyltetrahydropterin;
39	dp1ORF039	3	3306..3803	165	Citrulline biosynthesis;
40	dp1ORF040	1	7192..7683	163	
41	dp1ORF041	3	8208..8699	163	dUTPase;
42	dp1ORF042	1	48082..48561	159	
43	dp1ORF043	1	31699..32154	151	
44	dp1ORF044	-1	25211..25666	151	
45	dp1ORF045	2	25340..25777	145	
46	dp1ORF046	3	42774..43202	142	
47	dp1ORF047	1	47542..47961	139	
48	dp1ORF048	-3	16308..16709	133	
49	dp1ORF049	-3	43620..44018	132	
50	dp1ORF050	3	15081..15476	131	
51	dp1ORF051	2	29765..30154	129	
52	dp1ORF053	-3	49917..50300	127	
53	dp1ORF052	3	30516..30893	125	
54	dp1ORF054	2	14423..14800	125	
55	dp1ORF055	3	27627..28004	125	
56	dp1ORF056	-3	18780..19151	123	
57	dp1ORF057	1	9859..10218	119	
58	dp1ORF058	3	15633..15989	118	
59	dp1ORF059	1	30154..30507	117	
60	dp1ORF060	-2	37717..38070	117	
61	dp1ORF062	-3	44940..45284	114	
62	dp1ORF063	1	47200..47541	113	
63	dp1ORF064	2	29108..29449	113	

64	dp1ORF066	-3	28566..28898	110	
65	dp1ORF067	-1	44735..45061	108	
66	dp1ORF068	3	29451..29768	105	
67	dp1ORF069	-3	20094..20411	105	
68	dp1ORF061	-3	19161..19475	104	
69	dp1ORF070	1	15973..16284	103	
70	dp1ORF071	3	38904..39209	101	
71	dp1ORF072	-2	50749..51045	98	
72	dp1ORF073	3	14262..14555	97	
73	dp1ORF074	3	32298..32591	97	
74	dp1ORF075	-1	22154..22447	97	
75	dp1ORF076	-1	5435..5728	97	
76	dp1ORF077	1	14800..15084	94	
77	dp1ORF079	-3	35007..35288	93	
78	dp1ORF081	-3	55188..55466	92	
79	dp1ORF103	2	49352..49627	91	
80	dp1ORF080	1	42490..42759	89	
81	dp1ORF082	1	44728..44994	88	
82	dp1ORF083	-1	35720..35974	84	
83	dp1ORF065	-3	51246..51497	83	
84	dp1ORF085	-3	10602..10847	81	
85	dp1ORF087	-2	29794..30036	80	
86	dp1ORF088	3	5040..5279	79	
87	dp1ORF089	-2	12256..12495	79	
88	dp1ORF273	3	56256..56486	76	
89	dp1ORF078	-3	17280..17507	75	
90	dp1ORF090	1	27037..27261	74	
91	dp1ORF091	1	43189..43413	74	Holin;
92	dp1ORF092	3	46989..47213	74	
93	dp1ORF093	-2	45538..45756	72	
94	dp1ORF095	3	8877..9089	70	
95	dp1ORF096	-1	46469..46681	70	
96	dp1ORF097	-1	38888..39100	70	
97	dp1ORF098	1	43627..43836	69	
98	dp1ORF099	3	38298..38507	69	
99	dp1ORF100	1	1597..1803	68	
100	dp1ORF101	2	19220..19426	68	
101	dp1ORF094	1	8281..8484	67	
102	dp1ORF102	2	4034..4237	67	
103	dp1ORF104	-1	21224..21427	67	
104	dp1ORF105	-2	1828..2028	66	
105	dp1ORF106	-3	10329..10529	66	
106	dp1ORF108	-1	49250..49447	65	
107	dp1ORF109	-2	31435..31632	65	
108	dp1ORF110	1	16444..16638	64	
109	dp1ORF111	1	28657..28851	64	
110	dp1ORF113	-2	17521..17715	64	
111	dp1ORF084	1	15445..15636	63	
112	dp1ORF114	2	52952..53143	63	
113	dp1ORF115	-3	5151..5342	63	
114	dp1ORF116	-1	20474..20662	62	
115	dp1ORF117	-3	24492..24680	62	
116	dp1ORF118	2	15023..15208	61	
117	dp1ORF119	2	41054..41239	61	
118	dp1ORF120	1	28387..28569	60	
119	dp1ORF121	3	39222..39404	60	
120	dp1ORF122	-1	40220..40402	60	
121	dp1ORF123	-2	21145..21327	60	
122	dp1ORF124	-3	17712..17891	59	
123	dp1ORF125	-3	49740..49916	58	
124	dp1ORF126	-3	15960..16136	58	
125	dp1ORF127	-3	13335..13511	58	
126	dp1ORF128	1	4852..5025	57	
127	dp1ORF129	2	25133..25306	57	
128	dp1ORF130	-1	16619..16789	56	
129	dp1ORF131	1	43846..44013	55	
130	dp1ORF132	-1	15137..15304	55	
131	dp1ORF133	-2	7900..8061	53	
132	dp1ORF135	3	780..938	52	
133	dp1ORF136	-1	55094..55252	52	
134	dp1ORF137	-2	36988..37146	52	

135	dp1ORF138	-3	30504..30662	52	
136	dp1ORF139	-3	11934..12092	52	
137	dp1ORF140	3	20562..20717	51	
138	dp1ORF141	-1	42767..42922	51	
139	dp1ORF142	-3	31743..31898	51	
140	dp1ORF143	-3	7410..7565	51	
141	dp1ORF144	1	36517..36669	50	
142	dp1ORF145	1	42067..42219	50	
143	dp1ORF146	1	51484..51636	50	
144	dp1ORF147	1	55207..55359	50	
145	dp1ORF148	-1	28484..28636	50	
146	dp1ORF150	-3	15033..15185	50	
147	dp1ORF134	-2	349..498	49	
148	dp1ORF151	1	28027..28176	49	
149	dp1ORF152	1	42235..42384	49	
150	dp1ORF153	2	22307..22456	49	
151	dp1ORF086	2	52760..52906	48	
152	dp1ORF154	2	18446..18592	48	
153	dp1ORF155	3	13512..13658	48	
154	dp1ORF156	3	18777..18923	48	
155	dp1ORF157	-2	13135..13281	48	
156	dp1ORF158	-3	40581..40727	48	
157	dp1ORF159	-3	30225..30371	48	
158	dp1ORF149	-3	26331..26474	47	
159	dp1ORF160	2	41324..41467	47	
160	dp1ORF161	2	52175..52318	47	
161	dp1ORF162	3	13020..13163	47	
162	dp1ORF163	3	40224..40367	47	
163	dp1ORF164	-2	6553..6696	47	
164	dp1ORF165	-3	50361..50504	47	
165	dp1ORF166	-3	23376..23519	47	
166	dp1ORF167	3	1008..1148	46	
167	dp1ORF168	-2	54205..54345	46	
168	dp1ORF169	-2	45814..45954	46	
169	dp1ORF170	-2	27460..27600	46	
170	dp1ORF171	-3	47538..47678	46	
171	dp1ORF172	-1	10325..10462	45	
172	dp1ORF173	-2	32023..32160	45	
173	dp1ORF174	-2	29629..29766	45	
174	dp1ORF175	-2	15511..15648	45	
175	dp1ORF176	-3	42894..43031	45	
176	dp1ORF177	-3	19800..19937	45	
177	dp1ORF178	-3	11787..11924	45	
178	dp1ORF112	2	32207..32341	44	
179	dp1ORF179	3	56058..56192	44	
180	dp1ORF180	-1	41042..41176	44	
181	dp1ORF181	-1	12992..13126	44	
182	dp1ORF182	-2	45235..45369	44	
183	dp1ORF183	-2	13762..13896	44	
184	dp1ORF184	-3	53196..53330	44	
185	dp1ORF185	1	22522..22653	43	
186	dp1ORF186	2	21272..21403	43	
187	dp1ORF187	2	34415..34546	43	
188	dp1ORF188	2	35609..35740	43	
189	dp1ORF189	2	42587..42718	43	
190	dp1ORF190	3	39786..39917	43	
191	dp1ORF191	-1	40865..40996	43	
192	dp1ORF192	-1	2789..2920	43	
193	dp1ORF193	-2	42325..42456	43	
194	dp1ORF194	-2	40153..40284	43	
195	dp1ORF195	-3	42453..42584	43	
196	dp1ORF196	-3	11142..11273	43	
197	dp1ORF107	1	10750..10878	42	
198	dp1ORF197	2	7484..7612	42	
199	dp1ORF198	2	24119..24247	42	
200	dp1ORF199	-1	15614..15742	42	
201	dp1ORF200	-3	47715..47843	42	
202	dp1ORF201	1	38569..38694	41	
203	dp1ORF202	2	44483..44608	41	
204	dp1ORF203	-3	22656..22781	41	
205	dp1ORF204	1	1471..1593	40	

206	dp1ORF205	1	8524..8646	40	
207	dp1ORF206	1	19855..19977	40	
208	dp1ORF207	1	27502..27624	40	
209	dp1ORF208	2	47279..47401	40	
210	dp1ORF209	3	29784..29906	40	
211	dp1ORF210	-1	52955..53077	40	
212	dp1ORF211	-1	20837..20959	40	
213	dp1ORF212	-2	52861..52983	40	
214	dp1ORF213	-2	30169..30291	40	
215	dp1ORF214	-2	24151..24273	40	
216	dp1ORF215	-3	35700..35822	40	
217	dp1ORF216	-3	32727..32849	40	
218	dp1ORF217	1	23443..23562	39	
219	dp1ORF218	3	22029..22148	39	
220	dp1ORF219	-1	51269..51388	39	
221	dp1ORF220	-1	6215..6334	39	
222	dp1ORF221	1	43507..43623	38	
223	dp1ORF222	3	13212..13328	38	
224	dp1ORF223	3	14055..14171	38	
225	dp1ORF224	-1	13505..13621	38	
226	dp1ORF225	-2	32875..32991	38	
227	dp1ORF226	-2	25075..25191	38	
228	dp1ORF227	-2	22999..23115	38	
229	dp1ORF228	1	10450..10563	37	
230	dp1ORF229	1	27634..27747	37	
231	dp1ORF230	2	50723..50836	37	
232	dp1ORF231	-2	30958..31071	37	
233	dp1ORF232	-2	29272..29385	37	
234	dp1ORF233	-3	52779..52892	37	
235	dp1ORF234	1	36253..36363	36	
236	dp1ORF235	2	32768..32878	36	
237	dp1ORF236	-1	37418..37528	36	
238	dp1ORF237	-1	1568..1678	36	
239	dp1ORF238	-3	1191..1301	36	
240	dp1ORF239	1	26521..26628	35	
241	dp1ORF240	1	41893..42000	35	
242	dp1ORF241	-1	46913..47020	35	
243	dp1ORF242	-1	41231..41338	35	
244	dp1ORF243	-2	51199..51306	35	
245	dp1ORF244	-3	26976..27083	35	
246	dp1ORF245	-3	6171..6278	35	
247	dp1ORF246	-3	2724..2831	35	
248	dp1ORF247	1	29641..29745	34	
249	dp1ORF248	1	53560..53664	34	
250	dp1ORF249	2	2012..2116	34	
251	dp1ORF250	2	23837..23941	34	
252	dp1ORF251	-1	39101..39205	34	
253	dp1ORF252	-2	54667..54771	34	
254	dp1ORF253	-3	56151..56255	34	
255	dp1ORF254	-3	48375..48479	34	
256	dp1ORF255	-3	9468..9572	34	
257	dp1ORF256	1	15289..15390	33	
258	dp1ORF257	1	28216..28317	33	
259	dp1ORF258	1	44023..44124	33	
260	dp1ORF259	2	4298..4399	33	
261	dp1ORF260	2	24746..24847	33	
262	dp1ORF261	3	288..389	33	
263	dp1ORF262	3	9408..9509	33	
264	dp1ORF263	-1	26951..27052	33	
265	dp1ORF264	-1	6038..6139	33	
266	dp1ORF265	-1	4700..4801	33	
267	dp1ORF266	-2	50119..50220	33	
268	dp1ORF267	-2	47266..47367	33	
269	dp1ORF268	-2	12520..12621	33	
270	dp1ORF269	-3	53733..53834	33	
271	dp1ORF270	-3	50691..50792	33	
272	dp1ORF271	-3	19638..19739	33	
273	dp1ORF272	-3	1455..1556	33	

Table 30

Predicted Dp-1 amimo acid sequences

```
dp1ORF001
36698   atgattgacaataatttacctatgagtccaattcctggcgaaattgttcaagtatatgaccaaaacttcaatctaattggagca
1       M  I  D  N  N  L  P  M  S  P  I  P  G  E  I  V  Q  V  Y  D  Q  N  F  N  L  I  G  A
36782   agtgatgaaatctttagcaagcattacgaagacgaaattgtgactcgagctcgaggaaaagaaactttcacttttgaaagtatt
29      S  D  E  I  F  S  K  H  Y  E  D  E  I  V  T  R  A  R  G  K  E  T  F  T  F  E  S  I
36866   gaaacctcatctatctatcaacacttaaaggttgaaaacattatccagtatggaggaagatggtttcgaattaaatatgctcag
57      E  T  S  S  I  Y  Q  H  L  K  V  E  N  I  I  Q  Y  G  G  R  W  F  R  I  K  Y  A  Q
36950   gacgtagaagatgtcaaagggcttaccaagtttacctgctacgcattatggtatgaactagcagaaggcttgcctaggaagttg
85      D  V  E  D  V  K  G  L  T  K  F  T  C  Y  A  L  W  Y  E  L  A  E  G  L  P  R  K  L
37034   aaacacgttgcttcttctgtaggcgctgtcgcgctagatattatcaaagacgcaggtgaatgggttcgactagtttgtcctcct
113     K  H  V  A  S  S  V  G  A  V  A  L  D  I  I  K  D  A  G  E  W  V  R  L  V  C  P  P
37118   gacggtgctaacaaacaagttcgaagcataacagccgcagaaaattcaatgctttggcatcttcgatatcttgcaaagcaatac
141     D  G  A  N  K  Q  V  R  S  I  T  A  A  E  N  S  M  L  W  H  L  R  Y  L  A  K  Q  Y
37202   aatttagaattgacatttggttatgaagaaattatcaagcaagaggttagaattgttcaaaccgttgtatttcttcagccttat
169     N  L  E  L  T  F  G  Y  E  E  I  I  K  Q  E  V  R  I  V  Q  T  V  V  F  L  Q  P  Y
37286   gtcgagtctaaagtagactttcctcttgtagttgaagagaatttgaaatatgtcactaggcaggaagattctcgaaacctgtgt
197     V  E  S  K  V  D  F  P  L  V  V  E  E  N  L  K  Y  V  T  R  Q  E  D  S  R  N  L  C
37370   acggcttacaagttgacaggtaaaaaggaagaaggcagtcaagagcctttaacgtttgcttctatcaacaatggaagtgaatat
225     T  A  Y  K  L  T  G  K  K  E  E  G  S  Q  E  P  L  T  F  A  S  I  N  N  G  S  E  Y
37454   ctcattgatgtttcgtggtttactacacgccacatgaagcctcgatatattgctaaatctaaaagcgacgaacatttagaatt
253     L  I  D  V  S  W  F  T  T  R  H  M  K  P  R  Y  I  A  K  S  K  S  D  E  H  F  R  I
37538   aaagaaaatttgatgagtgctgcgcgtgcttatcttgacatctacagtcgcccactaattggatatgaggcttcagcggtcctt
281     K  E  N  L  M  S  A  A  R  A  Y  L  D  I  Y  S  R  P  L  I  G  Y  E  A  S  A  V  L
37622   tataacaaggttcctgacttgcatcatactcaactaattgtcgacgaccattatgatgttatcgagtggcgaaagatatctgct
309     Y  N  K  V  P  D  L  H  H  T  Q  L  I  V  D  D  H  Y  D  V  I  E  W  R  K  I  S  A
37706   cgaaaaattgactacgacgacctttcaaactctactatcattttccaagaccctcgaaaagacttgatggacttgctaaatgag
337     R  K  I  D  Y  D  D  L  S  N  S  T  I  I  F  Q  D  P  R  K  D  L  M  D  L  L  N  E
37790   gacggcgaaggagtcctttcaggggaaactgtaaatgagtcccaagttgttattagatacgcagatgacattttagggactaat
365     D  G  E  G  V  L  S  G  E  T  V  N  E  S  Q  V  V  I  R  Y  A  D  D  I  L  G  T  N
37874   tttaatgcagaatctgggaaatacattggtgtccttaatactaataagaaaccgagcgaattagttcctgacgactttacatgg
393     F  N  A  E  S  G  K  Y  I  G  V  L  N  T  N  K  K  P  S  E  L  V  P  D  D  F  T  W
37958   attcgactagaaggtcctaaaggtgacgcaggtttaccgggagctcctggcgtgatggagtcgacggtgtacctggaaagagc
421     I  R  L  E  G  P  K  G  D  A  G  L  P  G  A  P  G  R  D  G  V  D  G  V  P  G  K  S
38042   ggagtagggatagcagatacagctatcacttatgctgtatccgtttccggaacgcaagagcctgaaaatggatggagcgaacaa
449     G  V  G  I  A  D  T  A  I  T  Y  A  V  S  V  S  G  T  Q  E  P  E  N  G  W  S  E  Q
38126   gttcctgaactcataaaaggtcgattcttgtggactaaaacattttggagatatactgacggctcacatgaaactggatactcc
477     V  P  E  L  I  K  G  R  F  L  W  T  K  T  F  W  R  Y  T  D  G  S  H  E  T  G  Y  S
38210   gttgcctatatagggcaagacggaaattccggaaaagacggaatcgcaggtaaggacggagtaggtatagccgcaactgaagtc
505     V  A  Y  I  G  Q  D  G  N  S  G  K  D  G  I  A  G  K  D  G  V  G  I  A  A  T  E  V
38294   atgtatgcaagttcgccatctgctactgaagctccagctggtggatggtctacgcaagttcctaccgtcccaggtggtcagtat
533     M  Y  A  S  S  P  S  A  T  E  A  P  A  G  G  W  S  T  Q  V  P  T  V  P  G  G  Q  Y
38378   ttatggactcgaacaagatggcgctacactgaccaaactgatgaaattggatattcagtttcaagaatgggcgagcagggtcct
561     L  W  T  R  T  R  W  R  Y  T  D  Q  T  D  E  I  G  Y  S  V  S  R  M  G  E  Q  G  P
38462   aaaggtgacgcaggtcgtgacggtattgcaggaaagaacggaatagggttgaagtcaacttcagtttcttatggaattagtccc
589     K  G  D  A  G  R  D  G  I  A  G  K  N  G  I  G  L  K  S  T  S  V  S  Y  G  I  S  P
38546   actgattctgcgattcctggagtatgggcttcacaagttccttctttaatcaaaggtcaatatctttggactcgaactatttgg
617     T  D  S  A  I  P  G  V  W  A  S  Q  V  P  S  L  I  K  G  Q  Y  L  W  T  R  T  I  W
38630   acctataccgattcaactaccgaaacgggctatcaaaaaacctacattccaaaagacggaatgacggtaaaaatggaattgct
645     T  Y  T  D  S  T  T  E  T  G  Y  Q  K  T  Y  I  P  K  D  G  N  D  G  K  N  G  I  A
38714   ggtaaggatggggtaggaattaagtctacgaccattacctacgcaggctcaacctcaggaacagttgcgcctacttcaaattgg
673     G  K  D  G  V  G  I  K  S  T  T  I  T  Y  A  G  S  T  S  G  T  V  A  P  T  S  N  W
38798   acttctgctattccaaatgttcaaccgggattcttcttgtggacgaaaactgtttggaactatactgatgacactagcgaaaca
701     T  S  A  I  P  N  V  Q  P  G  F  F  L  W  T  K  T  V  W  N  Y  T  D  D  T  S  E  T
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337 I R G K Q I E Y I I L D P S A S A M I V E L Q K H P Y I
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141 D V D N I W I V R P E M N S A E E I L Q Y V L D I F E T
9203 ggtgaagttggcctagtagttctagattccttgccttacatggtcagtcaaaaccttattgatgaagagttgactaaaaaggcc
169 G E V G L V V L D S L P Y M V S Q N L I D E E L T K K A
9287 tatgcaggaatctcagcgcctttgactgaatttagtcgaaaggttactcctcttcttactcgctacaatgcaatattcctaggc
197 Y A G I S A P L T E F S R K V T P L L T R Y N A I F L G
9371 atcaatcaaattcgagaagatatgaatagtcagtacaatgcctattcaactccaggcggaaagatgtggaagcatgcttgtgca
225 I N Q I R E D M N S Q Y N A Y S T P G G K M W K H A C A
9455 gttcgacttaaatttagaaaggtgactaccttgacgaaaacggtgcatcattgacccgtactgctcgaaaccctgcagggaat
253 V R L K F R K G D Y L D E N G A S L T R T A R N P A G N
9539 gtagtagagtcattcgtcgagaagaccaaagcatttaagccggacagaaaattagtttcctatacgctttcctatcatgatgga
281 V V E S F V E K T K A F K P D R K L V S Y T L S Y H D G
9623 attcaaattgaaaatgaccttgtagatgtcgctgtcgaatttggagtcattcaaaaggcaggggcatggttcagtatcgtcgac
309 I Q I E N D L V D V A V E F G V I Q K A G A W F S I V D
9707 cttgaaactggagaaattatgacagatgaagacgaagaaccattgaagttccaaggcaaggcaaatctagttcgacgcttcaag
337 L E T G E I M T D E D E E P L K F Q G K A N L V R R F K
9791 gaggatgactacttattcgacatggtgatgactgcggttcacgaaattatcactcgagaagaaggctaa 9859
365 E D D Y L F D M V M T A V H E I I T R E E G *

dp1ORF011

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28101 ccaactcttttccctaatgctcaacaaacagggacagacatttcatggctcaagggtgcaaataatttgccagtaactatccag
29 P T L F P N A Q Q T G T D I S W L K G A N N L P V T I Q
28185 ccatctaactacgacgcgaaagcaagtcttcgtgaacgtgctggatttagcaaacaagctactgagatggcattcttccgtgag
57 P S N Y D A K A S L R E R A G F S K Q A T E M A F F R E
28269 tctatgcgacttggtgaaaaagaccgtcaaaacttgcaaatgctattgaaccaaagttcagctcttgcccaaccacttatcact
85 S M R L G E K D R Q N L Q M L L N Q S S A L A Q P L I T
28353 caactctataatgatactaagaaccttgtagacggtgttgaagcgcaagcagaatacatgcgtatgcaattgcttcaatacggt
113 Q L Y N D T K N L V D G V E A Q A E Y M R M Q L L Q Y G
28437 aaattcactgtcaaatcaactaacagcgaggctcaatacacttacgactacaacatggatgctaagcaacaatatgcagtcact
141 K F T V K S T N S E A Q Y T Y D Y N M D A K Q Q Y A V T
28521 aagaaatggactaacccagctgaaagtgaccctatcgctgacattttagcagcaatggatgacatcgaaaatcgtacaggtgtt
169 K K W T N P A E S D P I A D I L A A M D D I E N R T G V
28605 cgccctactcgaatggtcttgaaccgaaacacttataaccaaatgactaagagtgactctatcaagaaagctcttgcaattggt
197 R P T R M V L N R N T Y N Q M T K S D S I K K A L A I G
28689 gttcaaggttcttgggaaaacttcttgcttcttgcaagtgacgctgagaaattcatcgctgaaaaaacaggtcttcaaatcgct
225 V Q G S W E N F L L L A S D A E K F I A E K T G L Q I A
28773 gtctactctaagaaaattgctcagttcgctgacgctgacaaacttcctgacgttggtaacattcgtcagttcaacttgattgac
253 V Y S K K I A Q F A D A D K L P D V G N I R Q F N L I D
28857 gacggtaaagtggtattgcttccacctgacgcagttggtcacacttggtacggtactactccagaagcattcgacttggcttca
281 D G K V V L L P P D A V G H T W Y G T T P E A F D L A S
28941 ggcggaacagacgctcaagttcaagttctttcaggcggacctaccgttacaacttatcttgaaaaacatcctgtcaacattgca
309 G G T D A Q V Q V L S G G P T V T T Y L E K H P V N I A

29025 acagttgtatcagctgttatgattccatcattcgaaggaattgactatgtaggagttctcacaactaattag 29096
337 T V V S A V M I P S F E G I D Y V G V L T T N *
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1 M S I K F K T E E L S K I V S Q L N K L K P S K L L E I
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29 T N Y W H I F G D G E C V M F T A Y D G S N F L R C I I
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57 D S D V E I D V I V K A E Q F G K L V E K T T A A T V T
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85 L V P E E S S L K V I G N G E Y N I D I V T E D E E Y P
5682 acattcgaccacttgctcgaagacgtgagtgaagaaaatgctctcactttgaaaagctcgctgttctacggaatcgccaatatc
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5766 aacgattctgcggtatctaaatcaggagcagatggaatttataccggcttcctgttaaaggcggaaaagcaattactacagac
141 N D S A V S K S G A D G I Y T G F L L K G G K A I T T D
5850 atcattcgcgtatgtatcaaccctatcaaggaaaagggactagaaatgctcattccttacaacctaatgagtatttagcaagt
169 I I R V C I N P I K E K G L E M L I P Y N L M S I L A S
5934 attcctgatgagaagatgtacttctggcaaattgacgatactactgtctatatttcatcggcttcagtcgaaatttatggaaaa
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225 L M E G M E D Y E D V S Q L D S I E F E D D A A I P T A
6102 gaaatcctgagcgtattagaccgccttgtactattcacttcagcctttgacaaaggaaccgtcgaattcttattcttgaaagac
253 E I L S V L D R L V L F T S A F D K G T V E F L F L K D
6186 cgacttcgaattaaaacttctactagcagttatgaagacatcatgtacgcatctgctggcaagaaagtttcgaagaaagaattc
281 R L R I K T S T S S Y E D I M Y A S A G K K V S K K E F
6270 acttgccaccttaacagcttactcttgaaggaaattgtatcaaccgtcaccgaagaaaacttcactgtctcttatggaagcgaa
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6354 accgcaattaagatttcatcgaatggtgtcgtttacttcctagcacttcaagagccggaagaataa 6419
337 T A I K I S S N G V V Y F L A L Q E P E E *
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10215 atgaatttagcttctaaataccgtcctcaaactttcgaggaagtggtagctcaagaatatgtcaaagaaattcttttgaatcaa
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29 L Q N G A I K H G Y L F C G G A G T G K T T T A R I F A
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57 K D V N K G L G S P I E I D A A S N N G V E N V R N I I
10467 gaagattctagatacaagtctatggacagcgagttcaaagtttacatcattgacgaggttcatatgctttcaaccggagcattt
85 E D S R Y K S M D S E F K V Y I I D E V H M L S T G A F
10551 aatgcgctgttgaaaacattagaagagccctcatcgggaaccgtgttcattctatgtactactgaccctcaaaagattcctgac
113 N A L L K T L E E P S S G T V F I L C T T D P Q K I P D
10635 actattctcagtcgagttcaacggtttgactttactcgaattgataatgacgacatcgttaatcaacttcaatttattatcgaa
141 T I L S R V Q R F D F T R I D N D D I V N Q L Q F I I E
10719 agtgaaaatgaagaaggagctggttatagttatgagcgtgacgccctttcgtttattgggaaacttgcaaatggaggaatgcgt
169 S E N E E G A G Y S Y E R D A L S F I G K L A N G G M R
10803 gacagtatcacaaggctcgaaaaagtccttgattatagtcatcacgttgacatggaagccgtttctaatgcactaggagttccg
197 D S I T R L E K V L D Y S H H V D M E A V S N A L G V P
10887 gactacgaaacattcgcttcacttgttgaagctattgccaactatgacggctcaaagtgtttagaaattgtaaatgacttccac
225 D Y E T F A S L V E A I A N Y D G S K C L E I V N D F H
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253 Y S G K D L K L V T R N F T D F L L E V C K Y W L V R D
11055 atttcaatcactcaacttcctgctcatttgaaagtaagctagagcaattctgtgaggctttcaatatcctactctattgtgg
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11223 atgagcaaggaggagtga 11240
337 M S K E E *
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50961 atgaaagtaaatggtcttcaaattgaagcgactcctgaacaaataattgaaaaactttcgagacaacttgaagacgaaggaaca
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29 F I F R R T K S L G S N Y Q F S C P F H A G G T E K H P
51129 tcttgtggcatgagtagaaatccttcttattcaggaagtaaggtgacggaagctggaacggttcactgtttcacttgcggctac
57 S C G M S R N P S Y S G S K V T E A G T V H C F T C G Y
51213 acttcaggactaactgaattcgtctcgaatgtattaggtcgaaacgatggagggttctatggaaaccagtggctgaaaaggaat
85 T S G L T E F V S N V L G R N D G G F Y G N Q W L K R N
51297 tttggaacatctagcgaagtagttaggcaaggcgtcagccctgaagcgtttcgaagaaatgggagaactgaaaaagtcgagcat
113 F G T S S E V V R Q G V S P E A F R R N G R T E K V E H
51381 aaaatcattcctgaagaggaacttgataaataccggtttattcatccttatatgtatgaacggaaattgacggacgagctcatc
141 K I I P E E E L D K Y R F I H P Y M Y E R K L T D E L I
51465 gagatgtttgatgtaggttatgacaaactgcatgattgcatcacctttccagtacggaacctcaagggcgaaacagtattcttc
169 E M F D V G Y D K L H D C I T F P V R N L K G E T V F F
51549 aaccgtcgaagtgttcgttctaagtttcaccagtacggtgaagatgaccctaaaacggaatttctttatggccaatatgagctt
197 N R R S V R S K F H Q Y G E D D P K T E F L Y G Q Y E L
51633 gtagcatttcgagactatttgaaaaacctattagtcaagtattcgtgactgagtctgttatcaactgcttgactctttggtca
225 V A F R D Y F E K P I S Q V F V T E S V I N C L T L W S
51717 atgaagattccagcagtcgctcttatgggagtaggtggaggaaatcaaatcaatttactaaaacgacttccttatagaaatatt

253 M K I P A V A L M G V G G G N Q I N L L K R L P Y R N I
51801 gttctagcacttgaccctgataacgctgggcagacagcgcaggaaaaactctaccgacagttaaagcgaagcaaggtcgttaga
281 V L A L D P D N A G Q T A Q E K L Y R Q L K R S K V V R

51885 tttttgaactaccctaaagagttctatgataataagtgggatataaacgaccatccggaattattaaatttaatgatttagtc
309 F L N Y P K E F Y D N K W D I N D H P E L L N F N D L V
51969 ttgtag 51974
337 L *
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3793 atgggatttaatctatacttcgcaggaggtcacgctattagcactgacgattatttgaaggaaagaggagccaatcgcctattc
1 M G F N L Y F A G G H A I S T D D Y L K E R G A N R L F
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29 N Q L Y E R N G I G K R W I E H K K T N P S T T S K L F
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57 V D S S A Y S A H T K G A E V D I D A Y I E Y V N D N V
4045 ggaatgtttgactgtatcgccgaactcgataaaattcctggtgtatttagacagcctaagacacgtgaacagcttttggaagca
85 G M F D C I A E L D K I P G V F R Q P K T R E Q L L E A
4129 ccacaaatttcttgggataattatctatacatgcgcgagcgaatggttgagaaagacaagctcttacctattttccatatggga
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4213 gaagactttaaatggctcaacttgatgctcgaaactacattcgaaggcggaaagcatattccttacattggaatttcaccagcc
141 E D F K W L N L M L E T T F E G G K H I P Y I G I S P A
4297 aatgactcgactacgaagcataaagacaagtggatggaaagagtattcgaagttattcgaaacagttctaatccagacgttaag
169 N D S T T K H K D K W M E R V F E V I R N S S N P D V K
4381 actcacgcatttgggatgacagttactagccaattagagcgtcacccattctatagcgccgactctacttctgtactgctcaca
197 T H A F G M T V T S Q L E R H P F Y S A D S T S V L L T
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225 G A M G N I M T S K G L V D L S Q K N G G I D A V R R L
4549 ccaaaaccggttcaagttgaaattgaatccattatcgaagaaactggagcgcatttagcctagagcaattagttgaggactat
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4633 aaacttcgagcattgttcaatgttcaatacatgctgaattgggcagagaactatgaattcaagggaattaaaaatcgtcaacgt
281 K L R A L F N V Q Y M L N W A E N Y E F K G I K N R Q R
4717 cgactattttag 4728
309 R L F *
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85 F I W G R K G A S A G A G G H T G M F I D S D N I I H C
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44169 accaacggcgacatgaaatcgaatgcgtttatccgttataacgacggctggtatctactattaccggacggacgtctggcagat
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44253 aaacctcaattcaccgtagagccggacggctcattactgctaaagtttaa 44303
281 K P Q F T V E P D G L I T A K V *
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29 S G R K T L I R Y I A S K F D A D S I V V G T S V D D I
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57 R N I I Q D A Q T I F K A R I Y V I D G N S L S M S A L
11494 aactcgcttttgaagatagcggaagagccacctttaaactgtcatatagccatgactgttgatagcatcaataatgctttacct
85 N S L L K I A E E P P L N C H I A M T V D S I N N A L P
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113 T L A S R A K V L T M L P Y T N E E K M Q F V K S Y K K
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11914 acagttgtcatcaggaagcactatgtagaaatgtctttcgaagaacttgaggcccatgaccttttagtgagggaagcatctagg
225 T V V I R K H Y V E M S F E E L E A H D L L V R E A S R

11998 tgtttgcgaaaggtatctaaaaagggctcaaatgcgcgtgtctgcgtgaacgaatttatcaggagggtcaaacaagttgagtga
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253 C L R K V S K K G S N A R V C V N E F I R R V K Q V E *
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85 R S K S F W R I S T L E D P G Y Y R T G K F L G E T E Q
36183 ggaaaacttgtagacgttcaagcctttaaagatacttcccttgtagttaaattagggattcagttcaaagatgcttacgagtac
113 G K L V D V Q A F K D T S L V V K L G I Q F K D A Y E Y
36267 agcgactcaactgttcgaaaggtttataagtttcaacccgctttgggaggcgatagcttacctaacccaggaagacctactcga
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36351 caatttagagtagaaataagaactacttctcaaatcaaaggatatttcgaattggcgaaaaaagttcaggacagtttgttgag
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197 F G T N S V L M E S G S I I I L N L G T F E L I K I S S
36519 gcaaatcaagcgactaacttatttagatacattaaacgaggcgcattcttcaagattcctaatggaaattcaacaattaccatt
225 A N Q A T N L F R Y I K R G A F F K I P N G N S T I T I
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36686
253 E Y R A D D A A A W T S T L P A Q V E L F L N P S Y Y *
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1 M N V Y L N Q M G N V V R E T S V S T V W K T L T Q K G
12245 ctcgtttctaatcatcgaatattcgctgttcgagatgataaggagtttctgtctaatgagtcgaggtggaaaaggcttccggat
29 L V S N H R I F A V R D D K E F L S N E S R W K R L P D
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57 V R Y G T L V L M V T K I D K R S K L L K A F P D N C V
12413 gagtttgagaaaatgactgacgcgcagttgaaaaggcattttgtgtctaaatactcgactattgatagcgacatgattgacatg
85 E F E K M T D A Q L K R H F V S K Y S T I D S D M I D M
12497 gttatccagttctgtctaaacgattactctagaattgacaatgaattggacaagctgtcgcgattgaaaaaggttgacgcatca
113 V I Q F C L N D Y S R I D N E L D K L S R L K K V D A S
12581 gtagttgaatccattgtcaagcacaagaccgaaattgacatttcagcctagttgatgatgtattggaatataggccggagcag
141 V V E S I V K H K T E I D I F S L V D D V L E Y R P E Q
12665 gcaattatgaaagtgactgaacttttagccaaaggagaaagtcctattggattgcttaccttgctttatcaaaattttaataac
169 A I M K V T E L L A K G E S P I G L L T L L Y Q N F N N
12749 gcttgtcttgtgctaggagccgatgagcctaaagaagccaatctaggcattaagcagttcttaatcaataagattgtctataac
197 A C L V L G A D E P K E A N L G I K Q F L I N K I V Y N
12833 tttcaatacgagctggactcagcctttgaaggcatggctatttaggtcaagctatcgagggcataaagaatggtcgctataca
225 F Q Y E L D S A F E G M A I L G Q A I E G I K N G R Y T
12917 gaaagttcagtggtctatatttctttgtataaaatttttttcacttacttaa 12967
253 E S S V V Y I S L Y K I F S L T *
dp1ORF020
1864 atggttaatcaatacaatcagcctgaaagaggcaagattcgaatcaatgttcgcgaccctgagaaaatgcctatcatggaaatt
1 M V N Q Y N Q P E R G K I R I N V R D P E K M P I M E I
1948 ttcggtcctacaattcaaggtgaaggaatggttataggtcaaaagactattttcattcgaactggtggatgcgactatcattgc
29 F G P T I Q G E G M V I G Q K T I F I R T G G C D Y H C
2032 aactggtgtgactcagcctttacctggaacggtactactgagccggaatatatcacaggcaaagaagctgctagtcgaatcttg
57 N W C D S A F T W N G T T E P E Y I T G K E A A S R I L
2116 aaactagctttcaatgataaaggtgaacagatttgtaaccacgtgacattgactggaggaaatcctgccttaatcaacgagcct
85 K L A F N D K G E Q I C N H V T L T G G N P A L I N E P
2200 atggctaagatgatttcgattctaaaagaacatggattcaagtttggtctcgaaactcaaggaactcgattccaagaatggttc
113 M A K M I S I L K E H G F K F G L E T Q G T R F Q E W F
2284 aaagaagtaagcgatatcactattagtcctaaaccgccttcaagtggaatgagaactaatatgaaaattcttgaagctattgta
141 K E V S D I T I S P K P P S S G M R T N M K I L E A I V
2368 gatagaatgaatgatgaaaaccttgactggtcatttaaaatcgttatctttgacgaaaatgacctagcttatgcgcgtgatatg
169 D R M N D E N L D W S F K I V I F D E N D L A Y A R D M
2452 tttaaaactttcgaaggcaagttacgtccagtgaactacctttcagttgggaatgcaaacgcatacgaagaaggaaaaatcagt
197 F K T F E G K L R P V N Y L S V G N A N A Y E E G K I S
2536 gataggcttcttgaaaagttgggatggctttgggataaagtgtatgaagacccagctttcaacaatgttcgacctttaccgcaa
225 D R L L E K L G W L W D K V Y E D P A F N N V R P L P Q
2620 cttcatacacttgtttatgataataaaagaggagtataa 2658
253 L H T L V Y D N K R G V *
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1 M Q T H T K K E K S V I G F L K S W D G F G I K C M K T
2588 cagctttcaacaatgttcgacctttaccgcaacttcatacacttgtttatgataataaaagaggagtataaaatgaaaattgag
29 Q L S T M F D L Y R N F I H L F M I I K E E Y K M K I E
2672 catctagataaaatcggtaacgtattagggagagagaacggatgggcttcccttaagccggatgaaattgtaaccttggacaat
57 H L D K I G N V L G R E N G W A S L K P D E I V T L D N
2756 actgaggcagccgttcaaagactttttggtctattaggcgaggacgcagaacgtgacgggttgcaagatactccattccgtttt
85 T E A A V Q R L F G L L G E D A E R D G L Q D T P F R F

2840 gttaaagcactcgctgaacataccgtagggtatcgagaagaccctaaacttcatctcgaaaaaacattcgacgtcgaccatgaa
113 V K A L A E H T V G Y R E D P K L H L E K T F D V D H E
2924 gaccttgttcttgtgaaagacattccattcaattctttatgtgagcatcatttagctccgttcgtagggaaggtgcatattgca
141 D L V L V K D I P F N S L C E H H L A P F V G K V H I A
3008 tacattcctaaggataagattacaggtctttcaaaattcggtcgagtggttgaaggatacgctaaacgacttcaagtacaagag
169 Y I P K D K I T G L S K F G R V V E G Y A K R L Q V Q E
3092 cgcttgactcaacaaatcgctgacgctattcaggaagttctaaatcctcaagcagttgcggtcatcgtagaggctgagcatact
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3176 tgcatgagcggacgcggtattaagaagcacggggcaacgacagtgacttcaactatgcgaggtcttttccaagatgacgcatct
225 C M S G R G I K K H G A T T V T S T M R G L F Q D D A S
3260 gctcgagcagaattgcttcagttgattaaaaagtag 3295
253 A R A E L L Q L I K K *

dp1ORF022

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29 A N F V V D T A E T A E L E A V T S E G T E D V K R N D
31064 acgcgcattcttgctatcgtgcgtactccagaccttttatacggttatgacttaacattcaaggacaacacgtttgaccctgaa
57 T R I L A I V R T P D L L Y G Y D L T F K D N T F D P E
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31232 gcttctaatatgaaaccatttagaatgaacatctatgtgccaaactatgtaggtgactcaattgtcaactacgtgaaaatcact
113 A S N M K P F R M N I Y V P N Y V G D S I V N Y V K I T
31316 ttgaataactgtaccggtaaagctccagggctttcaatcgggaaagagttctacgctcctgagttcaacatcaaggcacgtgaa
141 L N N C T G K A P G L S I G K E F Y A P E F N I K A R E
31400 gcaaccaaagcaggtttgccagttaagtcaatggactatgtggcacaacttccagcggttcttcgtcgcgtgacattcgatttg
169 A T K A G L P V K S M D Y V A Q L P A V L R R V T F D L
31484 aacggtggaacaggaaccgccgacgcagttcgagttgaagcaggtaagaagatttctccaaaaccagttgaccctaccttaaca
197 N G G T G T A D A V R V E A G K K I S P K P V D P T L T
31568 ggtaaggctttcaaaggctggaaagttgaaggagaatcaactatttgggacttcgacaaccacatgatgcctgaccgagacgtc
225 G K A F K G W K V E G E S T I W D F D N H M M P D R D V
31652 aaactcgtagcacaatttgcatag 31675
253 K L V A Q F A *

dp1ORF023

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6503 ctgacccgggttattgaacgaactcagcctgaatataatccttcgacatattataagcccagcggggttggtggatgtattcga
29 L T R V I E R T Q P E Y N P S T Y Y K P S G V G G C I R
6587 aaaatgtatttcgaaagaatcggtgagtctattatagataacgcagattctaacctaattgcaatgggcgaagctggaacattt
57 K M Y F E R I G E S I I D N A D S N L I A M G E A G T F
6671 aggcacgaagttctccaagagtacatggttaaaatggctgaaatcgatgaggactttgaatggttgaatgtagcagagttcttg
85 R H E V L Q E Y M V K M A E I D E D F E W L N V A E F L
6755 aaagaaaatccagttgaaggaactatcgtcgacgagcgtttcaagaaaaacgattatgaaacgaagtgtaagaacgaacttctt
113 K E N P V E G T I V D E R F K K N D Y E T K C K N E L L
6839 caactttcattcttgtgtgacggactagttcgatataaaggcaagctctacatttagagattaagactgaaaccatgttcaag
141 Q L S F L C D G L V R Y K G K L Y I L E I K T E T M F K
6923 ttcactaaacatactgagccctatgaagaacacaagatgcaagcaacttgctacggaatgtgtctaggagtcgatgatgtcatt
169 F T K H T E P Y E E H K M Q A T C Y G M C L G V D D V I
7007 ttccttatgaaaatcgagataacttcgaaaagaaagcctacacgtttcacatcacagacgagatgaaaaatcaagtccttgga
197 F L Y E N R D N F E K K A Y T F H I T D E M K N Q V L G
7091 aaaattatgacctgcgaagagtatgtagagaaaggcgaaagtcctaaaatctattgctcttcagcctattgcccatattgtaga
225 K I M T C E E Y V E K G E S P K I Y C S S A Y C P Y C R
7175 aaggaaggtcgaaatctgtga 7195
253 K E G R N L *

dp1ORF024

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29 E V R A A S L V F S R R A A E A V V K G E I Y K D G K N
26160 ctctcgaaacgtgtttggtcttcagccgcacgcgcaggaaatgatgttcaacaaatagtcacacaaggcctagcaagtggaatg
57 L S K R V W S S A A R A G N D V Q Q I V T Q G L A S G M
26244 tctgctacagatatggctaaaatgctcgagaaatatatcgaccctaaggttcgaaaagattgggactttgataagatagctgag
85 S A T D M A K M L E K Y I D P K V R K D W D F D K I A E
26328 aagctagggaaacctgctgctcataaatatcaaaatctcgaatacaatgcccttcgacttgctcgaactaccattagccattcc
113 K L G K P A A H K Y Q N L E Y N A L R L A R T T I S H S
26412 gccacagctggagtgagacaatggggcaaggttaatccttatgctcgaaaagttcaatggcattctgttcacgctccaggtcga
141 A T A G V R Q W G K V N P Y A R K V Q W H S V H A P G R
26496 acgtgtcaagcgtgtatcgatttagatggtgaagtatttcctatcgaagaatgtcctttcgaccatcctaatggaatgtgctac
169 T C Q A C I D L D G E V F P I E E C P F D H P N G M C Y
26580 caaactgtatggtacgaaaactcactcgaagaaatcgctgatgagttgagaggctgggtagacggagaacctaatgatgtatta
197 Q T V W Y E N S L E E I A D E L R G W V D G E P N D V L
26664 gacgaatggtacgacgatttaagttcaggaaaagttgagaaatacagcgacctcgactttgttaaaagttattag 26738
225 D E W Y D D L S S G K V E K Y S D L D F V K S Y *

dp1ORF025

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1 M A K N K K R K K V N V K R K M L I P T N L S K K V N V

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18694      aaagcaatcgcttatagaaaagtcactgttaagtggctgcctaatacagatgaaattcaagtatatttcgacctttatataaat
29         K  A  I  A  Y  R  K  V  T  V  K  W  L  P  N  T  D  E  I  Q  V  Y  F  D  L  Y  I  N
18610      aaaaacaggctgacaatgttaggcactattgacccggacaagagctatttgaaggaattaggattgtttgtaagaaacctcag
57         K  N  R  L  T  M  L  G  T  I  D  P  D  K  S  Y  F  E  G  I  R  I  V  C  K  K  P  Q
18526      ccttggatgactgttaaggagctccaggttgcgcgtgcagacgccccaggtttttttgcagttcttaaagcctattgtcacacg
85         P  W  M  T  V  K  E  L  Q  V  A  R  A  D  A  P  G  F  F  A  V  L  K  A  Y  C  H  T
18442      gttggcgatgtactagatagcggagcagagcctactgaaattgttcaaggtattatgtataaagacggtgaactatttaaggac
113        V  G  D  V  L  D  S  G  A  E  P  T  E  I  V  Q  G  I  M  Y  K  D  G  E  L  F  K  D
18358      agtgaaattgtcagccttttcaaatacgatgtcaaagagccttatgagtttccaaaggaccttcctataaccttggacaacttt
141        S  E  I  V  S  L  F  K  Y  D  V  K  E  P  Y  E  F  P  K  D  L  P  I  T  L  D  N  F
18274      ttagagttcattatgtctagccagcatactagagcacttgttttgcgttgtgctaatataggtgagttttccaagaattggcgg
169        L  E  F  I  M  S  S  Q  H  T  R  A  L  V  L  R  C  A  N  I  G  E  F  S  K  N  W  R
18190      aaatggcaaaaagctatccagctcctgctcgactatgccaaggcggatgactttaaagtagacgaaactgtttgggacttttca
197        K  W  Q  K  A  I  Q  L  L  L  D  Y  A  K  A  D  D  F  K  V  D  E  T  V  W  D  F  S
18106      cccggctctaaagctggaaaggtagcacgtcgtaaaggctatgaggcaattcaacaagcccttgagcagataaataaataa
18026
225        P  G  S  K  A  G  K  V  A  R  R  K  G  Y  E  A  I  Q  Q  A  L  E  Q  I  N  K  *
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1          M  A  K  A  T  G  P  K  V  R  R  G  K  T  P  P  R  P  K  D  K  K  G  I  K  A  N  A
21596      cgtgtcaataaagaccagttcgtagagtatgactataaaggcatcaagatgacaattaaggaacgtgatgctagaatgaaattg
29         R  V  N  K  D  Q  F  V  E  Y  D  Y  K  G  I  K  M  T  I  K  E  R  D  A  R  M  K  L
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57         E  F  I  R  G  M  T  I  Q  E  I  A  A  R  Y  G  L  N  E  K  R  V  G  E  I  R  A  R
21764      gataaatgggtgaaggctaagaaagagttcgagaatgaaaaggctcttgttactaatgatacattgactcaaatgtatgcaggg
85         D  K  W  V  K  A  K  K  E  F  E  N  E  K  A  L  V  T  N  D  T  L  T  Q  M  Y  A  G
21848      tttaaagtctcagtcaatattaaatatcacgccgcctgggagaaactaatgaacatcgtcgaaatgtgtttagataatcctgac
113        F  K  V  S  V  N  I  K  Y  H  A  A  W  E  K  L  M  N  I  V  E  M  C  L  D  N  P  D
21932      agatatttatttactaaagaaggaaatattagatggggcgcattagatgtcctttcgaaccttatagatagagctcaaaaagga
141        R  Y  L  F  T  K  E  G  N  I  R  W  G  A  L  D  V  L  S  N  L  I  D  R  A  Q  K  G
22016      caagaaagagcgaatggaatgcttccggaagaggttcgatatagactacaaattgagcgcgagaaaattacattgctccgggcc
169        Q  E  R  A  N  G  M  L  P  E  E  V  R  Y  R  L  Q  I  E  R  E  K  I  T  L  L  R  A
22100      aaaatgggcgaccaggaaattgaaggcgaggttaaagataacttcgtagaagcactagataaagcagctcaagccgtttggcaa
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225        E  F  S  D  A  T  G  S  Y  I  K  G  V  T  D  N  D  N  K  P  E  K  *
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1          M  G  K  V  S  I  Q  K  S  G  T  F  S  S  G  S  N  N  E  F  F  T  L  A  D  H  G  D
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29         S  A  I  V  T  L  L  Y  D  D  P  E  G  E  D  M  D  Y  F  V  V  H  E  A  D  V  D  G
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57         R  R  R  Y  I  N  C  N  A  I  G  E  D  G  E  T  V  H  P  D  N  C  P  L  C  Q  N  G
53014      ttccctcgtattgaaaaactatttcttcaactttacaaccatgatacgggaaaagttgaaacatgggaccgaggccgttcttat
85         F  P  R  I  E  K  L  F  L  Q  L  Y  N  H  D  T  G  K  V  E  T  W  D  R  G  R  S  Y

53098      gttcaaaagattgttacatttatcaataaatatggaagccttgtgactcagccttttgaaattattcgttcaggagctaaaggt
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53182      gaccaacgaactacttatgaattccttccagagcgtccggaagacagtgctactcttgaagattttccagaaaagagcgaactt
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169        L  G  T  L  I  L  D  L  D  E  D  Q  M  F  D  V  V  D  G  K  F  T  L  Q  E  E  R  S
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225        E  R  T  P  S  V  S  R  R  T  P  P  T  R  G  R  G  F  *
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57         W  Y  T  M  E  D  E  T  E  P  K  K  E  E  A  A  K  P  A  K  K  A  A  P  A  V  A  R
44847      cctgctcgaaaaggtagagtcgttcccaaacctaaaaaagaagtccttgaggaagaaattcctgaagttaaggaacagccggaa
85         P  A  R  K  G  R  V  V  P  K  P  K  K  E  V  L  E  E  E  I  P  E  V  K  E  Q  P  E
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113        E  V  G  S  V  S  E  K  S  T  V  R  K  P  A  P  K  K  E  S  V  M  A  I  T  K  A  L
45015      gaaagtcgaattgttgaagcctttcctgcgtctactcgaatcgtcactcagtcttacatcgcctatcgctctaagaagaacttc
141        E  S  R  I  V  E  A  F  P  A  S  T  R  I  V  T  Q  S  Y  I  A  Y  R  S  K  K  N  F
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169        V  T  I  E  E  T  R  K  G  V  S  I  G  V  R  A  K  G  L  T  E  D  Q  K  K  L  L  A
45183      tctattgctcctgcatcttacgaatgggcgattgacggaattttaaactcgtcaaggaagaagatattgacaccgcaatggaa
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45267      ttgattgaagcttctcacctttcttcgctatga 45299
225        L  I  E  A  S  H  L  S  S  L  *
dp1ORF029
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662    atgaaatcagtagttttattatccggcggagtcgactcagccacttgtttagcaattgaagttgacaagtggggttctaaaaat
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746    gttcatgctatagcattcaattacggacaaaagcatgaagcagaacttgaaaatgctgctaatgttgcaatgttctacggagtc
29     V  H  A  I  A  F  N  Y  G  Q  K  H  E  A  E  L  E  N  A  A  N  V  A  M  F  Y  G  V
830    aagttcaccattcttgaaattgactcgaaaatctactcaagctctagctcttccttattacaaggaaaaggcgaaatttcacat
57     K  F  T  I  L  E  I  D  S  K  I  Y  S  S  S  S  S  S  L  L  Q  G  K  G  E  I  S  H
914    ggaaaatcttacgctgaaatcctagcagagaaggaagtagttgacacctatgttccatttagaaatggactaatgctttcacag
85     G  K  S  Y  A  E  I  L  A  E  K  E  V  V  D  T  Y  V  P  F  R  N  G  L  M  L  S  Q
998    gctgcggcttatgcttattcggttggagcttcttacgtcgtatatggtgctcacgcagacgatgcggctggaggtgcttaccct
113    A  A  A  Y  A  Y  S  V  G  A  S  Y  V  V  Y  G  A  H  A  D  D  A  A  G  G  A  Y  P
1082   gattgcactcctgagttctataattcaatgtcaaatgcaatggaatatggaactggaggcaaggtaacccttgtcgctcctcta
141    D  C  T  P  E  F  Y  N  S  M  S  N  A  M  E  Y  G  T  G  G  K  V  T  L  V  A  P  L
1166   cttactctaaccaaggcgcaagtcgttaaatggggaattgatttagatgttccttatttcttgactcgttcatgttatgaaagt
169    L  T  L  T  K  A  Q  V  V  K  W  G  I  D  L  D  V  P  Y  F  L  T  R  S  C  Y  E  S
1250   gacgctgaaagttgtggaacttgcgcaacttgtatcgaccgcaaaaaggcattcgaagaaaatggaatgactgaccctattcat
197    D  A  E  S  C  G  T  C  A  T  C  I  D  R  K  K  A  F  E  E  N  G  M  T  D  P  I  H
1334   tataaggagaattga 1348
225    Y  K  E  N  *
dp1ORF030
20088  atgaataacgaaaaaattattgaaaaattaaaatcttattcaattagcaaatgacaacccgagtgacgaagaggggcaaact
1      M  N  N  E  K  I  I  E  K  I  K  N  L  I  Q  L  A  N  D  N  P  S  D  E  E  G  Q  T
20004  gcccttcttatggctcaaaagttgatgctaaagaataatatcgcacttgctcaagttgaacaatttgatgaacctaaacagttc
29     A  L  L  M  A  Q  K  L  M  L  K  N  N  I  A  L  A  Q  V  E  Q  F  D  E  P  K  Q  F
19920  gagacttctcaagctgttgggaaagaagcaggtcgaatatttggtgggaacgtgaacttggtcatattctcgcgactaatttt
57     E  T  S  Q  A  V  G  K  E  A  G  R  I  F  W  W  E  R  E  L  G  H  I  L  A  T  N  F
19836  aggtgcttttgtattaatcagcgtgatatgcgcttgaataaaagtcgaataattttcttcggcgaaaaacaagacgctgaatta
85     R  C  F  C  I  N  Q  R  D  M  R  L  N  K  S  R  I  I  F  F  G  E  K  Q  D  A  E  L
19752  gtgtctaaaatatatgaggctgctttgctttatcttcgttaccgtattgaccgacttcctactcgcgaaccttcctacaagaat
113    V  S  K  I  Y  E  A  A  L  L  Y  L  R  Y  R  I  D  R  L  P  T  R  E  P  S  Y  K  N
19668  tcatacctcaaaggcttttgtcagccttagccattcgatttaaaaagcaggtggaagaatattcacttatggtcctacctagc
141    S  Y  L  K  G  F  L  S  A  L  A  I  R  F  K  K  Q  V  E  E  Y  S  L  M  V  L  P  S
19584  gagcaaacaaaaaatgcgcttcaggacacatttcgaaatttaaagaaggaaggaattgacagacctcaacatgacttcaatctt
169    E  Q  T  K  N  A  L  Q  D  T  F  R  N  L  K  K  E  G  I  D  R  P  Q  H  D  F  N  L
19500  gaagcgtatattgaagggcggtttcatggcgagaatgcaaagattatgcccgatgaaatttggaaggcggtaactaa 19423
197    E  A  Y  I  E  G  R  F  H  G  E  N  A  K  I  M  P  D  E  I  L  E  G  G  N  *


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26943  atggcttatcaattagaagacttgttaaaaggtctagatgaaccaactatcaaacaggtgaaggaaattatttcgaaaacttcg
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27027  aaagaactcgatgctaaaattttcattgacggcgacggtcaacatttgtacctcacgcacgtttcgatgaagttgttcaacag
29     K  E  L  D  A  K  I  F  I  D  G  D  G  Q  H  F  V  P  H  A  R  F  D  E  V  V  Q  Q
27111  cgcgatgcagctaacggctcaattaattcttataaagaacaagtcgcgacgctttctaaacaggtcaaagataacggtgatgcg
57     R  D  A  A  N  G  S  I  N  S  Y  K  E  Q  V  A  T  L  S  K  Q  V  K  D  N  G  D  A
27195  cagaccactatccaaaaccttcaagagcaactcgacaagcagtctcaacttgcaaaaggcgctgtgattacttcagctcttcat
85     Q  T  T  I  Q  N  L  Q  E  Q  L  D  K  Q  S  Q  L  A  K  G  A  V  I  T  S  A  L  H
27279  ccgttgattagtgactccattgctccagcagcagacattcttggatttatgaaccttgacaacattacggtcgaaagtgacggt
113    P  L  I  S  D  S  I  A  P  A  A  D  I  L  G  F  M  N  L  D  N  I  T  V  E  S  D  G
27363  aaagttaaaggtcttgatgaagagttgaaagctgttcgtgagtctcgtaaatacttattcaaagaagtcgaagttcccgcagaa
141    K  V  K  G  L  D  E  E  L  K  A  V  R  E  S  R  K  Y  L  F  K  E  V  E  V  P  A  E
27447  caagaggctcaagctaagtcgccagccgggactggaaatttaggaaatccaggtcgtgtcggtggtggtgttcccgaacctcgt
169    Q  E  A  Q  A  K  S  P  A  G  T  G  N  L  G  N  P  G  R  V  G  G  G  V  P  E  P  R
27531  gaaatcggctcttttggtaagcaacttgctgctgctcaacaaacggcaggagcacaagaacaatcatcattctttaaataa
27611
197    E  I  G  S  F  G  K  Q  L  A  A  A  Q  Q  T  A  G  A  Q  E  Q  S  S  F  F  K  *
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52033  atgaaagaagcgaatagactagtttctagctatgtaggattcgaatgctggactgacgaagaatgtatcaggaactttgaacta
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52117  gaccctgatatgtcaattgcgtctgcttatcatcgttatttgggatgctttattcctatgcaaaaaggtttaaatgcttatct
29     D  P  D  M  S  I  A  S  A  Y  H  R  Y  F  G  M  L  Y  S  Y  A  K  R  F  K  C  L  S
52201  cgacatgacattgaaagcattgcattcgagactatttcaaaatgtttggcaacgttcaaatcaaaccaaggggccaagttttca
57     R  H  D  I  E  S  I  A  F  E  T  I  S  K  C  L  A  T  F  K  S  N  Q  G  A  K  F  S
52285  acttaccttacaagactcttcaagaatagaatagtcttagaatataggtacctaaatgcaccttccatgaatcgaaattggtat
85     T  Y  L  T  R  L  F  K  N  R  I  V  L  E  Y  R  Y  L  N  A  P  S  M  N  R  N  W  Y
52369  gtagaagtgacgttcgatagcgtttcgacaaatgaagaaggcgacgatttagtatcctatcgacagttggctattgtgaagac
113    V  E  V  T  F  D  S  V  S  T  N  E  E  G  D  D  F  S  I  L  S  T  V  G  Y  C  E  D
52453  tacggaaaaattgaaattgaagcaagtcttgacttcatgacgctttctaatacagagtatgcttatatctcgtctgtcattcaa
141    Y  G  K  I  E  I  E  A  S  L  D  F  M  T  L  S  N  T  E  Y  A  Y  I  S  S  V  I  Q
52537  aacggtccttcagtaagcgacgcagaaattgcgcgtgaaattggagtaagcaggtctgctattagtcagtctaagaagtcacta
169    N  G  P  S  V  S  D  A  E  I  A  R  E  I  G  V  S  R  S  A  I  S  Q  S  K  K  S  L
52621  aaaaataaattaaaagatttatataa 52647
197    K  N  K  L  K  D  F  I  *
dp1ORF033
7670   atggcaagacctaagttacctcaaattgatattcgagaagaagaaatacgagatgctcaagacgtagcagactcgtatggtgcg
1      M  A  R  P  K  L  P  Q  I  D  I  R  E  E  E  I  R  D  A  Q  D  V  A  D  S  Y  G  A
7754   attatcaataaagtagtcgacgaaattgttgaagcagcttgcggttcacttgaccaggcaatggaagaaattcaaatagttgta
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29 I I N K V V D E I V E A A C G S L D Q A M E E I Q I V V
7838 agccaaaatcctgtcattatggaagaccttaactactacattggctatcttcccactcttctttatttcgccgcagatagggcg
57 S Q N P V I M E D L N Y Y I G Y L P T L L Y F A A D R A
7922 gaaatggtgggaatacaaatggattcaagttctgctatcaggaaagaaaaatacgataatctatacatttagccgccgggaaa
85 E M V G I Q M D S S S A I R K E K Y D N L Y I L A A G K
8006 actattcctgacaagcaagcagaaactcgaaaacttgtcatgaatgaagaagtcatcgaaaatgcttacaagcgagcctacaag
113 T I P D K Q A E T R K L V M N E E V I E N A Y K R A Y K
8090 aaagttcaattaaagctagaacaggccgataaggtattagcatctttaaaacgaattcaaacctggcaactagcagagttagaa
141 K V Q L K L E Q A D K V L A S L K R I Q T W Q L A E L E
8174 actcagtcaaataattcaaaaggagtattattaaatgcaaaaagacgtagacgtgaaaatgattga 8239
169 T Q S N N S K G V L L N A K R R R R E N D *

dp1ORF034
131 atgagtcaaaacactacacgcactgacgctgaattgacaggcgttactcttttaggaaaccaagacaccaaatacgattatgac
1 M S Q N T T R T D A E L T G V T L L G N Q D T K Y D Y D
215 tataatccagacgtccttgaaacttttccctaacaaacatcctgaaaataattacctagtaacatttgacggatatgaattcact
29 Y N P D V L E T F P N K H P E N N Y L V T F D G Y E F T
299 tccctttgccctaaaacaggacagcctgacttcgcgaatgttttcattagttacattccaaacgaaaagatggttgaatctaaa
57 S L C P K T G Q P D F A N V F I S Y I P N E K M V E S K
383 tcattgaaattgtacttattcagtttccgtaaccacggtgacttccacgaagattgcatgaacattatttgaatgacttgtat
85 S L K L Y L F S F R N H G D F H E D C M N I I L N D L Y
467 gaattgatggaacctaagtacattgaagtcatgggcctattcactcctcgtggtggaatttcaatttacccattcgtcaacaaa
113 E L M E P K Y I E V M G L F T P R G G I S I Y P F V N K
551 gtgaatcctcaatttgcaactcctgaacttgaacagcttcaacttcaacgcaaattgaacttccttggaaatgttcaaggtctt
141 V N P Q F A T P E L E Q L Q L Q R K L N F L G N V Q G L
635 ggacgagctattcgatag 652
169 G R A I R *

dp1ORF035
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1 M H L M K D S K M L R T W K S L A F E F E T K V R T T S
17341 gggttgaagttatcgcctgctatgaaaacgatgacgaggacgaagatttggaagggttataaaatgaaggtatttatcaacaat
29 G L K L S P A M K T M T R T K I W K G Y K M K V F I N N
17257 catactgaagctgatattgactacaaagatattctaaatttgtagcttatcgaaactctcctaaccctcaaattcaaatcact
57 H T E A D I D Y K D I L N F V A Y R N S P N P Q I Q I T
17173 agctggaacgctttgctttcctgctatacacggaatgagctttcttataaaggagtttcaataacggactttttgaagccatt
85 S W N A L L S C Y T R N E L S Y K G V S I T D F F E A I
17089 caaactattgcaagttccttcactcacctagactcgaaaacaattgatacacaaaatgaaaagcgactcgaaaggattgaggaa
113 Q T I A S S F T H L D S K T I D T Q N E K R L E R I E E
17005 cttcagtcaagaataggtcattgtaactgtactatcgacgaacttaaaaaaggagtccacgaaatgccggatattgaatcagct
141 L Q S R I G H C N C T I D E L K K G V H E M P D I E S A
16921 atttcttaccagtacggacagattcttgcttatgaagatgaacttaatttctgctaaactaa 16859
169 I S Y Q Y G Q I L A Y E D E L N F L L N *

dp1ORF036
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1 V L V E R K A D K E C W E W L E A V R A N I V E E V R N
48892 ggtcttagcattgttattgcttcgaatactgtcgggaatgggaaaactagctgggcggttcgacttttgcaacgctatttagca
29 G L S I V I A S N T V G N G K T S W A V R L L Q R Y L A
48976 gaaactgcacttgacggaagaattgttgagaaaggaatgtttgtagtgtcagctcaactattgactgagttcggcgactataat
57 E T A L D G R I V E K G M F V V S A Q L L T E F G D Y N
49060 tattttcaaaccatgcaagaatttctcgaacgtttcgagcgccttaagacttgtgagctattagtcatagacgaaataggtgga
85 Y F Q T M Q E F L E R F E R L K T C E L L V I D E I G G
49144 ggttccttaaccaaggcctcttatccttatctgtatgacttggttaattatagggttgacaataacttgtcgactatttatacg
113 G S L T K A S Y P Y L Y D L V N Y R V D N N L S T I Y T
49228 actaattatactgacgatgaaattattgaccttttaggccaaaggctttatagtcgtatatatgatacttcagtggttctagat
141 T N Y T D D E I I D L L G Q R L Y S R I Y D T S V V L D
49312 tttcaggcaagcaatgtaagaggattggaggtaagcgaaattgaatcatag 49362
169 F Q A S N V R G L E V S E I E S *

dp1ORF037
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1 M V K K L K S K I Y S V A Y I I L V V I A N L V T I Y F
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29 E P L N V K G I L I P P S S W F M G F T F L L I N L I S
56023 aagtacgagaagccaaaatttgcaggttctttgatatgggtagggttattccttacctcgttgatttgctttatgcaaaaccta
57 K Y E K P K F A G S L I W V G L F L T S L I C F M Q N L
56107 ccacaatcgcttgtcgtggcttcaggagttgcattttggataagtcaaaaagcaagtgtctttatattcgacaagctctcgaat
85 P Q S L V V A S G V A F W I S Q K A S V F I F D K L S N
56191 aaattagactcgaagattgcaaatgctttgtctagcaacatcggttctattatagacgcaaccatatggatttcattaggactg
113 K L D S K I A N A L S S N I G S I I D A T I W I S L G L
56275 agtcctcttggaattggaacggttgcatatatagatattccgtcagccgtactaggccaagttctagttcagtttatcttgcag
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56359 tcaattgcttcgagatatttgaaaaagtag 56388
169 S I A S R Y L K K *

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29 T Y K V E I S L A G G T Y D H G S S Q G M V V D F Y H V

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57 K K I A G T F I D R L D H A V L L Q G N E P I A L A N A
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1686 atgtggaagcatgctcgtatcgactctatcaaactatgggaaactcctacaggttgcgcagaatgtacttactacgagatttc
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1770 acagaagacgagattgaaatgttcaagaacgtaacctttatcgacaaagacgaaaagattactgtccgcgaaattttagagcag
141 T E D E I E M F K N V T F I D K D E K I T V R E I L E Q
1854 gagcaggataatggttaa 1871
169 E Q D N G *

dp1ORF039
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1 M N K S A T F W L V R T A L I A A L Y V T L T V A F S A
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29 I S Y G P I Q F R V S E A L I L L P L W N H R W T P G I
3474 gtattaggaacaattattgcaaacttcttttcacctcttggactgattgacgttttattcggttcacttgctaccttccttgga
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85 V V A M V K V A K M A S P L Y S L I C P V L A N A Y L I
3642 gcgctggaacttcgaatagtttactctttaccttttgggaatctgtcatctatgtaggaattagtgaagcgattatcgtttta
113 A L E L R I V Y S L P F W E S V I Y V G I S E A I I V L
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141 I S Y F L I S T L A K N N H F R T L I G A K N G I *

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29 Y D T T N G F R G V A N P C D Y I A A T N F G T L F I E
7360 ctgaaaactactaaagaagcttctttgagctttaataacatcactgataatcaatggttccagctatcacgcgcagatggatgc
57 L K T T K E A S L S F N N I T D N Q W F Q L S R A D G C
7444 aaatttattctcgccggaatttagtgtatttccaaaagcatgaaaagattatatggtatccaatttcaagccttgaaaaaatt
85 K F I L A G I L V Y F Q K H E K I I W Y P I S S L E K I
7528 aaacggtctggagttaaaagcgtcaacccaaacttcatcgatgcagggtatgaagtttcttacaagaagcgtcgaactagattg
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7612 accattcctttccaaaatgttctagatgcagttgagcttcattacaaggagaaaagcaatggcaagacctaa 7683
141 T I P F Q N V L D A V E L H Y K E K S N G K T *

dp1ORF041
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1 M Q K D V D V K M I D P K L D R L K Y T G D W V D V R I
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29 S S I T K I D A D S A D V S R C R K V L Q K A Q V Y S V
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57 A A G E C I K I A H G F A L E L P K G Y E A I L H P R S
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85 S L F K K T G L I F V S S G V I D E G Y K G D T D E W F
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113 S V W Y A T R D A D I F Y D Q R I A Q F R I Q E K Q P A
8628 atcaagttcaatttcgtagaatctttaggaaatgcggctcgtggaggccatggaagtacaggtgatttctaa 8699
141 I K F N F V E S L G N A A R G G H G S T G D F *

dp1ORF042
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29 T L F K K D V A T G L S K V E H D Y F Q I V E A L N G K
48250 caattcgaacctaatatgaagcaggtgtcatctttctttatagttcagtatgaatttattttcaatattaagtgcatcgattat
57 Q F E P N M K Q V S S F F I V Q Y E F I F N I K C I D Y
48334 aactggttcaacttttcgagcactatgaaaaatgttcgaacttatttaaacattgagtcgaacattgaactttgtcgattttta
85 N W F N F S S T M K N V R T Y L N I E S N I E L C R F L
48418 gctgaaagttttgttaaatatgaaaatgttcgaaaaagattgaacctaagcgaaaggttcataacggtctcgactttcaaaaga
113 A E S F V K Y E N V R K R L N L S E R F I T V S T F K R
48502 gcctggatttttggacgaactcgaaggaaaaacgggttcaaaattcgaaggattttattag 48561
141 A W I L D E L E G K T G S K F E G F Y *

dp1ORF043
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31783 cctatccatgttaaaattcgagcagcaggtgtcatgaacctaatcgctaacgggaaaatccctaatacgcttttaggtaaagtg
29 P I H V K I R A A G V M N L I A N G K I P N T L L G K V
31867 acagaactgtttggagaaacttcgacagtcactaaagacaatgctagtctagcatcaattactgaccaacagaagaaagaagcg
57 T E L F G E T S T V T K D N A S L A S I T D Q Q K K E A
31951 ctcgaccgattgaacaaaaccgataccggtattcaagacatggctgaacttcttcgagtattcgcagaagcttcaatggtagag
85 L D R L N K T D T G I Q D M A E L L R V F A E A S M V E
32035 cctacttacgctgaagtcggcgagtatatgacagatgagcaacttatgacaatcttcagtgcaatgtacggtgaagtgactcaa
113 P T Y A E V G E Y M T D E Q L M T I F S A M Y G E V T Q
32119 gctgaaacctttcgtacagacgaaggaaatgtctaa 32154
141 A E T F R T D E G N V *

dp1ORF044
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25582 gttttcaatttccttgtttcctacataagtggtgaaccgataatggcacttaggacattcgaagaatctccactctacgccctt
29 V F N F L V S Y I S G E P I M A L R T F E E S P L Y A L
25498 ttcgatatgtttcgaaataatctgtttagatgtaaggtcgaacttatgctcacaatggtcacaattaaccttgaacgtctgggt
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25414 cgactccttcttcggttggttgttcagtttgttctttttctttgtcatcaacttcgtcttcttcactcgtttcatcttgaggct
85 R L L L R L V V Q F V L F L C H Q L R L L H S F H L E A
25330 cctcttgttcgtttaattcgtttgctaatacaggcaatgctccagctgagatttcgtcaagctgagcaagttcttccaaaatgc
113 P L V R L I R L L I Q A M L Q L R F R Q A E Q V L P K C
25246 gttcccattccttgtccgccttttccttcttactga 25211
141 V P I P C P P F P S Y *
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1 M K R V K K T K L M T K K K N K L N N Q P K K E S T Q T
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29 F K V N C D H C E H K F D L T S K Q I I S K H I E K G V
25508 gagtggagattcttcgaatgtcctaagtgccattatcggttcaccacttatgtaggaaacaaggaaattgaaaaccttattcga
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25592 tttagaaatacttgtcgagctaaaatgaagcaggaacttcaaaaaggagctgctgctaatcaaaacacttaccattcatatcga
85 F R N T C R A K M K Q E L Q K G A A A N Q N T Y H S Y R
25676 attcaggatgagcaagctgggcataaaatctcagggcttatggcgaagctaaagaaggagataaacattgaaaaacgagaaaaa
113 I Q D E Q A G H K I S G L M A K L K K E I N I E K R E K
25760 gaatgggtatctatatag 25777
141 E W V S I *
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29 L F E W K S N K A K S V L E D I S T T L S T L K Q Q V D
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57 G I D Q T T V A I N H Q N D V I Q D G T R K I Q R Y R L
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85 Y H D L K R E V I T G Y T T L D H F R E L S I L F E S Y
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113 K N L G G N G E V E A L Y E K Y K K L P I R E E D L D E
43194 actatctaa 43202
141 T I *
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85 E E M C E K L S G L I E Y K P V I N T K L L E D M I Y H
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47961
113 G E I D Q E A I L P A V V I S V T E G I R F G K A K I *
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29 P V K E T E K Q Y K V T G I N P N L Y L D L G S V I R K
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57 S E L D I A V F K A C P V A E T G V T L T R D M E V D A
16457 agaattgaaatcatcaagaaattaactacaagaatcgaacgccttaacgaaagaattaaagcaagaaatgaacaaggtaaacaa
85 R I E I I K K L T T R I E R L N E R I K A R N E Q G K Q
16373 gaaagccgccacctagtatctgcgctagaagattgcgctcgtcaaattgctggaatttatcaataa 16308
113 E S R H L V S A L E D C A R Q I A G I Y Q *
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85 S V V G V V A V N D V I T V N E H P C M T S S A C A S T
43682 tttgcgtccccagatgaagatgtcgcctcgtttagcatcccacggagcattttcactaattag 43620
113 F A S P D E D V A S F S I P R S I F T N *
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1 M N N Q R K Q M N K R I V E L R E D Y Q R A R G R I N F

15165 cttcttgctgtaaaggaccacggcgaagaactcgaaaaccttgaagcctttgtgggatacattgacaatctagtcgaatgtttt
29 L L A V K D H G E E L E N L E A F V G Y I D N L V E C F
15249 cctgaaagccaacgaaatgtcttgaggctatgtgtattagatgaccttccagtcactaatgcggccgctgaaattggataccac
57 P E S Q R N V L R L C V L D D L P V T N A A A E I G Y H
15333 tatacatgggttcaccaacttcgagacaaagcagttgaaacacttgaagaaatttagatggggataacattattcgctctaaa
85 Y T W V H Q L R D K A V E T L E E I L D G D N I I R S K
15417 cacggaatcgaaattaaggagaaacttgatgaattatatggtaaaagtcattctagttag 15476
113 H G I E I K E K L D E L Y G K S H S S *

dp1ORF051
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29 S W V S D G Y G G K K K D K A N E V V A D D L V C L V D
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57 N S T V P D L L A N S T D A G K I F A Q N G V K I F I L
30017 tatgatgaaggcaaaatcattcaacgagccgatactatcgaaattaaaaactcaggaagacggtacagggtagtagaaacccac
85 Y D E G K I I Q R A D T I E I K N S G R R Y R V V E T H
30101 aatcttctcgagcaagacatttgatagaacttaaattggaggtgaacgactaa 30154
113 N L L E Q D I L I E L K L E V N D *

dp1ORF052
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29 V E F D E Q D T D R P D D Y I V L R Y S H R M P S A T N
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30768 gttcgaaacattatcaaggacatgggctacgaagtaacctatgcagaaactggtgactacttcgacacaatgctttctagatac
85 V R N I I K D M G Y E V T Y A E T G D Y F D T M L S R Y
30852 cgactagaaatcgaatatagaattccacaaggaggaaactaa 30893
113 R L E I E Y R I P Q G G N *

dp1ORF053
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29 P F F Q A V A S I L S I V H D L P C P G R A I M T I K S
50132 tcaccaggaagtaagcctccaagcacgtcgtccaatagttcaaaccctgtcgatattccaagtctttcaccgtcatggtttcta
57 S P G S K P P S T S S N S S N P V D I P S L S P S W F L
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113 S S F G I I F A I A M L L S T *

dp1ORF054
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29 Y K E I R D T A A A I S N R A V E K K D R D S L L V A T
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57 V M A L P V S H A E D L G K R L C I A N S R L E A F R E
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85 A V Q E A L E N E K A E D L K D V I L G L I D V D K K I
14759 ggcaaccttgcattgcaattagttgaatcaggagcattataa 14800
113 G N L A L Q L V E S G A L *

dp1ORF055
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29 A A Q I P A T A A T Q V G N K K Y I L A G T C V K N A T
27795 acatttgaaggacgcaaaactggactcgaagtagtatctaccggtgaacaattcgacggagttatcttcgctgaccaagaagtg
57 T F E G R K T G L E V V S T G E Q F D G V I F A D Q E V
27879 tttgaaggtgaagaaaaagtaaccgtgacagtattagttcacggattcgtcaaatatgcagcccttcgaaaagttggcgatgct
85 F E G E E K V T V T V L V H G F V K Y A A L R K V G D A
27963 gtgcctgaatctaaaaacgcaatgattcttgtcgttaaatag 28004
113 V P E S K N A M I L V V K *

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29 V P G T P Y R L Q V W V K M S L V K I E T R A G N G Y Y

18983 aaaaggctagtatgccaagacgatttgtattttatggtaaggagtcaatagatggttacttaattgacgccaccataactggc
57 K R L V C Q D D F V F Y G K E S I D G Y L I D A T I T G
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85 K S L A E Y C E P M N R H I L E T I A S R E A A E L N R
18815 gctaaaaagcaagaccaacagaaatggagatactag 18780
113 A K K Q D Q Q K W R Y *

dp1ORF057

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113 A E R L L R K *
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29 K V Q P N S G A T D Y Y K G D V V T D S M L I E C K T V
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15885 tctgctatcgctttcgactttggtgacggaggcgaacagtatatagcaatgtctataagtcagttcaagcgaatattagaggat
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15969 agaaatgataaccttatttaa 15989
113 R N D N L I *
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29 I T V C E V A A T K M E E Y A K T H A I W T D R T G N A
30322 cgacagaaactcaaaggagaagctgcttgggtaagcgcagaccaaatcatgatagctgtatcacatcacatggactacgggttt
57 R Q K L K G E A A W V S A D Q I M I A V S H H M D Y G F
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30490 agaaggttattagactag 30507
113 R R L L D *
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37734 tttgaaaggtcgtcgtag 37717
113 F E R S S *
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57 G N L V I E L E L D S L D D L I A L S N V V G T G L K L
19223 tcacggccttatagagaagataagcctttttcaattatggattgttgacgggtacatggaataa 19161
85 S R P Y R E D K P F Q L W I V D G Y M E *
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44948 actaactga 44940
113 T N *
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85 Y T R T L V G K T E R E A I Q E D A K A F K R E H G L E
47536 aattaa 47541
113 N *
dp1ORF064

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29 L A S S L I E R N F A F E I K A A E D G E T V E T V P Q
29276 acaattgaatcagttgaagaaattgacgaagttgaacaaatgcgcgaagagtatgcggctaaaaccgttcctgagctcgttgaa
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29360 ttagcaagagctaatggaattgacatttcttcaatttctcgaaaaagcgaatatatcgacgctttaattaagtacgaactagga
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29444 gagtaa 29449
113 E *

dp1ORF065
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1 M Q F V I T Y I K H L D E L V R Q F P F I H I R M N K P
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29 V F I K F L F R N D F M L D F F S S P I S S K R F R A D
51329 gccttgcctaactacttcgctagatgttccaaaattccttttcagccactggtttccatagaaccctccatcgtttcgacctaa
51246
57 A L P N Y F A R C S K I P F Q P L V S I E P S I V S T *

dp1ORF066
28898 gtgaccaactgcgtcaggtggaagcaataccactttaccgtcgtcaatcaagttgaactgacgaatgttaccaacgtcaggaag
1 V T N C V R W K Q Y H F T V V N Q V E L T N V T N V R K
28814 tttgtcagcgtcagcgaactgagcaatttcttagagtagacagcgatttgaagacctgtttttcagcgatgaatttctcagc
29 F V S V S E L S N F L R V D S D L K T C F F S D E F L S
28730 gtcacttgcaagaagcaagaagttttcccaagaaccttgaacaccaattgcaagagctttcttgatagagtcactcttagtcat
57 V T C K K Q E V F P R T L N T N C K S F L D R V T L S H
28646 ttggttataagtgtttcggttcaagaccattcgagtagggcgaacacctgtacgatttcgatgtcatccattgctgctaa
28566
85 L V I S V S V Q D H S S R A N T C T I F D V I H C C *

dp1ORF067
45061 gtgacgattcgagtagacgcaggaaaggcttcaacaattcgactttcaagagccttagtaatcgccatcacgctttctttttta
1 V T I R V D A G K A S T I R L S R A L V I A I T L S F L
44977 ggagcaggttttcgaacagtagatttctcactaactgaaccaacttcttccggctgttccttaacttcaggaatttcttcctca
29 G A G F R T V D F S L T E P T S S G C S L T S G I S S S
44893 aggacttctttttaggtttgggaacgactctacctttcgagcaggtcgagcaactgcaggagcagccttttagcaggttta
57 R T S F L G L G T T L P F R A G R A T A G A A F L A G L
44809 gcagcttcttctttttaggttcagtttcatcttccattgtgtaccaacgttcgagagttgaagctgaaaggtga 44735
85 A A S S F L G S V S S S I V Y Q R S R V E A E R *

dp1ORF068
29451 atggcagctcaaacggacattgaattagtcaaaatcaatatcgataacgataattctccgtcaccaatgactgaccaaagtatc
1 M A A Q T D I E L V K I N I D N D N S P S P M T D Q S I
29535 tcagctcttttagacaagcataaatctgtcgcctatgttagttatatgatttgcttaatgaagacccggaatgacgtggtaacc
29 S A L L D K H K S V A Y V S Y M I C L M K T R N D V V T
29619 cttggacctatcagtctaaaggtgacgcagactactggaaacaaatggcgcaattctattatgaccaatataagcaagaacag
57 L G P I S L K G D A D Y W K Q M A Q F Y Y D Q Y K Q E Q
29703 cttgaaactgatgaaaagtcgaacgctggttcgacaatcttaatgaaaagggctgatgggacatga 29768
85 L E T D E K S N A G S T I L M K R A D G T *

dp1ORF069
20411 atgaaactttatcacgccactgatttgataatcttggtaaaattctagctgaaggattgaagccttcagctggagttatttac
1 M K L Y H A T D F D N L G K I L A E G L K P S A G V I Y
20327 ctagcagaaagttatgaaaaggctctagccttttatcgcttcgaaatgttgatactattgtcgttctcgaacttgaagtagat
29 L A E S Y E K A L A F L S L R N V D T I V V L E L E V D

20243 attgaaaaatgtactgaaagtttcgaccataatgaaaagatgttttgtagcctatttcatttcgacacttgtcgcgcttggact
57 I E K C T E S F D H N E K M F C S L F H F D T C R A W T
20159 tatgacaagacaattgaagtagacgacattgacttttcgaaagctcgaaaatatgatagaaagtga 20094
85 Y D K T I E V D D I D F S K A R K Y D R K *

dp1ORF070
15973 atgataaccttatttaaaataaacagtgaaggaacagttactccaattaaagggtcagccatgcaactgtacgcagaccttatt
1 M I T L F K I N S E G T V T P I K G S A M Q L Y A D L I
16057 cctatacaagaggacgatatacagttcgttgatataactggacttgaccctattgttcgagaaaacgtacttgagctcatttca
29 P I Q E D D I Q F V D I T G L D P I V R E N V L E L I S
16141 cggagccgtgtaggagtttcaaaatatggtacaaacctcgaccagaatgatgtcgacgatttcctacagcacgccaaagaagaa
57 R S R V G V S K Y G T N L D Q N D V D D F L Q H A K E E
16225 gcgctcgactttgctaactacctaaccaagctacaaagtcaacaaaagcaaaataaatag 16284
85 A L D F A N Y L T K L Q S Q Q K Q N K *

dp1ORF071
38904 gtgaaacaggtcctagaggagttcaaggtcttcaaggtcctcaagggcttcaaggaattcctggacctgcaggagctgacggac
1 V K Q V L E E F K V F K V L K G F K E F L D L Q E L T D
38988 gttcgcaatatactcacctcgctttctctaatagtccaaacggtgagggatttagtcatactgacagcggacgagcatacgtcg
29 V R N I L T S L S L I V Q T V R D L V I L T A D E H T S
39072 gtcagtatcaagatttcaatcccgtccattcaaaagaccctgcagcctatacatggacgaaatggaaggggaatgacggagctc
57 V S I K I S I P S I Q K T L Q P I H G R N G R G M T E L
39156 aagggatacccgggaagccaggcgcagacggtaagactaattatttccatatag 39209
85 K G Y P G S Q A Q T V R L I I S I *

dp1ORF072
51045 atgttccttcgtcttcaagttgtctcgaaagtttttcaattatttgttcaggagtcgcttcaatttgaagaccatttactttca

1 M F L R L Q V V S K V F Q L F V Q E S L Q F E D H L L S
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29 S K C F N S F P C N L T S K T S S R P R G F C F Q W R A
50877 ttcgccttttcagttccttcttcgccttcctctttgaatcctataagagtataggttccagtttcaacgtcccacatatattc
57 F A F F S S F F A F L F E S Y K S I G S S F N V P H I F
50793 gatgattttcggtcttcgccatatcggttttaacgacagatag 50749
85 D D F S V F A I S V F N D R *
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14262 gtgaacgcttgccggaagaatacgacgaagaaacttgggaacctatcactgaagcagaatacatcaagcgaacagaaaaaccta
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14346 aagcagttgcaaaacctactcgaaaaactccagcgccttctcgtcgccctcgcccttaaaagaaaggttgaaataaaatgtgtg
29 K Q L Q N L L E K L Q R L L V A L A L K R K V E I K C V
14430 aaaattgtcaaaacgaaacattcaatactagaattttcaatgaagatgaaagtggctatgtcgacgcctcattcacttacaagg
57 K I V K T K H S I L E F S M K M K V A M S T P H S L T R
14514 agattcgcgacaccgcagcagctattagcaatcgagcggtag 14555
85 R F A T P Q Q L L A I E R *
dp1ORF074
32298 gtgacgaaaagaaaaatccaggattgcaaatgcttatggagtgactattttcagtcgctcctctttttgtatatagaaaggaaa
1 V T K R K I Q D C K C L W S D Y F Q S L L F L Y I E R K
32382 ttacatggatttgggtcaattgcagcaaaaatgactttggatatctcaaacttcacaagtcaattaaatcttgctcaaagtca
29 L H G F W V N C S K N D F G Y L K L H K S I K S C S K S
32466 agcgcaacggctcgcactagagtcttcgaagtcctttcaaattggttctgctttaacaggattagggaaaggacttacgactgc
57 S A T A R T R V F E V L S N W F C F N R I R E R T Y D C
32550 ggttacccttcctcttatgggatttgcagccgcctctattaa 32591
85 G Y P S S Y G I C S R L Y *
dp1ORF075
22447 atggcaaagttttgtccgttgaattccgtcatggcccaaagggaaaatgaaagagccatcgatactgtttttcctgaacgaatg
1 M A K F C P L N S V M A Q R E N E R A I D T V F P E R M
22363 gaaccgtctgctatgacgatatcgaaagttcgaaaaggtgagccctttgtccaccatgttaggagctggagttgtttcttacta
29 E P S A M T I S K V R K G E P F V H H V R S W S C F L L
22279 aaagggacgaagttgaacttaggtagtttatttctcaggcttattgtcattatcagtcactcctttaatgtaggaacctgttgc
57 K G T K L N L G S L F L R L I V I I S H S F N V G T C C
22195 gtcactaaattcttgccaaacggcttgagctgctttatctag 22154
85 V T K F L P N G L S C F I *
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5728 gtgagagcatttcttcactcacgtcttcgagcaagtggtcgaatgtagggtactcttcatcttctgtaacaatatcaatattg
1 V R A F S S L T S S S K W S N V G Y S S S S S V T I S I L
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29 Y S P F P I T F S E D S S G T N V T V A A V V F S T S F
5560 ccaaactgctctgctttcacaatcacgtcaatttcaacatcgctgtcgataatgcatcgaaggaagtttgagccatcatacgct
57 P N C S A F T I T S I S T S L S I M H R R K F E P S Y A
5476 gtaaacatgacgcattcgccgtcaccaaaaatatgccaatag 5435
85 V N M T H S P S P K I C Q *
dp1ORF077
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1 M E R I K T L F H V I Y A N G T H L E V A A L F D T V D
14884 gattatgatgacgttatagaggacatccaggggtatattgatacccctgacctttataatcaaaggagcattagaatggcgcct
29 D Y D D V I E D I Q G Y I D T P D L Y N Q R S I R M A P
14968 tacaatcctgacatcaatggtgacgctattgctactgacattttactacgactagatgatattatctacgtcgacgcaacttgt
57 Y N P D I N G D A I A T D I L L R L D D I I Y V D A T C
15052 gaaactattaaatacgaggagcctattgcatga 15084
85 E T I K Y E E P I A *
dp1ORF078
17507 atggcaacagtaaaggaaacagtaaaatttgacggacgtcttgtaactatcttcgactacgacgatttagagtgggaaggatat
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17423 gcacctaatgaaggattcgaagatgttgaggacatggaagtccttagcattcgagttcgaaacgaaggtgaggacgacgagtgg
29 A P N E G F E D V E D M E V L S I R V R N E G E D D E W
17339 gttgaagttatcgcctgctatgaaaacgatgacgaggacgaagatttggaagggttataa 17280
57 V E V I A C Y E N D D E D E D L E G L *
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35288 atggaactgataccattgataaatcctcgaacaaggttgacccctgcgcttaccatttgtccagcgaatccagtaaccttagaa
1 M E L I P L I N P R T R L T P A L T I C P A N P V T L E
35204 acaattgaagttcccatgctgccaattttagagacagctgaaccaatcattgacccaataccactaatgaagtttcgaatcagg
29 T I E V P M L P I L E T A E P I I D P I P L M K F R I R
35120 ttcgcacctcctgaaaccatctgtcccacaaagctagcaatcttgctaactaatgatgaaagcatgtttccagctgtcgataaa
57 F A P P E T I C P T K L A I L L T N D E S M F P A V D K
35036 agtgagccgagaagtgaagcaataccttga 35007
85 S E P R S E A I P *
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42490 atgttgaaccttacaaaatcgcgccaaattgtggcagagttcactattggacaaggagctgaaaagaaacttgtcaaaacaacg
1 M L N L T K S R Q I V A E F T I G Q G A E K K L V K T T
42574 attgtgaacattgatgcaaacgcagtatcaaccgtctctgaaactcttcatgacccagacttgtatgctgcgaaccgtcgagaa
29 I V N I D A N A V S T V S E T L H D P D L Y A A N R R E
42658 cttcgagctgacgagcaaaaacttcgcgaaactcgttacgcaatcgaagatgaaattctagctgaacagtcaaagactgaaaca
57 L R A D E Q K L R E T R Y A I E D E I L A E Q S K T E T
42742 gctctaacagctgaataa 42759

85 A L T A E *
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55466 atgttcaggaacagtatcgtccatctgttggtctgcgtcaaagttaaaggggtcgaaatcttcgttcttgctagcgtcgatata
1 M F R N S I V H L L V C V K V K G V E I F V L A S V D I
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29 L E L V F R K T H I R K P S S S T G S C L N I S Q V L R
55298 ctgctgttgaacgaatatgatatagtctgccactttagggaactcggtgaagaaatcttcaataaccttattcgcttctttgac
57 L L L N E Y D I V C H F R E L G E E I F N N L I R F F D
55214 agatacattcatctgctcagcgattga 55188
85 R Y I H L L S D *
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1 V N F T F Q L Q L S N V G T Q W K M K L N L K K K K L L
44812 aacctgctaaaaggctgctcctgcagttgctcgacctgctcgaaaaggtagagtcgttcccaaacctaaaaagaagtccttg
29 N L L K R L L L Q L L D L L E K V E S F P N L K K K S L
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57 R K K F L K L R N S R K K L V Q L V R N L L F E N L L L
44980 aaaaagaaagcgtga 44994
85 K K K A *
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1 M P S G F L N P E S L N P A K V S P T Y S S T V A P L S
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29 T R S I P S T N S V C L L A I Y F S F T V L Q C Y Q T L
35806 atagagtttctttacttctattatacaatcctctcgacagtttgtcaacgtcgtcattgtttcgaactacgattgttccaatgt
57 I E F L Y F Y Y T I L S T V C Q R R H C F E L R L F Q C
35722 tga 35720
85 *
dp1ORF084
15445 atgaattatatggtaaaagtcattctagttagtgtctttgtactgtcagccttttgcatgacttgctcaatggtttatttggtt
1 M N Y M V K V I L V S V F V L S A F C M T C S M V Y L V
15529 acaggtaagcaagaggaccaccgtagtaccgtcgcccttgtatttggcgctctcgtaagctctgcggcgttctattcgacactc
29 T G K Q E D H R S T V A L V F G A L V S S A A F Y S T L

15613 tttatcctcgcctatctgccatga 15636
57 F I L A Y L P *
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10847 gtgatgactataatcaaggactttttcgagccttgtgatactgtcacgcattcctccatttgcaagtttcccaataaacgaaag
1 V M T I I K D F F E P C D T V T H S S I C K F P N K R K
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29 G V T L I T I T S S F F I F T F D N K L K L I N D V V I
10679 atcaattcgagtaaagtcaaaccgttgaactcgactgagaatagtgtcaggaatcttttgagggtcagtagtacatag 10602
57 I N S S K V K P L N S T E N S V R N L L R V S S T *
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52760 atatgggaaaagtatcaattcaaaaatcaggaacatttagctcagggtctaataacgagttttcacactcgctgaccacggtg
1 I W E K Y Q F K N Q E H L A Q G L I T S F S H S L T T V
52844 acagcgcaattgtcactctattgtatgatgacccggaaggcgaagacatggattatttcgtag 52906
29 T A Q L S L Y C M M T R K A K T W I I S *
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30036 atgatttgccttcatcatatagaatgaaaattttcactccatttgggcaaaaatttttcccgcgtcagtagaattggctaaa
1 M I L P S S Y R M K I F T P F W A K I F P A S V E L A K
29952 aggtcaggaacagttgaattatcaactaaacaaacaaggtcgtctgctacgacttcattcgctttatcctttttctttcctcca
29 R S G T V E L S T K Q T R S S A T T S F A L S F F F P P
29868 tatccatcactgacccaagagtttcgaagtaccttgattttagtaggagcggtttcaatggctctacgaacttga 29794
57 Y P S L T Q E F R S T L I L V G A V S M A L R T *
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5040 atgaaaaaagttcaaacttatcaagaatatctaaaactagttgagttcaaacgtcaactttctttaaatcttcgagaaggaaaa
1 M K K V Q T Y Q E Y L K L V E F K R Q L S L N L R E G K
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29 I G V D E A V I Q L F T F Y S F N N I E E P P F I V L K
5208 atgcaagaggctgccgtgaacgggacttatgaagcaaaactcaatatgcttaaaagatttaaaattatttag 5279
57 M Q E A A V N G T Y E A K L N M L K R F K I I *
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1 M S I M S L S I V E Y L D T K C L F N C A S V I F S N S
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29 T Q L S G K A F S N L L R L S I L V T I K T S V P Y L T
12327 tccggaagccttttccacctcgactcattagacagaaactccttatcatctcgaacagcgaatattcgatga 12256
57 S G S L F H L D S L D R N S L S S R T A N I R *
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27037 atgctaaaattttcattgacggcgacggtcaacatttgtacctcacgcacgtttcgatgaagttgttcaatcagcgcgatgcag
1 M L K F S L T A T V N I L Y L T H V S M K L F N S A M Q
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29 L T A Q L I L I K N K S R R F L N R S K I T V M R R P L
27205 tccaaaaccttcaagagcaactcgacaagcagtctcaacttgcaaaggcgctgtga 27261
57 S K T F K S N S T S S L N L Q K A L *

dp1ORF091
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1 M K L S N E Q Y D V A K N V V T V V V P A A I A L I T G
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29 L G A L Y Q F D T T A I T G T I A L L A T F A G T V L G
43357 gtttctagccgaaactaccaaaaggaacaagaagctcaaaacaatgaggtggaataa 43413
57 V S S R N Y Q K E Q E A Q N N E V E *
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1 M K T I S I L R K D T K R K P D R N G R K T A L E L A Q
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29 E I D M S P S E L A E L L Q I P E R T A T R I L K L D K
47157 ctgctcaacaaagagcaatgctcaataatagaaaggtatataaatgaaattcactga 47213
57 L L N K E Q C S I I E R Y I N E I H *
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1 M Q H T I K Q C L K L A F L L T A I S I A C L V F P K P
45672 tgctcatcgcctaaaaggaaacatggatgctcttgtgcgtattcgaaacattcaacctggtgcgcgaatggagtagtcttgaac
29 C S S P K R K H G C S C A Y S K H S T W C A N G V V L N
45588 gaaaactgctcattgcttgaagaagctattcggtttcgagagtcaatgtag 45538
57 E N C S L L E E A I R F R E S M *
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8281 atgtacgaattagttctatcactaaaattgacgccgacagcgccgatgtctcaagatgtcgaaaagtgcttcaaaaggctcaag
1 M Y E L V L S L K L T P T A P M S Q D V E K C F K R L K

8365 tatattcagtggcggcaggtgaatgcattaaaattgcacacggatttgctcttgaacttcctaagggatatgaagcaatcttgc
29 Y I Q W R Q V N A L K L H T D L L L N F L R D M K Q S C
8449 atcctcgttccagtctttttaagaaaactggtctaa 8484
57 I L V P V F L R K L V *
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1 V G K L L Q L S T L S R M R K W Y L S R N G N R R L K N
8961 tcaaggaaaagctggaaaatgcgcgtgcatccaaagctagcaagactgctgtcaaggaacttgaaatgcaactcgatagtcttc
29 S R K S W K M R V H P K L A R L L S R N L K C N S I V F
9045 aagagcctcttaagattgtatatcttgaccttgagaatacattag 9089
57 K S L L R L Y I L T L R I H *
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46681 gtgattcataaattcttcaatttcgttgaacttatctgcggtttctcctgttaccaggttgcatttgactgtcttcgaaagtat
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46597 cttagcaagaggttcaataacctttttcccaattgctaaatatcacgcaggactttccttgctggatacattcctcgacaatttc
29 L S K R F N N L F P I A K Y H A G L S L L D T F L D N F
46513 gatacatctttcgaacttgcaagacttgacatcttgagtagttaa 46469
57 D T S F E L A R L D I L S S *
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39100 atggacgggattgaaatcttgatactgaccgacgtatgctcgtccgctgtcagtatgactaaatccctcaccgtttggactatt
1 M D G I E I L I L T D V C S S A V S M T K S L T V W T I
39016 agagaaagcgaggtgagtatattgcgaacgtccgtcagctcctgcaggtccaggaattccttgaagcccttgaggaccttgaag
29 R E S E V S I L R T S V S S C R S R N S L K P L R T L K
38932 accttgaactcctctaggacctgtttcacctatcttggaaactga 38888
57 T L N S S R T C F T Y L G N *
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1 V K M L R G M L N E A T S S S G D A K V L A Q A L E V I
43711 cagggatgttcattgacagtgataacatcattcactgcaactacgcctacgacggaatttccgtcaacgaccacgatgagcgtt
29 Q G C S L T V I T S F T A T T P T T E F P S T T T M S V
43795 ggtactatgcaggtcaaccttactactacgtctatcgcttga 43836
57 G T M Q V N L T T T S I A *
dp1ORF099
38298 atgcaagttcgccatctgctactgaagctccagctggtggatggtctacgcaagttcctaccgtcccaggtggtcagtatttat
1 M Q V R H L L L K L Q L V D G L R K F L P S Q V V S I Y
38382 ggactcgaacaagatggcgctacactgaccaaactgatgaaattggatattcagtttcaagaatgggcgagcagggtcctaaag
29 G L E Q D G A T L T K L M K L D I Q F Q E W A S R V L K
38466 gtgacgcaggtcgtgacggtattgcaggaaagaacggaatag 38507
57 V T Q V V T V L Q E R T E *
dp1ORF100
1597 atgcagttgacaccaagcgagttctatttggatttagaactacggctgagaatatgtcaagattccttacctggactctcacgg
1 M Q L T P S E F Y L D L E L R L R I C Q D S L P G L S R
1681 agcttatgtggaagcatgctcgtatcgactctatcaaactatgggaaactcctacaggttgcgcagaatgtacttactacgaga
29 S L C G S M L V S T L S N Y G K L L Q V A Q N V L T T R
1765 ttttcacagaagacgagattgaaatgttcaagaacgtaa 1803
57 F S Q K T R L K C S R T *
dp1ORF101
19220 gtgataatttagtccagttcccactacatttgaaagcgcgattaggtcatctaggctgtctagctcgagttcgattacaaggt
1 V I L V Q F P L H L K A R L G H L G C L A R V R L Q G
19304 tgccagtatcaatttcacaaaagtaagcgacatttccaactttctctagtgcttcacgatacctatcatatgtcgcctcttcgt
29 C Q Y Q F H K S K R H F Q L S L V L H D T Y H M S P L R

19388 caaatagtcgcgcagaataaacttcgaatttcatttag 19426
57 Q I V A Q N K L R I S F *

dp1ORF102
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1 M I T W E C L T V S P N S I K F L V Y L D S L R H V N S
4118 ttttggaagcaccacaaatttcttgggataattatctatacatgcgcgagcgaatggttgagaaagacaagctcttacctattt
29 F W K H H K F L G I I I Y T C A S E W L R K T S S Y L F
4202 tccatatgggagaagactttaaatggctcaacttga 4237
57 S I W E K T L N G S T *

dp1ORF103
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49436 gcaggagtgcataatgagcgagagtctcaagataaggtgattcaaagttataagcagaaagaaaagtcagccgtctacttgaca
29 A G V H N E R E S Q D K V I Q S Y K Q K E K S A V Y L T
49520 gtcgatagttcaggagcttggctaggaagtgctccgggagccaaggaaagtcctctctacaatgaaaagggacagcatgtagga
57 V D S S G A W L G S A P G A K E S P L Y N E K G Q H V G
49604 aaattgaaagaggtgggagagtga 49627
85 K L K E V G E *

dp1ORF104
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1 M R K R V I L K L K R L N W Y V L N S Y S R M V E F F E
21343 cttttgaacttttcgaatggttcgactttcgaaggattgaggttttcgaaccggttgagttttcgagcattctcgactttc
29 L L N F S N G S T F R R I E V F E P V E F F E H S R L F
21259 gaccccttttctatgctcgacttttcgagtgttttga 21224
57 D P F L C S T F R V F *

dp1ORF105
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29 F H D R H F L R V A N I D S N L A S F R L I V L I N H Y
1860 cctgctcctgctctaaaatttcgcggacagtaa 1828
57 P A P A L K F R G Q *

dp1ORF106
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29 Y P I I R S S I N F N R R A K S F V H I L R E N S S S S
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57 G F T S S S A T T E *

dp1ORF107
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29 I I V I T L T W K P F L M H *

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29 S M I Q F R L P P I L L H C L P E N L E P L K Y H I Y D
49279 tataaagcctttggcctaaaaggtcaataa 49250
57 Y K A F G L K G Q *

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29 G F G E I F L P A S T R T A S A V P V P P F K S N V T R
31464 cgaagaaccgctggaagttgtgccacatag 31435
57 R R T A G S C A T *

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29 M S S S L F L I T E P R S K Y K L G L I P V T L Y C F S
16612 gtttcttttacaggaatgctttcatag 16638
57 V S F T G M L S *

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29 S S L K K Q V F K S L S T L R K L L S S L T L T N P L T
28825 ttggtaacattcgtcagttcaacttga 28851
57 L V T F V S S T *

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29 Y P G D E K K N P G L Q M L M E *

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1 M K T V K E A I K Q F G D E W W Y E I I N E N G Q M I Q
17631 gacggaagaatcgaagacatgggcgaatacatggaagaaacggtcgaccaagttaagttcatcaactatggtgacatcgaatct
29 D G R I E D M G E Y M E E T V D Q V K F I N Y G D I E S

17547 caaattatcaaactatatatcgcataa 17521
57 Q I I K L Y I A *

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29 F F N F T T M I R E K L K H G T E A V L M F K R L L H L
53120 tcaataaatatggaagccttgtga 53143
57 S I N M E A L *

dp1ORF115
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5258 aagcatattgagttttgcttcataagtcccgttcacggcagcctcttgcatttgagtacaatgaaaggaggttcctcgatatt
29 K H I E F C F I S P V H G S L L H F E Y N E R R F L D I
5174 gttgaaactatagaaggtgaataa 5151
57 V E T I E G E *

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29 G N I E N I L N G S N F A N V V A E A T V L K L E K L S
20494 gaagaggaagctattgagtag 20474
57 E E E A I E *

dp1ORF117
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1 M I T G C S N I L N R S E S R K S L I V L F K L S A T V
24596 ataaggtctttgacatcgcttgtcccgtatatgtcattagtcaatggttcattaagaataactcgacaaggaatttgcttcaag
29 I R S L T S L V P Y M S L V N G S L R I T R Q G I C F K
24512 ccggttggggcggattcttga 24492
57 P V G A D S *

dp1ORF118
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1 M I L S T S T Q L V K L L N T R S L L H E Q S A K A N E
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29 Q T N R R T S R R L S T C K R S N K L P S C C K G P R R
15191 agaactcgaaaaccttga 15208
57 R T R K P *

dp1ORF119
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1 M E V Q H P R F S T S Y F F G H F F S R H D F S G S T D
41138 tttaacagggaacaacttcctccaaatcatgtcgaacattcaagtcaacttcaacaatgcttccggcgcttacggatccactat
29 F N R E Q L P P N H V E H S S Q L Q Q C F R R L R I H Y
41222 ccaagcatttcacgctga 41239
57 P S I S R *

dp1ORF120
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1 V L K R K Q N T C V C N C F N T V N S L S N Q L T A R L
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29 N T L T T T T W M L S N N M Q S L R N G L T Q L K V T L
28555 tcgctgacattttag 28569
57 S L T F *

dp1ORF121
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1 V Q T D H V S S V W K I I I N N I W V I T P I M S K Q I
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29 A G I E L S I D G L T A L P M F K W E V E T S S L I L Y
39390 ttgaatttggtttaa 39404
57 L N L V *

dp1ORF122
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1 M L F S L S Y I P N H V H V W I K R V L F R S K S A D L
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29 N G L G K D P V I D V N E P L R K V H N F I P C G E H R
40234 aattcggtcacttga 40220
57 N S V T *

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1 M V R L F E G L R F S N R L S F S S I L D F S T P F Y A
21243 cgacttttcgagtgtttgaggtttcgagcaggttcgacttttcgagaaattgagtttttcgacctctaaattaggctcgatt
29 R L F E C F E V F E Q V R L F E K L S F S T S K L G S I
21159 attcgaaaagtttag 21145
57 I R K V *

dp1ORF124
17891 atggtaaaagttaaagatttgcaagtaggaatgaaagttgtaaatgcaaaaggtactgaatttaaagtaactgaccgtcaaggt
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17807 cgtaaatgggtaagcctagaacgtcttagtgatggacgtattcggttctatgataacgaatcactaatggacgaaaaagtggag
29 R K W V S L E R L S D G R I R F Y D N E S L M D E K V E
17723 gtagtaaaatga 17712
57 V V K *

dp1ORF125
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29 V S P I S K N S N P G K W S R I V S S S G T L P Y L E K
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57 C S *

dp1ORF126
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29 R S A Y S C M A D P L I G V T V P S L F I L N K V I I S
15968 atcctctaa 15960
57 I L *

dp1ORF127
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29 E I V L R L Q L F P L G K C L P S L C L P W Y P F R K V
13343 gttgattga 13335
57 V D *

dp1ORF128
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1 M T A V Q Q V K F Y L E E A G A H F L K D V E Y S D N L
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29 E Q A I M K D I L K W N G A H R D E H D M K I T S Y E V
5020 ttatag 5025
57 L *

dp1ORF129
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29 R R K R R T R N G N A F W K N L L S L T K S Q L E H C L
25301 tattag 25306
57 Y *

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29 K Q H F I S V I L Q Q I G K T V T R T T L S T M K A F L
16621 taa 16619
57 *

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1 M L N R L R R N L A G R K M L L V S G T L E Q T E L I Q
43930 aagatgagttcgagtatatcgaagaaaacaagtcttggttctactttgacgaccaaggctacatgctcgctgagaaatggttga
44013
29 K M S S S I S K K T S L G S T L T T K A T C S L R N G *

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15220 cccacaaaggcttcaaggttttcgagttcttcgccgtggtcctttacagcaagaaggaagtttattcgacctcttgcacgttga
15137
29 P T K A S R F S S S S P W S F T A R R K F I R P L A R *

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29 S Y F S F L I A E L E S I C I P T I S A L S A A K *

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29 L R K L N K Y N F N D L D S T I F S F G M *
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1 M K Q N L K M L L M L Q C S T E S S S P F L K L T R K S
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29 T Q A L A L P Y Y K E K A K F H M E N L T L K S *
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1 V K K S S I T L F A S L T D T F I C S A I E L A P R P Y
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29 I R P K R T D L T E F L R S F P S L L V V P S G *
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1 M L R T C L L A P S G G Q T S R T H S P A S L I I S S A
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29 T A P T E E A T C F N F L G K P S A S S Y H N A *
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1 M T I S K N N V V I R P I C I L L V K F N S W K H R S R
30578 cgagagctgaaatgtaggaagaatttccttcaatctgtccatcattgtcgttcgtttagtcatgttcactcctag 30504
29 R E L K C R K N F L Q S V H H C R S F S H V H S *
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1 M I L N H S T C L T L L I N S F T Q T R A F E P F L D T
12008 tttcgcaaacacctagatgcttccctcactaaaaggtcatgggcctcaagttcttcgaaagacatttctacatag 11934
29 F R K H L D A S L T K R S W A S S S S K D I S T *
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1 M F S I F P A P K T S A W S L F T T I R Y S L V S A L A
20646 aagtttgaaaatttcatttatttccctttatttgtttttctttatactattattatacaataatgattga 20717
29 K F E N F I L F S L Y L F F F I L L L Y N N D *
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1 V L R V V E I S S K T L L A L F D F H S N N L F S R T V
42838 agcactccgctgcacgctgtaataatcgtcgtcaagactgctgtgtcgtttagccacattggcatagattga 42767
29 S T P L H A V I I V V K T A V S F S H I G I D *
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31898 gtgactgtcgaagtttctccaaacagttctgtcactttacctaaaagcgtattagggattttcccgttagcgattaggttcatg
1 V T V E V S P N S S V T L P K S V L G I F P L A I R F M
31814 acacctgctgctcgaattttaacatggataggttcactaccttttgaaaatcctggaagtgcgatgatttga 31743
29 T P A A R I L T W I G S L P F E N P G S A M I *
dp1ORF143
7565 atgaagtttgggttgacgcttttaactccagaccgtttaatttttcaaggcttgaaattggataccatataatcttttcatgc
1 M K F G L T L L T P D R L I F S R L E I G Y H I I F S C
7481 ttttggaaatacactaaaattccggcgagaataaatttgcatccatctgcgcgtgatagctggaaccattga 7410
29 F W K Y T K I P A R I N L H P S A R D S W N H *
dp1ORF144
36517 gtgcaaatcaagcgactaacttatttagatacattaaacgaggcgcattcttcaagattcctaatggaaattcaacaattacca
1 V Q I K R L T Y L D T L N E A H S S R F L M E I Q Q L P
36601 ttgaataccgagccgatgacgcagcagcttggacctctactcttcccgctcaagttgaactgtttctaa 36669
29 L N T E P M T Q Q L G P L L F P L K L N C F *
dp1ORF145
42067 atggaaacagctggagacctaacaagtggaaagaggttctatttaagcaagacttcgaacagaataattggcagaaacttgttc
1 M E T A G D L T S G K R F Y L S K T S N R I I G R N L F

42151 ttcaaagtgggtggaaccatcactcaacctatggcgacgcattctattcgaaaactcttgacggcatag 42219
29 F K V G G T I T Q P M A T H S I R K L L T A *
dp1ORF146
51484 atgacaaactgcatgattgcatcacctttccagtacggaacctcaagggcgaaacagtattcttcaaccgtcgaagtgttcgtt
1 M T N C M I A S P F Q Y G T S R A K Q Y S S T V E V F V
51568 ctaagtttcaccagtacggtgaagatgaccctaaaacggaatttctttatggccaatatgagcttgtag 51636
29 L S F T S T V K M T L K R N F F M A N M S L *
dp1ORF147
55207 atgtatctgtcaaagaagcgaataaggttattgaagatttcttcaccgagttccctaaagtggcagactatatcatattcgttc
1 M Y L S K K R I R L L K I S S P S S L K W Q T I S Y S F
55291 aacagcaggcgcaggacttgggatatgttcaaacagctaccggtcgaagaagaaggcttcctgatatga 55359
29 N S R R R T W D M F K Q L P V E E E G F L I *
dp1ORF148
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1 V F R F K T I R V G R T P V R F S M S S I A A K M S A I
28552 gggtcactttcagctgggttagtccatttcttagtgactgcatattgttgcttagcatccatgttgtag 28484
29 G S L S A G L V H F L V T A Y C C L A S M L *
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1 M P L N F S S I R I N L A P L S H S S C G G M A N G S S
26390 agcaagtcgaagggcattgtattcgagatttgatatttatgagcagcaggtttccctag 26331

29 S K S K G I V F E I L I F M S S R F P *
dp1ORF150
15185 gtggtcctttacagcaagaaggaagtttattcgacctcttgcacgttgatagtcttcgcgaagttcgacgattcgtttgttcat
1 V V L Y S K K E V Y S T S C T L I V F A K F D D S F V H
15101 ttgctttcgctgattgttcatgcaataggctcctcgtatttaatagtttcacaagttgcgtcgacgtag 15033
29 L L S L I V H A I G S S Y L I V S Q V A S T *
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1 M I I S T Q G R L L A T F K H F L Q T L F N T L D Q L F
28111 tccctaatgctcaacaaacagggacagacatttcatggctcaagggtgcaaataatttgccagtaa 28176
29 S L M L N K Q G Q T F H G S R V Q I I C Q *
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42235 atgtgcataaaggacttatcgacaaagaggctactattgcagtacttcctgaaggatttagaccgaaagtttcaatgtatcttc
1 M C I K D L S T K R L L L Q Y F L K D L D R K F Q C I F
42319 aggctctcaataactcatatggaaatgccattctatgtatatacactgacggaagacttgtggtga 42384
29 R L S I T H M E M P F Y V Y T L T E D L W *
dp1ORF153
22307 atggtggacaaagggctcacctttcgaactttcgatatcgtcatagcagacggttccattcgttcaggaaaaacagtatcgat
1 M V D K G L T F S N F R Y R H S R R F H S F R K N S I D
22391 ggctctttcatttccctttgggccatgacggaattcaacggacaaaactttgccatctgtggtaa 22456
29 G S F I F P L G H D G I Q R T K L C H L W *
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1 V T I G F K N C K K T W G V C T R N L E L L N S H P R L
18530 aggtttcttacaaacaatcctaattccttcaaaatagctcttgtccgggtcaatagtgcctaa 18592
29 R F L T N N P N S F K I A L V R V N S A *
dp1ORF155
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1 M N T T L S N L Q W D M V Q N L I S F F N V S F N S R Q
13596 ttgaagctcaagcaattttctggcatatgggagcctatgatattagtccttatgcaaatttga 13658
29 L K L K Q F S G I W E P M I L V L M Q I *
dp1ORF156
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1 M L V S P F L L V L L F S S V Q F S C F S R C N S F E N
18861 atgcctgttcataggctcacaatattccgccaaagatttgccagttatggtggcgtcaattaa 18923
29 M P V H R L T I F R Q R F A S Y G G V N *
dp1ORF157
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1 V L A G L E K K L V S F S S Q S I R F S I P S R L I V S
13197 gttactgctttcttgaagcgtttttaaagtctgtcatattagacccctttcatttctataa 13135
29 V T A F L K R F L K S V I L D P F H F L *
dp1ORF158
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1 V N A V I R V K R S P N G H C L C P V T I V R N S H F S
40643 acttgcgagcgttacctcttcgccggacgtgtcgtagtctgggtgactgctatgaacacttga 40581
29 T C E R Y L F A G R V V V W V T A M N T *
dp1ORF159
30371 atgatttggtctgcgcttacccaagcagcttctccctttgagtttctgtcgagcattccctgtacggtctgtccaaatagcatgc
1 M I W S A L T Q A A S P L S F C R A F P V R S V Q I A C
30287 gtctttgcgtattcttccatcttagtagcagcgacttcgcagactgttatgacagcgacttga 30225
29 V F A Y S S I L V A A T S Q T V M T A T *
dp1ORF160
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1 M G Y R H A R K T I E R P R R I Y Q C Y R I L W T V Y Q
41408 tttctccgttcaacgtactcgtcaaaatcctgcaattatccaagctcttcgaaatgctaa 41467
29 F L R S T Y S S K S C N Y P S S S K C *
dp1ORF161
52175 atgcaaaaaggtttaaatgcttatctcgacatgacattgaaagcattgcattcgagactatttcaaaatgtttggcaacgttca
1 M Q K G L N A Y L D M T L K A L H S R L F Q N V W Q R S
52259 aatcaaaccaagggggccaagttttcaacttaccttacaagactcttcaagaatagaatag 52318
29 N Q T K G P S F Q L T L Q D S S R I E *
dp1ORF162
13020 atgacagaagttgcggtaaatagcccgcaaaaggtgagagtagttatggtcgggaatattgaatttctcgaatatttaaaaagg
1 M T E V A V N S P Q K V R V V M V G N I E F L E Y L K R
13104 aagtacggaacagaaacttccatcagttatattatagaaaatgaaaggggtctaatatga 13163
29 K Y G T E T S I S Y I I E N E R G L I *
dp1ORF163
40224 gtgaccgaatttctatgttctccgcagggaatgaagttatgtaccttacgcaagggttcattcacatcgataacgggatcttta
1 V T E F L C S P Q G M K L C T L R K G S F T S I T G S L
40308 cccaatccattcaagtcggccgatttagaacggaacaatactcgtttaatccagacatga 40367
29 P N P F K S A D L E R N N T R L I Q T *
dp1ORF164
6696 atgtactcttggagaacttcgtgcctaaatgttccagcttcgcccattgcaattaggttagaatctgcgttatctataatagac
1 M Y S W R T S C L N V P A S P I A I R L E S A L S I I D
6612 tcaccgattctttcgaaatacatttttcgaatacatccaccaaccccgctgggcttataa 6553
29 S P I L S K Y I F R I H P P T P L G L *

dp1ORF165
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1 M S E S W S I P T T D G L Y L D I M L S K I A G V R F F
50420 cctccaatcataaagggcgtgactaccacaagggaattttcagcctcagtcattgcttga 50361
29 P P I I K G V T T T R E F S A S V I A *

dp1ORF166
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1 V V M L F N D S I F S R L A R F T V P A V S I V F I N V
23435 gtgcgtgttgctagggtcgagtgtaaatctattctcagccaagagttcagcgtgaaatga 23376
29 V R V A R V E C K S I L S Q E F S V K *

dp1ORF167
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1 M L I R L E L L T S Y M V L T Q T M R L E V L T L I A L
1092 ctgagttctataattcaatgtcaaatgcaatggaatatggaactggaggcaaggtaa 1148
29 L S S I I Q C Q M Q W N M E L E A R *

dp1ORF168
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1 M R L F P G Y I L H I V Q F L E S S I V L E I H R V R K
54261 tttgcaaagggtcataggccgcatacatataggcaacatcaggaggaattaaactaa 54205
29 F A K G H R P H T Y R Q H Q E E L N *

dp1ORF169
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1 M N T A S R R V S M L V I R K N S S W P P S K S S A R L
45870 gaaactccgtcaatcactaatttcccatctttagtgactcgacttcctaaaatatga 45814
29 E T P S I T N F P S L V T R L P K I *

dp1ORF170
27600 atgatgattgttcttgtgctcctgccgtttgttgagcagcagcaagttgcttaccaaaagagccgatttcacgaggttcgggaa
1 M M I V L V L L P F V E Q Q Q V A Y Q K S R F H E V R E
27516 caccaccaccgacacgacctggatttcctaaatttccagtcccggctggcgacttag 27460
29 H H H R H D L D F L N F Q S R L A T *

dp1ORF171
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1 M S F S F M Y S F R A S R R L L T C F S M S P L V A F N
47594 tcaccggcttcttcaattgcagcgatgaactgtttttcatcttcaaatttcatttaa 47538
29 S P A S S I A A M N C F S S S N F I *

dp1ORF172
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1 M F R T F S T P L L E A A S I S I G E P S P L F T S F A
10378 aaaattcgagcagtagtggttttaccagttccagcgccaccacagaatagatag 10325
29 K I R A V V V L P V P A P P Q N R *

dp1ORF173
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1 M T L D I S F V C T K G F S L S H F T V H C T E D C H K
32076 ttgctcatctgtcatatactcgccgacttcagcgtaagtaggctctaccattga 32023
29 L L I C H I L A D F S V S R L Y H *

dp1ORF174
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1 M S H Q P F S L R L S N Q R S T F H Q F Q A V L A Y I G
29682 cataatagaattgcgccatttgtttccagtagtctgcgtcacctttagactga 29629
29 H N R I A P F V S S S L R H L L D *

dp1ORF175
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1 M R V M S W Q I G E D K E C R I E R R R A Y E S A K Y K
15564 ggcgacggtactacggtggtcctcttgcttacctgtaaccaataaaccattga 15511
29 G D G T T V V L L L T C N Q I N H *

dp1ORF176
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1 V I K T V T L N F S S S V L N D V I L V I D C Y C R L V
42947 aatcccgtcgacctgctgtttaagagtgctaagagttgtagagatatcctctaa 42894
29 N P V D L L F K S A K S C R D I L *

dp1ORF177
19937 atgaacctaaacagttcgagacttctcaagctgttgggaaagaagcaggtcgaatatttggtgggaacgtgaacttggtcata
1 M N L N S S R L L K L L G K K Q V E Y F G G N V N L V I
19853 ttctcgcgactaattttaggtgcttttgtattaatcagcgtgatatgcgcttga 19800
29 F S R L I L G A F V L I S V I C A *

dp1ORF178
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1 M T T V D Q F K R Q L R K S L G S I F P S S V S L N L S
11840 caattagtaacctttagcgaattgctagcacttgcctccatattaagtcataa 11787
29 Q L V T F S E L L A L A S H I K S *

dp1ORF179
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1 M G R V I P Y L V D L L Y A K P T T I A C R G F R S C I
56142 ttggataagtcaaaaagcaagtgtctttatattcgacaagctctcgaataa 56192

29 L D K S K S K C L Y I R Q A L E *

dp1ORF180
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1 M F D M I W R K L F P V K I C R T A E V V S T K E M P E
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29 K V G R T E S G M L N L H P F E *

dp1ORF181
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1 M E V S V P Y F L F K Y S R N S I F P T I T T L T F C G
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29 L F T A T S V I G C P P L L I L *

dp1ORF182
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1 V L A H V S I N R V R P R L A F E R A I T I S I I A K K
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29 G E K L Q S I P L R C Q Y L L P *

dp1ORF183
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1 V I P A F G F S S A S S T F S S L G A G F L R V E L L G
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29 F S S T T S S T S A S C S T G P *

dp1ORF184
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1 V N L P S T T S N I W S S S R S K I R V P R S S L F S G
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29 K S S R V A L S S G R S G R N S *

dp1ORF185
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1 M K F E M F E M K I Y L L L D T L E M A K K L S T T S I
22606 tatttggaggaaaagatgagtcgagtcaagaccttatacaggggtaa 22653
29 Y L E E K M S R V K T L Y R G *

dp1ORF186
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1 M L E K L N R F E N L N P S K S R T I R K V Q K F E K L
21356 aaccattcgagagtaggaattaaggacataccagttcaaccttttag 21403
29 N H S R V G I K D I P V Q P F *

dp1ORF187
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1 M V L F N L F L L S F K Q L F K L S L L Y S M V L F R H
34499 ttcctacgcttattcaagcaggtcttcaaatttgtcagctctcataa 34546
29 F L R L F K Q V F K F C Q L S *

dp1ORF188
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1 M F V K Q P V R L E W T C S I Q E V T T L T N L S H N L
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29 K T I K A S K P L S T L E Q S *

dp1ORF189
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1 M Q T Q Y Q P S L K L F M T Q T C M L R T V E N F E L T
42671 agcaaaaacttcgcgaaactcgttacgcaatcgaagatgaaattctag 42718
29 S K N F A K L V T Q S K M K F *

dp1ORF190
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1 M Y S L K V V Q C G S I I L K S N L V I S L L L L V K Q
39870 aggaagaccttaaatatcgaattgactcaaaagccgatcaaaagctaa 39917
29 R K T L N I E L T Q K P I K S *

dp1ORF191
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29 L P K S I Q S L P K T R Y Q T *

dp1ORF192
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1 M V D V E C F F E M K F R V F S I P Y G M F S E C F N K
2836 acggaatggagtatcttgcaacccgtcacgttctgcgtcctcgcctaa 2789
29 T E W S I L Q P V T F C V L A *

dp1ORF193
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1 M I S A Q I K Y E M R H C L N L T K N Y L H S L S P Q V
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29 F R Q C I Y I E W H F H M S Y *

dp1ORF194
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40200 ccgtcgttcttaccgataattagaccttcattagaagagctcatgtaa 40153
29 P S F L P I I R P S L E E L M *

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1 M F T I V V L T S F F S A P C P I V N S A T I W R D F V
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29 R F N I V L T S F L K N I I T *

dp1ORF196
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1 M V D L T S P C P I M S L L L A H Q K K F G F N Y R F S
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29 I R L P F N N S S K F I H F F *

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1 M K R L Y G I Q F Q A L K K L N G L E L K A S T Q T S S
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29 M Q G M K F L T R S V E L D *

dp1ORF198
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24203 tttctgttgacattgtttatcaggacgagcgtacaaaaggaatga 24247
29 F L L T L F I R T S V Q K E *

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1 V A P E L G C T F P P N C L A T A F S C L A L A L R V G
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29 I G L Y A R D V M A D R R G *

dp1ORF200
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1 M T G L Y S I S P E S F S H I S S V S A S S T N F S I I
47759 tctttcaagcgttcttcgtccatagttgagcgctctgtcgtgtag 47715
29 S F K R S S S I V E R S V V *

dp1ORF201
38569 atgggcttcacaagttccttctttaatcaaaggtcaatatctttggactcgaactatttggacctataccgattcaactaccga
1 M G F T S S F F N Q R S I S L D S N Y L D L Y R F N Y R
38653 aacgggctatcaaaaaacctacattccaaaagacgggaatga 38694
29 N G L S K N L H S K R R E *

dp1ORF202
44483 gtggggcgtttatttttttataaaaattttttacaaaatgcttgacaacattcactcattatcgtataatacaattataaaaata
1 V G R L F F I K I F Y K M L D N I H S L S Y N T I I K I
44567 aataaagccgaaaggcgaggaggacattatgtcaaaaattaa 44608
29 N K A E R R G G H Y V K N *

dp1ORF203
22781 gtgattaggattggccgggttacaagagaaccacattttcgaacctgttacggaacagcgccctgtcgcttggttgacaaacga
1 V I R I G R V T R E P H F R T C Y G T A P C R L V D K R
22697 ttcaggcatcagtgccacctcatcacagaagatacctgctaa 22656
29 F R H Q C H L I T E D T C *

dp1ORF204
1471 atgaccacggttcgagtcaagggatggttgttgacttttatcacgtcaagaaaatcgcaggtacattcattgacagacttgacc
1 M T T V R V K G W L L T F I T S R K S Q V H S L T D L T
1555 acgctgttcttcttcaagggaatgaaccaatcgctttag 1593
29 T L F F F K G M N Q S L *

dp1ORF205
8524 gtgacactgatgaatggttctcagtttggtatgctactcgtgacgcagatatcttctacgaccaaagaattgcccaatttagaa
1 V T L M N G S Q F G M L L V T Q I S S T T K E L P N L E
8608 ttcaggaaaagcaacctgctatcaagttcaatttcgtag 8646
29 F R K S N L L S S S I S *

dp1ORF206
19855 atgaccaagttcacgttcccaccaaaatattcgacctgcttctttcccaacagcttgagaagtctcgaactgtttaggttcatc
1 M T K F T F P P K Y S T C F F P N S L R S L E L F R F I
19939 aaattgttcaacttgagcaagtgcgatattattctttag 19977
29 K L F N L S K C D I I L *

dp1ORF207
27502 gtgtcggtggtggtgttcccgaacctcgtgaaatcggctcttttggtaagcaacttgctgctgctcaacaaacggcaggagcac
1 V S V V V F P N L V K S A L L V S N L L L L N K R Q E H
27586 aagaacaatcatcattctttaaataataggaggaactaa 27624
29 K N N H H S L N N R R N *

dp1ORF208
47279 atgtttggtatgaagcaaaagacttcgctgaagaaaataacattcacttcccgtttgttcttcctgaacctagaacagaccttg
1 M F G M K Q K T S L K K I T F T S R L F F L N L E Q T L
47363 accatcgtggttctcgattctgggatgacgaaggcgtga 47401
29 T I V V L D S G M T K A *

dp1ORF209
29784 atgttaagaatcaagttcgtagagccattgaaaccgctcctactaaaatcaaggtacttcgaaactcttgggtcagtgatggat

1 M L R I K F V E P L K P L L L K S R Y F E T L G S V M D
29868 atggaggaaagaaaaaggataaagcgaatgaagtcgtag 29906
29 M E E R K R I K R M K S *

dp1ORF210
53077 atgtttcaacttttcccgtatcatggttgtaaagttgaagaaatagtttttcaatacgagggaatccgttttggcataatggac
1 M F Q L F P Y H G C K V E E I V F Q Y E G I R F G I M D
52993 aattatcaggatggactgtttccccgtcttcgccaatag 52955
29 N Y Q D G L F P R L R Q *

dp1ORF211
20959 gtgctcgacttttatgtcgcccctaattttgtttttacttacggactatgggatttgtaggtattttcagggcgctttttat
1 V L D F Y V A P N F C F Y L R T M G F V G I F R A L F Y
20875 ttacttattaagtccttttctatattagattgtttataa 20837
29 L L I K S F S I L D C L *

dp1ORF212
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1 M D C F P V F A N S I A I D I A S T T V N V C F V D Y E
52899 ataatccatgtcttcgccttccgggtcatcatacaatag 52861
29 I I H V F A F R V I I Q *

dp1ORF213
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1 M R L C V F F H L S S S D F A D C Y D S D L K L V S I P
30207 ttcacagttactaacaaattcttcaggcttccatactaa 30169
29 F T V T N K F F R L P Y *

dp1ORF214
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1 M M P K L F F S A H S F C T L V L I N N V N R K Q A G R
24189 gtttctagggtcaactgtataggtgaactgaggcattga 24151
29 V S R V N C I G E L R H *

dp1ORF215
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35738 acgattgttccaatgttgacaacggtttgctcgccttga 35700
29 T I V P M L T T V C S P *

dp1ORF216
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1 M A S E L A A T S P P D T A A R S S T P G I A S M I S F
32765 acctggaaaccggctgaagctagatttccatacccttga 32727
29 T W K P A E A R F S I P *

dp1ORF217
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1 M N T M L T A G T V K R A K R E K I E S L K S M T T A W
23527 ataggaacagatatgcctgtctcactgacgctctaa 23562
29 I G T D M P V S L T L *

dp1ORF218
22029 atggaatgcttccggaagaggttcgatatagactacaaattgagcgcgagaaaattacattgctccgggccaaaatgggcgacc
1 M E C F R K R F D I D Y K L S A R K L H C S G P K W A T
22113 aggaaattgaaggcgaggttaaagataacttcgtag 22148
29 R K L K A R L K I T S *

dp1ORF219
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1 M I L C S T F S V L P F L R N A S G L T P C L T T S L D
51304 gttccaaaattccttttcagccactggtttccatag 51269
29 V P K F L F S H W F P *

dp1ORF220
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1 V K F S S V T V D T I S F K S K L L R W Q V N S F F E T
6250 ttcttgccagcagatgcgtacatgatgtcttcataa 6215
29 F L P A D A Y M M S S *

dp1ORF221
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43591 acgcatggcttattgaaaacggttatgaactaa 43623
29 T H G L L K T V M N *

dp1ORF222
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1 V T V S R T L W I G S K M I P I S S Q V Q Q A L D T M E
13296 gctatgaaggtggacttgtcgagcactcattaa 13328
29 A M K V D L S S T H *

dp1ORF223
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1 M W W Y L L D M F E M S T T S T V K S L T F T T R K M S
14139 acgagcctgacgatgacagcgacattcttgtag 14171
29 T S L T M T A T F L *

dp1ORF224
13621 atgccagaaaattgcttgagcttcaactggcgtgagttgaatgaaacgttgaagaaggaaattagattttgcaccatgtcccat
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13537 tgtaagttgctcagggtcgtattcatatgctaa 13505
29 C K L L R V V F I C *
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1 V S N G C D V F H R L C H V A S F C V R I S C C S S K Y
32907 gtcagccacgtgacccgcctggtttgcctctaa 32875
29 V S H V T R L V C L *
dp1ORF226
25191 gtggctgcgtacattagtttgaacttcagtgagcgcaagttgcttagcagaaagttcatcgctaggaattggatagtggtgttc
1 V A A Y I S L N F S E R K L L S R K F I A R N W I V V F
25107 gatagtcattgtcgtaagtgtttgataacttga 25075
29 D S H C R K C L I T *
dp1ORF227
23115 atgactcaattagatggtagcgcttatgacgtttcgagaatccataaaggccgaaggttgttgcattatagataccaaagtcgc
1 M T Q L D G S A Y D V S R I H K G R R L L H Y R Y Q S R
23031 ctgctacgaataaacggtcgaattctatattga 22999
29 L L R I N G R I L Y *
dp1ORF228
10450 atgttcgaaacattattgaagattctagatacaagtctatggacagcgagttcaaagtttacatcattgacgaggttcatatgc
1 M F E T L L K I L D T S L W T A S S K F T S L T R F I C
10534 tttcaaccggagcatttaatgcgctgttga 10563
29 F Q P E H L M R C *
dp1ORF229
27634 atgtgcgagttaagaaaactgattttaatcaaaccactcgaagcattgtcgcaattcctgaccactacgttgctttggctgctc
1 M C E L R K L I L I K P L E A L S Q F L T T T L L W L L
27718 aaattccagctaccgcagcaactcaagtag 27747
29 K F Q L P Q Q L K *
dp1ORF230
50723 gtgacgaaaaatccggcatacttgaactatctgtcgttaaaaaccgatatggcgaagaccgaaaaatcatcgaatatatgtggg
1 V T K N P A Y L N Y L S L K T D M A K T E K S S N I C G
50807 acgttgaaactggaacctatactcttatag 50836
29 T L K L E P I L L *
dp1ORF231
31071 atgcgcgtgtcattgcgtttcacatcttcagttccctccgaggtcacggcttcgagttctgctgtttctgccgtatctacgaca
1 M R V S L R F T S S V P S E V T A S S S A V S A V S T T
30987 aagttagctccgccgacttttggcaactga 30958
29 K L A P P T F G N *
dp1ORF232
29385 atgtcaattccattagctcttgctaattcaacgagctcaggaacggttttagccgcatactcttcgcgcatttgttcaacttcg
1 M S I P L A L A N S T S S G T V L A A Y S S R I C S T S
29301 tcaatttcttcaactgattcaattgtttga 29272
29 S I S S T D S I V *
dp1ORF233
52892 atgtcttcgccttccgggtcatcatacaatagagtgacaattgcgctgtcaccgtggtcagcgagtgtgaaaaactcgttatta
1 M S S P S G S S Y N R V T I A L S P W S A S V K N S L L
52808 gaccctgagctaaatgttcctgatttttga 52779
29 D P E L N V P D F *
dp1ORF234
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1 M L T S T A T Q L F E R F I S F N P L W E A I A Y L T Q
36337 gaagacctactcgacaatttagagtag 36363
29 E D L L D N L E *
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32768 atgaaatcatggacgctatgccaggggtacttgacctggctgccgtatctggaggagatgtggccgcgagctccgaggccatgg
1 M K S W T L C Q G Y L T W L P Y L E E M W P R A P R P W
32852 ctagttcacttcgagcctttggattag 32878
29 L V H F E P L D *
dp1ORF236
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1 M F V A F R F S N I S R L H V A C S K P R N I N E I F T
37444 tccattgttgatagaagcaaacgttaa 37418
29 S I V D R S K R *

dp1ORF237
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1 V R V Q V R N L D I F S A V V L N P N R T R L V S T A F
1594 gctaaagcgattggttcattcccttga 1568
29 A K A I G S F P *
dp1ORF238
1301 atgccttttgcggtcgatacaagttgcgcaagttccacaactttcagcgtcactttcataacatgaacgagtcaagaaataag
1 M P F C G R Y K L R K F H N F Q R H F H N M N E S R N K

1217 gaacatctaaatcaattccccatttaa 1191
29 E H L N Q F P I *
dp1ORF239
26521 atggtgaagtatttcctatcgaagaatgtcctttcgaccatcctaatggaatgtgctaccaaactgtatggtacgaaaactcac
1 M V K Y F L S K N V L S T I L M E C A T K L Y G T K T H
26605 tcgaagaaatcgctgatgagttga 26628
29 S K K S L M S *
dp1ORF240
41893 atgtttggaataagcgtgaaacagagtttacatggcgaagtaacaaatacgaggacaaccctacgggaactcgaggtgaatggg
1 M F G I S V K Q S L H G E V T N T R T T L R E L E V N G
41977 gactatttcaaaatttctggttag 42000
29 D Y F K I S G *
dp1ORF241
47020 gtgtctttccttaatatggagatagttttcattctatttaagcaggatatcgaaaaggttaccaatttagatttcataggctt
1 V S F L N M E I V F I L F K Q D I E K V T N F R F H R L
46936 accatctacgatataatctgctaa 46913
29 T I Y D I I C *
dp1ORF242
41338 gtgtctgtaacccatgctcttacggtagcggagccattaaagttcatcatacccaatttgccgccgttttcgttgatagcttgg
1 V S V T H A L T V A E P L K F I I P N L P P F S L I A W
41254 tttttacctacgagctcagcgtga 41231
29 F L P T S S A *
dp1ORF243
51306 atgttccaaaattccttttcagccactggtttccatagaaccctccatcgtttcgacctaatacattcgagacgaattcagtta
1 M F Q N S F S A T G F H R T L H R F D L I H S R R I Q L
51222 gtcctgaagtgtagccgcaagtga 51199
29 V L K C S R K *
dp1ORF244
27083 gtgaggtacaaaatgttgaccgtcgccgtcaatgaaaattttagcatcgagttctttcgaagttttcgaaataatttccttcac
1 V R Y K M L T V A V N E N F S I E F F R S F R N N F L H
26999 ctgtttgatagttggttcatctag 26976
29 L F D S W F I *
dp1ORF245
6278 gtggcaagtgaattctttcttcgaaactttcttgccagcagatgcgtacatgatgtcttcataactgctagtagaagttttaat
1 V A S E F F L R N F L A S R C V H D V F I T A S R S F N
6194 tcgaagtcggtctttcaagaataa 6171
29 S K S V F Q E *
dp1ORF246
2831 atggagtatcttgcaacccgtcacgttctgcgtcctcgcctaatagaccaaaaagtctttgaacggctgcctcagtattgtcca
1 M E Y L A T R H V L R P R L I D Q K V F E R L P Q Y C P
2747 aggttacaatttcatccggcttaa 2724
29 R L Q F H P A *
dp1ORF247
29641 gtgacgcagactactggaaacaaatggcgcaattctattatgaccaatataagcaagaacagcttgaaactgatgaaaagtcga
1 V T Q T T G N K W R N S I M T N I S K N S L K L M K S R
29725 acgctggttcgacaatcttaa 29745
29 T L V R Q S *
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53644 acatttcaggaaacgctctaa 53664
29 T F Q E T L *
dp1ORF249
2012 gtggatgcgactatcattgcaactggtgtgactcagcctttacctggaacggtactactgagccggaatatatcacaggcaaag
1 V D A T I I A T G V T Q P L P G T V L L S R N I S Q A K
2096 aagctgctagtcgaatcttga 2116
29 K L L V E S *

dp1ORF250
23837 atgggcaaacatggaagattgacgaagactcagtcgactataaacctactcgagaaattcgaaactatattcgacaacttatca
1 M G K H G R L T K T Q S T I N L L E K F E T I F D N L S
23921 aaaagcaatcacgctttatga 23941
29 K S N H A L *
dp1ORF251
39205 atggaaataattagtcttaccgtctgcgcctggcttcccgggtatcccttgagctccgtcattccccttccatttcgtccatgt
1 M E I I S L T V C A W L P G Y P L S S V I P L P F R P C
39121 ataggctgcagggtcttttga 39101
29 I G C R V P *
dp1ORF252
54771 gtgttgtataggtcgaaactaattttgcatattttctatatttcaaaagtgcttttgagatatcgttatcaaaatgctcgacaa
1 V L Y R S K L I L H I F Y I S K V L L R Y R Y Q N A R Q
54687 tactttcgcctgttcctctag 54667
29 Y F R L F L *
dp1ORF253
56255 atggttgcgtctataatagaaccgatgttgctagacaaagcatttgcaatcttcgagtctaatttattcgagagcttgtcgaat

1 M V A S I I E P M L L D K A F A I F E S N L F E S L S N
56171 ataaagacacttgcttttga 56151
29 I K T L A F *
dp1ORF254
48479 atgaacctttcgcttaggttcaatctttttcgaacattttcatatttaacaaaactttcagctaaaaatcgacaaagttcaatg
1 M N L S L R F N L F R T F S Y L T K L S A K N R Q S S M
48395 ttcgactcaatgtttaaataa 48375
29 F D S M F K *
dp1ORF255
9572 atgctttggtcttctcgacgaatgactctactacattccctgcagggtttcgagcagtacgggtcaatgatgcaccgttttcgt
1 M L W S S R R M T L L H S L Q G F E Q Y G S M M H R F R
9488 caaggtagtcaccttttctaa 9468
29 Q G S H L F *
dp1ORF256
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1 M T F Q S L M R P L K L D T T I H G F T N F E T K Q L K
15373 cacttgaagaaattttag 15390
29 H L K K F *
dp1ORF257
28216 gtgaacgtgctggatttagcaaacaagctactgagatggcattcttccgtgagtctatgcgacttggtgaaaaagaccgtcaaa
1 V N V L D L A N K L L R W H S S V S L C D L V K K T V K
28300 acttgcaaatgctattga 28317
29 T C K C Y *
dp1ORF258
44023 atggaaattggtattggttcgaccgtgacggatacatggctacgtcatggaaacggattggcgagtcatggtactacttcaatc
1 M E I G I G S T V T D T W L R H G N G L A S H G T T S I
44107 gcgatggttcaatggtaa 44124
29 A M V Q W *
dp1ORF259
4298 atgactcgactacgaagcataaagacaagtggatggaaagagtattcgaagttattcgaaacagttctaatccagacgttaaga
1 M T R L R S I K T S G W K E Y S K L F E T V L I Q T L R
4382 ctcacgcatttgggatga 4399
29 L T H L G *
dp1ORF260
24746 gtgaccctacttcctcaatcggcggtactggaggcaagcaagctcaagtcacttccatttcaggaaacttcaacttccttccag
1 V T L L P Q S A V L E A S K L K S L P F Q E T S T S F Q
24830 cggctgaatattatttag 24847
29 R L N I I *
dp1ORF261
288 atgaattcacttccctttgccctaaaacaggacagcctgacttcgcgaatgttttcattagttacattccaaacgaaaagatgg
1 M N S L P F A L K Q D S L T S R M F S L V T F Q T K R W
372 ttgaatctaaatcattga 389
29 L N L N H *
dp1ORF262
9408 atgcctattcaactccaggcggaaagatgtggaagcatgcttgtgcagttcgacttaaatttagaaaaggtgactaccttgacg
1 M P I Q L Q A E R C G S M L V Q F D L N L E K V T T L T
9492 aaaacggtgcatcattga 9509
29 K T V H H *

dp1ORF263
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1 M K I L A S S S F E V F E I I S F T C L I V G S S R P F
26968 aacaagtcttctaattga 26951
29 N K S S N *
dp1ORF264
6139 gtgaatagtacaaggcggtctaatacgctcaggatttctgctgtagggatagccgcatcatcttcaaactcaattgagtcaagc
1 V N S T R R S N T L R I S A V G I A A S S S N S I E S S
6055 tgtgaaacgtcttcataa 6038
29 C E T S S *
dp1ORF265
4801 gtgaataaagtcaagcgtttttgtataaaaagttcatttttttttaaaaaaaataagagcgaaaagctcttatctaaaatagtc
1 V N K V K R F C I K S S F F F K K N K S E K L L S K I V
4717 gacgttgacgatttttaa 4700
29 D V D D F *
dp1ORF266
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1 M P V L P S S C K H F I N S P R L T L S R S S H Y D N Q
50136 atcctcaccaggaagtaa 50119
29 I L T R K *
dp1ORF267
47367 atggtcaaggtctgttctaggttcaggaagaacaaacgggaagtgaatgttattttcttcagcgaagtcttttgcttcatacca
1 M V K V C S R F R K N K R E V N V I F F S E V F C F I P
47283 aacattaatcgtagatag 47266
29 N I N R R *
dp1ORF268

12621 atgtcaatttcggtcttgtgcttgacaatggattcaactactgatgcgtcaacctttttcaatcgcgacagcttgtccaattca
1 M S I S V L C L T M D S T T D A S T F F N R D S L S N S
12537 ttgtcaattctagagtaa 12520
29 L S I L E *

dp1ORF269
53834 gtgaatagtatcgagtccatcagtttctacgtcaatagaacctattccgtcttcaatcattttgtctacatactgctcgagttt
1 V N S I E S I S F Y V N R T Y S V P N H F V Y I L L E F
53750 tgcttcctcagtgattaa 53733
29 C F L S D *

dp1ORF270
50792 atgatttttcggtcttcgccatatcggtttttaacgacagatagttcaagtatgccggattttcgtcacgcttcatagcgata
1 M I F R S S P Y R F L T T D S S S M P D F S S R F I A I
50708 actctgctagcattttga 50691
29 T L L A F *

dp1ORF271
19739 atgaggctgctttgctttatcttcgttaccgtattgaccgacttcctactcgcgaaccttcctacaagaattcatacctcaaag
1 M R L L C F I F V T V L T D F L L A N L P T R I H T S K
19655 gctttttgtcagccttag 19638
29 A F C Q P *

dp1ORF272
1556 gtggtcaagtctgtcaatgaatgtacctgcgatttcttgacgtgataaaagtcaacaaccatcccttgactcgaaccgtggtc
1 V V K S V N E C T C D F L D V I K V N N H P L T R T V V
1472 ataagttccgcctgctaa 1455
29 I S S A C *

dp1ORF273
56256 atggatttcattaggactgagtcctcttggaattggaacggttgcatatatagatattccgtcagccgtactaggccaagttct
1 M D F I R T E S S W N W N G C I Y R Y S V S R T R P S S
56340 agttcagtttatcttgcagtcaattgcttcgagatatttgaaaaagtagtcaggaaaattcctgattatcttgcagtcaattgc
29 S S V Y L A V N C F E I F E K V V R K I P D Y L A V N C
56424 ttcgagatatttgaaaaagtagtcaggaaaattcctgattattttttacaaaaacgcttga 56486
57 F E I F E K V V R K I P D Y F F Y K N A *

Table 31

```
Query= sid|114822|lan|dp1ORF001 Phage dp1 ORF|36698-40390|2
        (1230 letters)

>gi|928828 (L44593) ORF1904; putative [Lactococcus lactis phage BK5-T]
          Length = 1904

 Score =  427 bits (1086), Expect = e-118
 Identities = 226/475 (47%), Positives = 281/475 (58%), Gaps = 45/475 (9%)

Query: 395  AESGKYIGVLNTNKKPSELVPDDFTWIRLEGPKGDAGLPGAPGRDGVDGVPGKSGVGIAD 454
            A+   YIG        +       P D+TW  +     +G+ G  GA G+DGV      GK GVGI
Sbjct: 820  ADYPSYIGQYTDFIQYDSAKPSDYTWSLI---RGNDGKDGATGKDGV---AGKDGVGIKT 873

Query: 455  TAITYAVSVSGTQEPENGWSEQVPELIKGRFLWTKTFWRYTDGSHETGYSVAYIGQDGNS 514
            T ITYA+S SGT +P  GW+ QVP L+KG++LWTKT W YTD S ETGYSV YI +DGN+
Sbjct: 874  TVITYALSSSGTDKPNTGWTSQVPTLVKGQYLWTKTVWTYTDSSSETGYSVTYIAKDGNN 933

Query: 515  GKDGIAGKDGVGIAATEVMYASSPSATEAPAGGWSTQVPTVPGGQYLWTRTRWRYTDQTD 574
            G DGIAGKDGVGI   T + YA   S T APA GW++QVP VP GQ+LWT+T W YTD T
Sbjct: 934  GNDGIAGKDGVGIKKTTITYAVGTSGTTAPASGWNSQVPNVPAGQFLWTKTVWTYTDNTS 993

Query: 575  EIGYSVSRMGEQGPKGDAGR---DGIAGKNGIGLKSTSVSYGISPTDSAIP-GVWASQVP 630
            E GYSV+ MG +G KGD G      +GIAGK+G G+K+T+++Y  SP   +  P G W++ VP
Sbjct: 994  ETGYSVAMMGVKGDKGDPGNNGTNGIAGKDGKGIKATAITYQASPNGTTAPTGTWSASVP 1053

Query: 631  SLIKGQYLWTRTIWTYTDSTTETGYQKTYIPKDGNDGKNGIAGKDGVGIKSTTITYAGST 690
             + KG +LWTRTIWTYTD+TTETGY    Y+  +GN+G +G  GKDG GIK+TTITYAGST
Sbjct: 1054 PVAKGSFLWTRTIWTYTDNTTETGYAVAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGST 1113

Query: 691  SGTVAPTSNWTSAIPNVQPGFFLWTKTVWNYTDDTSETGYSVSKIGETXXXXXXXXXXXX 750
            SGT   P + WTS +P V   G +LWTKTVW YTD+TSETGYSV+ +G
Sbjct: 1114 SGTTPPNNGWTSTVPTVAEGNYLWTKTVWTYTDNTSETGYSVAMMG------VKGDKGDP 1167

Query: 751  XXXXXXXXXXADGRS-QYTHLAFSNSPNGEGFSHTDSGRAYVGQYQDFNPVHSKDPAAYT 809
                        DG+  + T + +  SPNG           A  G +     P  +K    +T
Sbjct: 1168 GNNGTNGIAGKDGKGIKATAITYQASPNGT--------TAPTGTWSASVPPVAKGSFLWT 1219

Query: 810  WTKW------------------KGNDGAQGIPGKPGADGKTNYFHIAYASSADGS 846
             T W                    GN+G  G PGK G   KT     I YA S  G+
Sbjct: 1220 RTIWTYTDNTTETGYAVAYMGTNGNNGHDGFPGKDGTGIKTT--TITYAGSTSGT 1272


 Score =  396 bits (1007), Expect = e-109
 Identities = 208/449 (46%), Positives = 260/449 (57%), Gaps = 42/449 (9%)

Query: 421  IRLEGPKGDAGLPGAPGRDGVDGVPGKSGVGIADTAITYAVSVSGTQEPENGWSEQVPEL 480
            + + G KGD G     PG +G +G+ GK G GI  TAITY  S +GT  P   WS  VP +
Sbjct: 1155 VAMMGVKGDKG---DPGNNGTNGIAGKDGKGIKATAITYQASPNGTTAPTGTWSASVPPV 1211

Query: 481  IKGRFLWTKTFWRYTDGSHETGYSVAYIGQDGNSGKDGIAGKDGVGIAATEVMYASSPSA 540
             KG FLWT+T W YTD + ETGY+VAY+G +GN+G DG  GKDG GI  T + YA S S
Sbjct: 1212 AKGSFLWTRTIWTYTDNTTETGYAVAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGSTSG 1271

Query: 541  TEAPAGGWSTQVPTVPGGQYLWTRTRWRYTDQTDEIGYSVSRMGEQGPKGDAGR---DGI 597
            T  P  GW+++ VPTV  G YLWT+T W YTD T E GYSV+ MG +G KGD G     +GI
Sbjct: 1272 TTPPNNGWTSTVPTVAEGNYLWTKTVWTYTDNTSETGYSVAMMGVKGDKGDPGNNGTNGI 1331

Query: 598  AGKNGIGLKSTSVSYGISPTDSAIP-GVWASQVPSLIKGQYLWTRTIWTYTDSTTETGYQ 656
            AGK+G G+K+T+++Y  SP   +  P G W++ VP + KG +LWTRTIWTYTD+TTETGY
Sbjct: 1332 AGKDGKGIKATAITYQASPNGTTAPTGTWSASVPPVAKGSFLWTRTIWTYTDNTTETGYA 1391

Query: 657  KTYIPKDGNDGKNGIAGKDGVGIKSTTITYAGSTSGTVAPTSNWTSAIPNVQPGFFLWTK 716
             Y+  +GN+G +G  GKDG GIK+TTITYAGSTSGT  P + WTS +P V  G +LWTK
Sbjct: 1392 VAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGSTSGTTPPNNGWTSTVPTVAEGNYLWTK 1451


Query: 717  TVWNYTDDTSETGYSVSKIGETXXXXXXXXXXXXXXXXXXXXXXXXADGRS-QYTHLAFSNS 775
            TVW YTD+TSETGYSV+ +G                          DG+  + T + +  S
Sbjct: 1452 TVWTYTDNTSETGYSVAMMG------VKGDKGDPGNNGTNGIAGKDGKGIKATAITYQAS 1505
```

```
Query: 776  PNGEGFSHTDSGRAYVGQYQDFNPVHSKDPAAYTWTKW------------------KGND 817
            PNG          A G +    P +K    +T T W                   GN+
Sbjct: 1506 PNGT--------TAPTGTWSASVPPVAKGSFLWTRTIWTYTDNTTETGYAVAYMGTNGNN 1557

Query: 818  GAQGIPGKPGADGKTNYFHIAYASSADGS 846
            G G PGK G   KT   I YA S  G+
Sbjct: 1558 GHDGFPGKDGTGIKTT--TITYAGSTSGT 1584
```

Score = 384 bits (977), Expect = e-105
Identities = 179/322 (55%), Positives = 222/322 (68%), Gaps = 7/322 (2%)

```
Query: 421  IRLEGPKGDAGLPGAPGRDGVDGVPGKSGVGIADTAITYAVSVSGTQEPENGWSEQVPEL 480
            + + G KGD G    PG +G +G+ GK G GI  TAITY  S +GT  P   WS  VP +
Sbjct: 1311 VAMMGVKGDKG---DPGNNGTNGIAGKDGKGIKATAITYQASPNGTTAPTGTWSASVPPV 1367

Query: 481  IKGRFLWTKTFWRYTDGSHETGYSVAYIGQDGNSGKDGIAGKDGVGIAATEVMYASSPSA 540
             KG FLWT+T W YTD + ETGY+VAY+G +GN+G DG  GKDG GI  T + YA S S
Sbjct: 1368 AKGSFLWTRTIWTYTDNTTETGYAVAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGSTSG 1427

Query: 541  TEAPAGGWSTQVPTVPGGQYLWTRTRWRYTDQTDEIGYSVSRMGEQGPKGDAGR---DGI 597
            T  P  GW++ VPTV  G YLWT+T W YTD T E GYSV+ MG +G KGD G    +GI
Sbjct: 1428 TTPPNNGWTSTVPTVAEGNYLWTKTVWTYTDNTSETGYSVAMMGVKGDKGDPGNNGTNGI 1487

Query: 598  AGKNGIGLKSTSVSYGISPTDSAIP-GVWASQVPSLIKGQYLWTRTIWTYTDSTTETGYQ 656
            AGK+G G+K+T+++Y  SP  +  P G W++ VP + KG +LWTRTIWTYTD+TTETGY
Sbjct: 1488 AGKDGKGIKATAITYQASPNGTTAPTGTWSASVPPVAKGSFLWTRTIWTYTDNTTETGYA 1547

Query: 657  KTYIPKDGNDGKNGIAGKDGVGIKSTTITYAGSTSGTVAPTSNWTSAIPNVQPGFFLWTK 716
             Y+  +GN+G +G  GKDG GIK+TTITYAGSTSGT  P + WTS +P V  G +LWTK
Sbjct: 1548 VAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGSTSGTTPPNNGWTSTVPTVAEGNYLWTK 1607

Query: 717  TVWNYTDDTSETGYSVSKIGET 738
            TVW YTD++ ETGYSV K+G T
Sbjct: 1608 TVWAYTDNSFETGYSVGKMGNT 1629
```

Score = 201 bits (507), Expect = 2e-50
Identities = 121/297 (40%), Positives = 156/297 (51%), Gaps = 19/297 (6%)

```
Query: 421  IRLEGPKGDAGLPGAPGRDGVDGVPGKSGVGIADTAITYAVSVSGTQEPENGWSEQVPEL 480
            + + G KGD G    PG +G +G+ GK G GI  TAITY  S +GT  P   WS  VP +
Sbjct: 1467 VAMMGVKGDKG---DPGNNGTNGIAGKDGKGIKATAITYQASPNGTTAPTGTWSASVPPV 1523

Query: 481  IKGRFLWTKTFWRYTDGSHETGYSVAYIGQDGNSGKDGIAGKDGVGIAATEVMYASSPSA 540
             KG FLWT+T W YTD + ETGY+VAY+G +GN+G DG  GKDG GI  T + YA S S
Sbjct: 1524 AKGSFLWTRTIWTYTDNTTETGYAVAYMGTNGNNGHDGFPGKDGTGIKTTTITYAGSTSG 1583

Query: 541  TEAPAGGWSTQVPTVPGGQYLWTRTRWRYTDQTDEIGYSVSRMGEQGPKGDAGRDGIAGK 600
            T  P  GW++ VPTV  G YLWT+T W YTD + E GYSV +MG  GP   AG +G  GK
Sbjct: 1584 TTPPNNGWTSTVPTVAEGNYLWTKTVWAYTDNSFETGYSVGKMGNTGP---AGSNGNPGK 1640

Query: 601  NGIGLKSTSVSYGISPTDSAIPGVWASQVPSLIKG-QYLWTRTIWTYTDSTTE--TGYQK 657
                + T+    G++    S  +   +     ++ G +Y W    W   +       G
Sbjct: 1641 VVSDTEPTTKFKGLTWKYSGVVDMPLGNGTKILAGTEYYWNGNNWALYEINAHNINGDNL 1700

Query: 658  TYIPKDGNDGK-NGIAGKDGVGIKSTTITYAGS-----TSGTVAPTSNWTSAIPNVQ 708
            +        DGK   I G +GV   + T T  GS     +S +  T N T AI N Q
Sbjct: 1701 SVTNGTFKDGKIESIWGSNGV---NGTTTIEGSHLQIHSSDSTTNTEN-TLAIDNRQ 1753
```

Query= sid|114823|lan|dp1ORF002 Phage dp1 ORF|32386-35835|1
(1149 letters)

>dbj|BAA31888| (AB009866) orf 15 [bacteriophage phi PVL]
Length = 694

Score = 280 bits (709), Expect = 3e-74
Identities = 157/465 (33%), Positives = 257/465 (54%), Gaps = 28/465 (6%)

```
Query: 40   QIGSALTGLGKGLTTAVTLPLMGFAAASIKVGNEFQAQMSRVQAIAGATAEELGRMKTQA 99
            +IG+++   +G+ +T  VT P++   A + K G EF   M +V+A +GAT EE   +K +A
Sbjct: 151  EIGNSMKNVGRNMTMYVTAPVVAGFAVAAKKGIEFDDSMRKVKATSGATGEEFEALKKKA 210
```

```
Query: 100 IDLGAKTAFSAKEAAQGMENLASAGFQVNEIMDAMPGVLDLXXXXXXXXXXXXXXXMASSL 159
           ++GA T FSA ++A+ +  +A AG+    ++M+ + GV+DL                +    L
Sbjct: 211 REMGATTKFSASDSAEALNYMALAGWDSKQMMEGLSGVMDLAAASGEELGAVSDIVTDGL 270

Query: 160 RAFGLEANQAGHVADVFARAAADTNAETSDMAEAMKYVAPVAHSMGLSLEETAASIGIMA 219
            AFGL+A  +GH+ADV A+ ++  N +   + EA KYVAPVA ++G ++E+T+ +IG+M+
Sbjct: 271 TAFGLKAKDSGHLADVLAQTSSKANTDVRGLGEAFKYVAPVAGALGYTIEDTSIAIGLMS 330

Query: 220 DAGIKGSQAGTTLRGALSRIAKPTKAMVKSMQELGVSFYDANGNMIPLREQIAQLKTATA 279
           +AGIKG +AGT LR    + ++ PT+AM   M+ LG+S  D+NG MIP+R+ + QL+
Sbjct: 331 NAGIKGEKAGTALRTMFTNLSSPTRAMGNEMERLGISITDSNGKMIPMRKLLDQLREKFK 390

Query: 280 GLTQEERNRHLVTLYGQNSLSGMLALLDAGPEKLDKMTNALVNSDGAAKEMAETMQDNLA 339
            L+++++      T++G+ ++SG LA+++A  E   K+T ++ +S GA+K MA+TM+  L
Sbjct: 391 HLSKDQQASSAATIFGKEAMSGALAIINASDEDYQKLTKSIDSSTGASKRMADTMESGLG 450

Query: 340 SKIEQMGGAFESVAIIVQQILEPALAKIVGAITKVLEAFVNMSPIGQKMVVIFAGMVAAL 399
            K+  +     E +A+ +  +EPAL  IV A +KV+      +    Q  VV F   VA L
Sbjct: 451 GKLRTLRSQLEELALTIYDRIEPALKIIVSAFSKVVTWVTKLPTSIQLAVVGFGLFVAVL 510

Query: 400 GPLLLIAGM-------VMTTIVKLRIAIQFLGPAFMGTMGTIAGVIAIF----------- 441
           GPL+ + G+         MT +  L I +         F        IA ++ +F
Sbjct: 511 GPLVFMFGLFISVMGNAMTVLGPLLINVNKASGLFAFLRTKIASLVKLFPILGVSISSLT 570

Query: 442 -------YALVAV---FMIAYTKSERFRNFINSLAPAIKAGFGGA 476
                  ALV +   F  AY +SE FRN +N      +  F  A
Sbjct: 571 LPITLIVGALVGIGIAFYQAYKRSETFRNIVNQAISGVANAFKAA 615
```

```
Query= sid|114824|lan|dp1ORF003 Phage dp1 ORF|53538-55877|3
       (779 letters)

>sp|P43741|DPO1_HAEIN DNA POLYMERASE I (POL I) >gi|1074025|pir||E64098 DNA polymerase I
          (polA) homolog - Haemophilus influenzae (strain Rd KW20)
          >gi|1573871 (U32767) DNA polymerase I (polA)
          [Haemophilus influenzae Rd]
          Length = 930

 Score = 191 bits (481), Expect = 1e-47
 Identities = 148/553 (26%), Positives = 262/553 (46%), Gaps = 60/553 (10%)

Query: 63  RLELITEEAKLEQYVDKMIEDGIGSIDVETDGLDTIHDELAGVCLYSPSQKGIYAPVNHV 122
            + E +  +A L ++++K+     + ++D ETD LD +    L G+        + +  Y P+
Sbjct: 333 KYETLLTQADLTRWIEKLNAAKLIAVDTETDSLDYMSANLVGISFALENGEAAYLPLQLD 392

Query: 123 SNMTKMRIKNQISPEFMKKMLQRIVDSGIPVIYHNSKFDMKSIYWRLGVKMNEPAWDTYL 182
                ++   +    +K +L+   +  I  I  N KFD +SI+ R G+++     +DT L
Sbjct: 393 YLDAPKTLEKSTALAAIKPILE---NPNIHKIGQNIKFD-ESIFARHGIELQGVEFDTML 448

Query: 183 AAMLLNENESHSLKSLHSKYVRNEENAEVAKFNDLFKGIPFSLIPPDVAYMYAAYDPLQT 242
            +  LN      H++  L  +Y+ +E  A  +          + F+ IP + A  YAA D   T
Sbjct: 449 LSYTLNSTGRHNMDDLAKRYLGHETIAFESLAGKGKSQLTFNQIPLEQATEYAAEDADVT 508

Query: 243 FELYEFQEQYLTPGTEQCEEYNLEKVSWVLHNIEMPLIKVLFDMEVYGVDLDQDKLAEIR 302
            +L +       L           E Y            +E+PL+ VL  ME  GV +D D L
Sbjct: 509 MKLQQALWLKLQEEPTLVELYK---------TMELPLLHVLSRMERTGVLIDSDALFMQS 559

Query: 303 EQFTANMNEAEQEFQQLVSEWQPEIEELRQTNFQSYQKLEMDARGRVTVSISSPTQLAIL 362
            +  +  +  E++   L  +                              +++S  QL  +
Sbjct: 560 NEIASRLTALEKQAYALAGQ---------------------------PFNLASTKQLQEI 592

Query: 363 FYDIMGLKSPERDKPRG---TGESIVEH--FDNDISXXXXXXXXXXXXXVSTYTT-LDQHL 416
            +D + L   ++  P+G   T E ++E   + +++                STYT  L Q +
Sbjct: 593 LFDKLELPVLQKT-PKGAPSTNEEVLEELSYSHELPKILVKHRGLSKLKSTYTDKLPQMV 651

Query: 417 AKPDNRIHTTFKQYGAKTGRMSSENPNLQNIPSRGE-GAVVRQIFAASEGHYIIGSDYSQ 475
                R+HT++ Q    TGR+SS +PNLQNIP R E G  +RQ F A EG+ I+ +DYSQ
Sbjct: 652 NSQTGRVHTSYHQAVTATGRLSSSDPNLQNIPIRNEEGRHIRQAFIAREGYSIVAADYSQ 711

Query: 476 QEPRSLAELSGDESMRHAYEQNLDLYSVIGSKLYGVPYEECLEFYPDGTTNKEGKLRRNS 535
            E R +A LSGD+ + +A+ Q  D++     ++++GV  +E          T+++    R +
Sbjct: 712 IELRIMAHLSGDQGLINAFSQGKDIHRSTAAEIFGVSLDE--------VTSEQ----RRN 759

Query: 536 VKSVLLGLMYGRGANSIAEQMNVSVKEANKVIEDFFTEPPKVADYIIFVQQQAQDLGYVQ 595
            K++  GL+YG  A   ++ Q+ +S  +A K ++ +F  +P V  ++ ++++A+  GYV+
```

```
Sbjct: 760 AKAINFGLIYGMSAFGLSRQLGISRADAQKYMDLYFQRYPSVQQFMTDIREKAKAQGYVE 819

Query: 596 TATGRRRRLPDMS 608
           T  GRR  LPD++
Sbjct: 820 TLFGRRLYLPDIN 832

 Score = 46.9 bits (109), Expect = 5e-04
 Identities = 34/123 (27%), Positives = 66/123 (53%), Gaps = 16/123 (13%)

Query: 663 EIKDQAKAEGI-------------LIKDNGGKIADAQRQCLNSVIQGTAADMTKYAMIKV 709
           +I+++AKA+G              +   N  +   A+R  +N+ +QGTAAD+ K AMIK+
Sbjct: 807 DIREKAKAQGYVETLFGRRLYLPDINSSNAMRRKGAERVAINAPMQGTAADIIKRAMIKL 866

Query: 710 HNDAELKELGFHLMIPVHDELLGEVPIKNAKRGAERLTEVMIEAAKDIISLPMKCDPSIV 769
            ++     +     +++ VHDEL+ EV   +       E++ + M EAA +++ +P+  +  +
Sbjct: 867 -DEVIRHDPDIEMIMQVHDELVFEVRSEKVAFFREQIKQHM-EAAAELV-VPLIVEVGVG 923

Query: 770 ERW 772
           + W
Sbjct: 924 QNW 926

Query= sid|114825|lan|dp1ORF004 Phage dp1 ORF|40401-42440|3
        (679 letters)

>emb|CAB07981| (Z93946) hypothetical protein [bacteriophage Dp-1]
          Length = 532

 Score = 1011 bits (2585), Expect = 0.0
 Identities = 497/499 (99%), Positives = 498/499 (99%)

Query: 1   MTKFINSYGPLHLNLYVEQVSQDVTNNSSRVSWRATVDRDGAYRTWTYGNISNLSVWLNG 60
           MTKFINSYGPLHLNLYVEQVSQDVTNNSSRVSWRATVDRDGAYRTWTYGNISNLSVWLNG
Sbjct: 1   MTKFINSYGPLHLNLYVEQVSQDVTNNSSRVSWRATVDRDGAYRTWTYGNISNLSVWLNG 60

Query: 61  SSVHSSHPDYDTSGEEVTLASGEVTVPHNSDGTKTMSVWASFDPNNGVHGNITISTNYTL 120
           SSVHSSHPDYDTSGEEVTLASGEVTVPHNSDGTKTMSVWASFDPNNGVHGNITISTNYTL
Sbjct: 61  SSVHSSHPDYDTSGEEVTLASGEVTVPHNSDGTKTMSVWASFDPNNGVHGNITISTNYTL 120

Query: 121 DSIPRSTQISSFEGNRNLGSLHTVIFNRKVNSFTHQVWYRVFGSDWIDLGKNHTTSVSFT 180
           DSIPRSTQISSFEGNRNLGSLHTVIFNRKVNSFTHQVWYRVFGSDWIDLGKNHTTSVSFT
Sbjct: 121 DSIPRSTQISSFEGNRNLGSLHTVIFNRKVNSFTHQVWYRVFGSDWIDLGKNHTTSVSFT 180

Query: 181 PSLDLARYLPKSSSGTMDICIRTYNGTTQIGSDVYSNGWRFNIPDSVRPTFSGISLVDTT 240
           PSLDLARYLPKSSSGTMDICIRTYNGTTQIGSDVYSNGWRFNIPDSVRPTFSGISLVDTT
Sbjct: 181 PSLDLARYLPKSSSGTMDICIRTYNGTTQIGSDVYSNGWRFNIPDSVRPTFSGISLVDTT 240

Query: 241 SAVRQILTGNNFLQIMSNIQVNFNNASGAYGSTIQAFHAELVGKNQAINENGGKLGMMNF 300
           SAVRQILTGNNFLQIMSNIQVNFNNASGAYGSTIQAFHAELVGKNQAINENGGKLGMMNF
Sbjct: 241 SAVRQILTGNNFLQIMSNIQVNFNNASGAYGSTIQAFHAELVGKNQAINENGGKLGMMNF 300

Query: 301 NGSATVRAWVTDTRGKQSNVQDVSINVIEYYGPSINFSVQRTRQNPAIIQALRNAKVAPI 360
           NGSATVRAWVTDTRGKQSNVQDVSINVIEYYGPSINFSVQRTRQNPAIIQALRNAKVAPI
Sbjct: 301 NGSATVRAWVTDTRGKQSNVQDVSINVIEYYGPSINFSVQRTRQNPAIIQALRNAKVAPI 360

Query: 361 TVGGQQKNIMQITFSVAPLNTTNFTEDRGSASGTFTTISLMTNSSANLAGNYGPDKSYIV 420
           TVGGQQKNIMQITFSVAPLNTTNFTEDRGSASGTFTTISL+TNSSANLAGNYGPDKSYIV
Sbjct: 361 TVGGQQKNIMQITFSVAPLNTTNFTEDRGSASGTFTTISLLTNSSANLAGNYGPDKSYIV 420

Query: 421 KAKIQDRFTSTEFSATVATESVVLNYDKDGRLGVGKVVEQGKAGSIDAAGDIYAGGRQVQ 480
           KAKIQDRFTSTEFSATV TESVVLNYDKDGRLGVGKVVEQGKAGSIDAAGDIYAGGRQVQ
Sbjct: 421 KAKIQDRFTSTEFSATVPTESVVLNYDKDGRLGVGKVVEQGKAGSIDAAGDIYAGGRQVQ 480

Query: 481 QFQLTDNNGALNRGQYNDV 499
           QFQLTDNNGALNRGQYNDV
Sbjct: 481 QFQLTDNNGALNRGQYNDV 499


Query= sid|114827|lan|dp1ORF006 Phage dp1 ORF|45296-46987|2
        (563 letters)

>gb|AAD18987| (AE001666) SWI/SNF family helicase_2 [Chlamydia pneumoniae]
          Length = 1166

 Score =  171 bits (429), Expect = 1e-41
 Identities = 150/522 (28%), Positives = 254/522 (47%), Gaps = 55/522 (10%)
```

```
Query: 46   SSNNFE-LPYKYFNNVIDALDEWELHIFGELDKDVQDYIDSRNRIASSSNEQFSFKTTPF 104
            S + FE LP  +  ++ + L E +  I GE++ D QD          +           T
Sbjct: 659  SLDQFEALPVNF--SMSERLIEIQKQIRGEIEFDFQD-------VPQQIQATLRSYQTEG 709

Query: 105  AHQVECFEYAQEHPCFLLGDEQGLGKTKQAIDIAVSRKASFKH--CLIVCCISGLKWNWA 162
             H +E     + H   +L D+ GLGKT QAI IAV++     K   C ++ C + L +NW
Sbjct: 710  VHWLE--RLRKMHLNGILADDMGLGKTLQAI-IAVTQSKLEKGSGCSLIVCPTSLVYNWK 766

Query: 163  KEVGIHSNESAHILGSRVTKDGKLVIDGV-SKRAEDLLGGHDEFFLITNIETLRDAVFIK 221
            +E    + E                 LVIDGV S+R + L    D    IT+    L+  V
Sbjct: 767  EEFRKFNPEFR-----------TLVIDGVPSQRRKQLTALADRDVAITSYNLLQKDV--- 812

Query: 222  YLNELTKSGEIGMVIIDEIHKCKNPSSKQGASIQKLQSYYKMGLTGTPLMNNPIDVFNVM 281
               EL KS    V++DE H  KN +++   S++ +QS +++ LTGTP+ N+  +++++
Sbjct: 813  ---ELYKSFRFDYVVLDEAHHIKNRTTRNAKSVKMIQSDHRLILTGTPIENSLEELWSLF 869

Query: 282  KWLGAEHHTLTQFKERYCIVDQFNQITGYR-----NLAELRELVNDYMLRRTKEEVL-DL 335
             +L        L       +R+  V ++  +   Y      N+  L++ V+ ++LRR KE+VL DL
Sbjct: 870  DFLMPG---LLSSYDRF--VGKYIRTGNYMGNKADNMVALKKKVSPFILRRMKEDVLKDL 924

Query: 336  PEKIRVTEYVDMNSKQSKIY-------KEVLTKLVQEIDKVKLMPNPLAETIRLRQATGN 388
            P    +  +  +    Q ++Y        K+ L++LV++      ++  + LA   RL+Q   +
Sbjct: 925  PPVSEILYHCHLTESQKELYQSYAASAKQELSRLVKQEGFERIHIHVLATLTRLKQICCH 984

Query: 389  PSILTTQDVK---SCKFERCIEIVEECIQQGKSCVIFSNWEKVIEPLAKIL-SKTVKCNL 444
            P+I      +   S K++  ++++   +  G   V+FS  + K++  + K L S+ +
Sbjct: 985  PAIFAKDAPEPGDSAKYDMLMDLLSSLVDSGHKTVVFSQYTKMLGIIKKDLESRGIPFVY 1044

Query: 445  VTGETADKFNEIEEFMNHRKASVILGTIGALGTGFTLTKADTVIFLDSPWTRAEKDQAED 504
            + G T ++  +  +  +F       V L ++ A GTG   L   ADTVI   D   W   A  ++QA D
Sbjct: 1045 LDGSTKNRLDLVNQFNEDPSLLVFLISLKAGGTGLNLVGADTVIHYDMWWNPAVENQATD 1104

Query: 505  RCHRIGAKSSVTIYTLVAKGTVDERIEDLIERKGELADYIVD 546
            R HRIG    SV+ Y LV   T++E+I   L   RK  L    +++
Sbjct: 1105 RVHRIGQSRSVSSYKLVTTLNTIEEKILTLQNRKKSLVKKVIN 1146
```

Query= sid|114828|lan|dp1ORF007 Phage dp1 ORF|22230-23621|3
(463 letters)

>gi|2444105 (U88974) ORF26 [Streptococcus thermophilus temperate bacteriophage O1205]
Length = 411

Score = 88.9 bits (217), Expect = 7e-17
Identities = 80/315 (25%), Positives = 133/315 (41%), Gaps = 48/315 (15%)

```
Query: 139 QGVTLAGIFCDEVALMPESFVNQATGRCSVTGSKMWFSCNPANPNHYFKKNWIDKQVEKR 198
           +G T  G + +E +L  E     +   RCS  G+++ +  NP NPNH+  +++I K  + +
Sbjct: 121 RGFTAFGAYVNEASLANELVFKEIISRCSGDGARVVWDSNPDNPNHWLNRDYIGKN-DGK 179

Query: 199 ILYLHFTMDDNPSLT----DSIKRRYEKMYAGVFRKRFILGLWVTADGLVYSMFNEEQHV 254
           I+    F +DDN  L+      DSIK    K   G F  R ILGLW  A+G +Y+ ++ + HV
Sbjct: 180 IIDFSFKLDDNTFLSKRYIDSIKAATPK---GKFYDRDILGLWTVAEGAIYADYDSKIHV 236

Query: 255 KKLNIEFDRLFVAGDFGIYNATTFGLYGFSKRHKRYHLIESYYHSGREAEEQLTEADVNS 314
                  E  R F  D+G  +  +  +G        ++L++         +E +  +  +A
Sbjct: 237 VDELPEMKRYFGGIDWGYTHYGSIVIVG-EGVDNNFYLVDGVAAQFKEIDWWVEQA---- 291

Query: 315 NIQFSSVLQKTTKEYANDLVDMIRGKQIEYIILDPSASAMIVELQKHPYIAR---KNIPI 371
                     +K T  Y N                          +  +  ++AR   +  I
Sbjct: 292 --------RKLTGIYGN--------------------IPFYADSARPEHVARFENEGFDI 323

Query: 372 IPARNDVTLGISFHAELLAENRFTLDPSNT-HDIDEYYAYSWDSKASQTGEDRVIKEHDH 430
           + A   V  GI   A+L  E +  +           DE Y Y W   ++   +D  +KE D
Sbjct: 324 MNANKSVIAGIELIAKLFKEKKLYVKRGFVPRFFDEIYQYRWKENST---KDEPLKEFDD 380

Query: 431 CMDRNRYACLTDALI 445
           +D  RYA  +D +I
Sbjct: 381 VLDSVRYAIYSDYVI 395
```

Query= sid|114829|lan|dp1ORF008 Phage dp1 ORF|49624-50961|1
(445 letters)

>gb|AAD19901| (AF100420) DnaB replication fork helicase [Thermus aquaticus]

```
          Length = 444

 Score = 67.5 bits (162), Expect = 2e-10
 Identities = 69/248 (27%), Positives = 111/248 (43%), Gaps = 14/248 (5%)

Query: 147 GERLGISTGFEXXXXXXXXXXXXXXXXXIVIMARPGQGKS-WTIDKMLATAWKNGHDVLLYS 205
           GE  G+ TGF+                 I I ARP  GK+ + +      A K G  V +YS
Sbjct: 178 GEVAGVRTGFKELDQLIGTLGPGSLNI-IAARPAMGKTAFALTIAQNAALKEGVGVGIYS 236

Query: 206 GEMSEMQVGARIDTILSNVSINSITKGIWNDHQFEKYEDHIQAMTEAENSLVVVTPFMIG 265
            EM    Q+  R+    + + +N +  G    D  F + D      ++EA     +  TP +
Sbjct: 237 LEMPAAQLTLRMMCSEARIDMNRVRLGQLTDRDFSRLVDVASRLSEAP-IYIDDTPDLTL 295

Query: 266 GKNLTPAILDSMISKYRPSVVGIDQLSLMS--ESYPSREQKRIQYANITMDLYKISAKYG 323
            +     A    ++S+ +  ++ ID L LMS   S  S E ++ + A I+  L  ++ + G
Sbjct: 296 ME--VRARARRLVSQNQVGLIIIDYLQLMSGPGSGKSGENRQQEIAAISRGLKALARELG 353

Query: 324 IPIVLNVQAGRSAKTEGAESMELEHIAESDGVGQNASRVIAMKRD-------EKSGILEL 376
           IPI+    Q  R+ +     +    L  + ES  + Q+A  V+ + RD        EK+GI E+
Sbjct: 354 IPIIALSQLSRAVEARPNKRPMLSDLRESGSIEQDADLVMFIYRDEYYNPHSEKAGIAEI 413

Query: 377 SVVKNRYG 384
            V K R G
Sbjct: 414 IVGKQRNG 421
```

```
Query= sid|114831|lan|dp1ORF010 Phage dp1 ORF|8699-9859|2
         (386 letters)

>gi|2760912 (AF037258) RecA protein [Chlorobium tepidum]
          Length = 346

 Score =  133 bits (331), Expect = 2e-30
 Identities = 99/340 (29%), Positives = 164/340 (48%), Gaps = 66/340 (19%)

Query: 44  GGLPRKRVVEFFGPESSGKTTSALDIVKNAQMVFXXXXXXXXXXXXXXXXXXNARASKASKT 103
            GGLPR RV E +GPESSGKTT AL  +  AQ
Sbjct: 67  GGLPRGRVTEIYGPESSGKTTLALHAIAEAQ--------------------------KNG 100

Query: 104 AVKELEMQLDSLQEPLKIVYLDLENTLDTEWAKKIGVDVDNIWIVRPEMNSAEEILQYVL 163
             + L                +D E+  D  +A+K+GVD++ + + +PE  S E+ L V
Sbjct: 101 GIAAL---------------VDAEHAFDPTYARKLGVDINALLVSQPE--SGEQALSIVE 143

Query: 164 DIFETGEVGLVVLDSLPYMVSQNLIDEELTKKAYAGISAPLTEFSRKVTPLLTRYNAIFL 223
            +  +G V ++V+DS+  +V Q  ++ E+        +  +++  RK+T  +++ +++ L
Sbjct: 144 TLVRSGAVDIIVIDSVAALVPQAELEGEMGDSVVGLQARLMSQALRKLTGAISKSSSVCL 203

Query: 224 GINQIREDMNSQYNA-YSTPGGKMWKHACAVRLKFRKGDYLDENGASLTRTARNPAGNVV 282
            INQ+R+ +   Y +  +T GGK  K   +VRL  RK   + ++G  L        GN
Sbjct: 204 FINQLRDKIGVMYGSPETTTGGKALKFYSSVRLDIRKIAQI-KDGEELV-------GNRT 255

Query: 283 ESFVEKTKAFKPDRKLVSYTLSYHDGIQIENDLVDVAVEFGVIQKAGAWFSIVDLETGEI 342
            +  V K K   P  K   + + Y +GI  +  +L+D+AVEFG+I+K+GAWFS    + G
Sbjct: 256 KVKVVKNKV-APPFKTAEFDILYGEGISVLGELIDLAVEFGIIKKSGAWFSYGTEKLG-- 312

Query: 343 MTDEDEEPLKFQGKANLVRRFKEDDYLFDMVMTAVHEIIT 382
                       QG+ N+ +   KED+ L + +    V +++T
Sbjct: 313 -----------QGRENVKKLLKEDETLRNTIRQQVRDMLT 341
```

```
Query= sid|114832|lan|dp1ORF011 Phage dp1 ORF|28017-29096|3
         (359 letters)

>gi|2444110 (U88974) ORF31 [Streptococcus thermophilus temperate bacteriophage
          O1205]
          Length = 348

 Score =  187 bits (469), Expect = 1e-46
 Identities = 118/358 (32%), Positives = 187/358 (51%), Gaps = 21/358 (5%)

Query: 3   IYDYINAGEIASYIQALPSNALQYLGPTLFPNAQQTGTDISWLKGANNLPVTIQPSNYDA 62
            IYD + A  IA Y  AL  N    LG ++FP  +Q GT +S++KGA+    V ++ + +D
Sbjct: 4   IYDKVTASNIAGYFNALQENVSSTLGESIFPARKQLGTKLSYIKGASGQSVALKAAAFDT 63

Query: 63  KASLRERAGFSKQATEMAFFRESMRLGEKDRQNLQMLLNQSSA-LAQPLITQLYNDTKNL 121
```

```
             ++R+R          +M FF+E+M + E DRQ L ++ +  +A L   ++   ++ND   L
Sbjct: 64   NVTIRDRVSAEMHDEQMPFFKEAMLVKENDRQQLNLVKDSGNAVLVNTIVAGIFNDNLTL 123

Query: 122 VDGVEAQAEYMRMQLLQYGKFTVKSTNSEAQYTYDYNMDAKQQYAVTKKWTNPAESDPIA 181
            V+G  A+ E MRMQ+L  GK     S          Y      D K+Q  V+K W  P  + P+A
Sbjct: 124 VNGARARLEAMRMQVLATGKIAFTSDGVNKDIDYGVKPDHKKQ--VSKSWAEPG-ATPLA 180

Query: 182 DILAAMDDIENRTGVRPTRMVLNRNTYNQMTKSDSIKKAL-AIGVQGSWENFLLLASDAE 240
            D+  A+ +     G+ P R V+N  T+  + K+ S  K +  +  GS      +  ++ E
Sbjct: 181 DLEDAI-ETARELGLNPERAVMNAKTFGLIRKAASTVKVIKPLAGDGS----AVTKAELE 235

Query: 241 KFIAEKTGLQIAVYSKKIAQFADADKLPDVGNIRQFNLIDDGKVVLLPPDAVGHTWYGTT 300
             +IA+  G+ I + +                D G + +F    DG + L+P  +G+T +GTT
Sbjct: 236 NYIADNFGVSIVLENGTYRN--------DKGEVSKF--YPDGHLTLIPNGPLGNTVFGTT 285

Query: 301 PEAFDLASGGT-DAQVQVLSGGPTVTTYLEKHPVNIATVVSAVMIPSFEGIDYVGVLT 357
            PE  DL  +  T +A+V+++  G  VTT      PVN+ T VS V +PSFE +D V +LT
Sbjct: 286 PEESDLFADNTVNAEVEIVDNGIAVTTTKTTDPVNVQTKVSMVALPSFERLDDVYMLT 343
```

```
Query= sid|114834|lan|dp1ORF013 Phage dp1 ORF|10215-11240|3
         (341 letters)

>sp|P09122|DP3X_BACSU DNA POLYMERASE III SUBUNITS GAMMA AND TAU
           Length = 563

 Score =  182 bits (458), Expect = 2e-45
 Identities = 118/353 (33%), Positives = 176/353 (49%), Gaps = 31/353 (8%)

Query: 7    YRPQTFEEVVAQEYVKEILLNQLQNGAIKHGYLFCXXXXXXXXXXXXRIFAKDVN------ 60
            +RPQ FE+VV QE++ + L N L      H YLF               +IFAK VN
Sbjct: 10   FRPQRFEDVVGQEHITKTLQNALLQKKFSHAYLFSGPRGTGKTSAAKIFAKAVNCEHAPV 69

Query: 61   ----------KGL-----GSPIEIDAASNNGVENVRNIIEDSRYKSMDSEFKVYIIDEVH 105
                       KG+          IEIDAASNNGV+ +R+I +  ++        +KVYIIDEVH
Sbjct: 70   DEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDIRDKVKFAPSAVTYKVYIIDEVH 129

Query: 106 MLSTGAFNALLKTLEEPSSGTVFILCTTDPQKIPDTILSRVQRFDFTRIDNDDIVNQLQF 165
            MLS GAFNALLKTLEEP     +FIL TT+P KIP TI+SR QRFDF RI  +  IV ++
Sbjct: 130 MLSIGAFNALLKTLEEPPEHCIFILATTEPHKIPLTIISRCQRFDFKRITSQAIVGRMNK 189

Query: 166 IIESENEEGAGYSYERDALSFIGKLANGGMRDSITRLEKVLDYSHHVDMEAVSNAL---G 222
            I+++E           E  +L  I    A+GGMRD+++ L++ + +S    D+  V +AL   G
Sbjct: 190 IVDAEQ-----LQVEEGSLEIIASAAHGGMRDALSLLDQAISFSG--DILKVEDALLITG 242

Query: 223 VPDYETFASLVEAIANYDGSKCLEIVNDFHYSGKDLKLVTRNFTDFLLEVCKYWLVRDIS 282
                       L +++ + + S  LE +N+      GKD  +  +    +  ++   Y      +
Sbjct: 243 AVSQLYIGKLAKSLHDKNVSDALETLNELLQQGKDPAKLIEDMIFYFRDMLLYKTAPGLE 302

Query: 283 ITQLPAHFESKLEQFCEAFQYPTLLWMLEEMNELAGVVKWEPNAKPIIETKLL 335
                 +     +  E          L  M++ +N+      +KW  + +      E  ++
Sbjct: 303 GVLEKVKVDETFRELSEQIPAQALYEMIDILNKSHQEMKWTNHPRIFFEVAVV 355
```

```
Query= sid|114835|lan|dp1ORF014 Phage dp1 ORF|50961-51974|3
         (337 letters)

>sp|P47492|PRIM_MYCGE DNA PRIMASE >gi|1361496|pir||F64227 DNA primase (dnaE) homolog
           MG250 - Mycoplasma genitalium (SGC3) >gi|3844848
           (U39704) DNA primase (dnaE) [Mycoplasma genitalium]
           Length = 607

 Score = 57.0 bits (135), Expect = 2e-07
 Identities = 53/190 (27%), Positives = 89/190 (45%), Gaps = 17/190 (8%)

Query: 146 EELDKYRFIHP-------YMYERKLTDELIEMFDVGYDK--LHDCITFPVRNLKGETVFF 196
            E +++Y FI+P          Y++  K    + +  FD     K     + I  P+ +  G  V F
Sbjct: 170 ESMERYPFINPKIKPSELYLFS-KTNQQGLGFFDFNTKKATFQNQIMIPIHDFNGNPVGF 228

Query: 197 NRRSVRSKFHQYGEDDPKTEFLYGQYELVAFRDYFEKPISQVFVTESVINCLTLWSMKIP 256
            + RSV +          ++      EF + + EL+          K ++Q+F+ E    +  TL + K
Sbjct: 229 SARSVDNINKLKYKNSADHEF-FKKGELLFNFHRLNKNLNQLFIVEGYFDVFTLTNSKFE 287

Query: 257 AVALMGVGGGN-QINLLKR--LPYRNIVLALDPDNAGQTAQEKLYRQLKRSK-VVRFLNY 312
            AVALMG+     + QI   +K          + +VLALD D +GQ A    L   +L   +   +V   + +
Sbjct: 288 AVALMGLALNDVQIKAIKAHFKELQTLVLALDNDASGQNAVFSLIEKLNNNNFIVEIVQW 347
```

```
Query: 313 PKEFYDNKWD 322
             + D  WD
Sbjct: 348 EHNYKD--WD 355



Query= sid|114837|lan|dp1ORF016 Phage dp1 ORF|43413-44303|3
         (296 letters)

>emb|CAB07986| (Z93946) N-acetylmuramoyl-L-alanine amidase [bacteriophage Dp-1]
          Length = 296

 Score =  661 bits (1686), Expect = 0.0
 Identities = 296/296 (100%), Positives = 296/296 (100%)

Query: 1    MGVDIEKGVAWMQARKGRVSYSMDFRDGPDSYDCSSSMYYALRSAGASSAGWAVNTEYMH 60
            MGVDIEKGVAWMQARKGRVSYSMDFRDGPDSYDCSSSMYYALRSAGASSAGWAVNTEYMH
Sbjct: 1    MGVDIEKGVAWMQARKGRVSYSMDFRDGPDSYDCSSSMYYALRSAGASSAGWAVNTEYMH 60

Query: 61   AWLIENGYELISENAPWDAKRGDIFIWGRKGASAGAGGHTGMFIDSDNIIHCNYAYDGIS 120
            AWLIENGYELISENAPWDAKRGDIFIWGRKGASAGAGGHTGMFIDSDNIIHCNYAYDGIS
Sbjct: 61   AWLIENGYELISENAPWDAKRGDIFIWGRKGASAGAGGHTGMFIDSDNIIHCNYAYDGIS 120

Query: 121 VNDHDERWYYAGQPYYYVYRLTNANAQPAEKKLGWQKDATGFWYARANGTYPKDEFEYIE 180
            VNDHDERWYYAGQPYYYVYRLTNANAQPAEKKLGWQKDATGFWYARANGTYPKDEFEYIE
Sbjct: 121 VNDHDERWYYAGQPYYYVYRLTNANAQPAEKKLGWQKDATGFWYARANGTYPKDEFEYIE 180

Query: 181 ENKSWFYFDDQGYMLAEKWLKHTDGNWYWFDRDGYMATSWKRIGESWYYFNRDGSMVTGW 240
            ENKSWFYFDDQGYMLAEKWLKHTDGNWYWFDRDGYMATSWKRIGESWYYFNRDGSMVTGW
Sbjct: 181 ENKSWFYFDDQGYMLAEKWLKHTDGNWYWFDRDGYMATSWKRIGESWYYFNRDGSMVTGW 240

Query: 241 IKYYDNWYYCDATNGDMKSNAFIRYNDGWYLLLPDGRLADKPQFTVEPDGLITAKV 296
            IKYYDNWYYCDATNGDMKSNAFIRYNDGWYLLLPDGRLADKPQFTVEPDGLITAKV
Sbjct: 241 IKYYDNWYYCDATNGDMKSNAFIRYNDGWYLLLPDGRLADKPQFTVEPDGLITAKV 296

Query= sid|114841|lan|dp1ORF020 Phage dp1 ORF|1864-2658|1
         (264 letters)

>emb|CAB13247| (Z99111) similar to coenzyme PQQ synthesis [Bacillus subtilis]
          Length = 243

 Score =  217 bits (548), Expect = 5e-56
 Identities = 117/248 (47%), Positives = 163/248 (65%), Gaps = 15/248 (6%)

Query: 23   MPIMEIFGPTIQGEGMVIGQKTIFIRTGGCDYHCNWCDSAFTWNGTTEPE--YITGKEAA 80
            +P++EIFGPTIQGEGMVIGQKT+F+RT GCDY C+WCDSAFTW+G+ + +  ++T +E
Sbjct: 5    IPVLEIFGPTIQGEGMVIGQKTMFVRTAGCDYSCSWCDSAFTWDGSAKKDIRWMTAEEIF 64

Query: 81   SRILKLAFNDKGEQICNHVTLTGGNPALINEPMAKMISILKEHGFKFGLETQGTRFQEWF 140
            + +       D G     +HVT++GGNPAL+ + +    I +LKE+  +  LETQGT +Q+WF
Sbjct: 65   AEL-----KDIGGDAFSHVTISGGNPALLKQ-LDAFIELLKENNIRAALETQGTVYQDWF 118

Query: 141 KEVSDITISPKPPSSGMRTNMKILEAIVDRM--NDENLDWSFKIVIFDENDLAYARDMFK 198
             + D+TISPKPPSS M TN + L+ I+ +  ND      S K+VIF++ DL +A+ + K
Sbjct: 119 TLIDDLTISPKPPSSKMVTNFQKLDHILTSLQENDRQHAVSLKVVIFNDEDLEFAKTVHK 178

Query: 199 TFEGKLRPVNYLSVGNANAY--EEGKISDRLLEKLGWLWDKVYEDPAFNNVRPLPQLHTL 256
            + G       YL VGN + +  ++ +  LL K  L DKV  D  N VR LPQLHTL
Sbjct: 179 RYPG---IPFYLQVGNDDVHTTDDQSLIAHLLGKYEALVDKVAVDAELNLVRVLPQLHTL 235

Query: 257 VYDNKRGV 264
            ++ NKRGV
Sbjct: 236 LWGNKRGV 243
```

```
Query= sid|114842|lan|dp1ORF021 Phage dp1 ORF|2504-3295|2
        (263 letters)

>sp|P19465|GCH1_BACSU GTP CYCLOHYDROLASE I (GTP-CH-I) >gi|98411|pir||A38256 GTP
           cyclohydrolase I (EC 3.5.4.16) - Bacillus subtilis
           >gi|143231 (M37320) regulatory protein [Bacillus
           subtilis] >gi|143799 (M80245) MtrA [Bacillus subtilis]
           >gi|2634696|emb|CAB14194| (Z99115) GTP cyclohydrolase I
           [Bacillus subtilis]
           Length = 190

 Score = 208 bits (523), Expect = 4e-53
 Identities = 103/185 (55%), Positives = 133/185 (71%), Gaps = 1/185 (0%)

Query: 80  VTLDNTEAAVQRLFGLLGEDAERDGLQDTPFRFVKALAEHTVGYREDPKLHLEKTFDVDH 139
           V  +  E AV+++    +GED  R+GL DTP R  K  AE   G  EDPK H +  F  +H
Sbjct: 4   VNKEQIEQAVRQILEAIGEDPNREGLLDTPKRVAKMYAEVFSGLNEDPKEHFQTIFGENH 63

Query: 140 EDLVLVKDIPFNSLCEHHLAPFVGKVHIAYIPKD-KITGLSKFGRVVEGYAKRLQVQERL 198
           E+LVLVKDI F+S+CEHHL PF GK H+AYIP+  K+TGLSK  R VE  AKR Q+QER+
Sbjct: 64  EELVLVKDIAFHSMCEHHLVPFYGKAHVAYIPRGGKVTGLSKLARAVEAVAKRPQLQERI 123

Query: 199 TQQIADAIQEVLNPQAVAVIVEAEHTCMSGRGIKKHGATTVTSTMRGLFQDDASARAELL 258
           T  IA++I E L+P  V V+VEAEH CM+ RG++K GA TVTS +RG+F+DDA+ARAE+L
Sbjct: 124 TSTIAESIVETLDPHGVMVVVEAEHMCMTMRGVRKPGAKTVTSAVRGVFKDDAAARAEVL 183

Query: 259 QLIKK 263
           + IK+
Sbjct: 184 EHIKR 188


Query= sid|114843|lan|dp1ORF022 Phage dp1 ORF|30896-31675|2
        (259 letters)

>gi|2347102 (U77367) internalin [Listeria monocytogenes]
           Length = 821

 Score = 55.0 bits (130), Expect = 5e-07
 Identities = 44/149 (29%), Positives = 63/149 (41%), Gaps = 13/149 (8%)

Query: 119 FRMNIYVPNYVG--DSIVNYVKITLNNCTGKAPGLSIGKEFYAPEFNIKAREATKAGLPV 176
           F   + VPN +   D  +   +   NN T  AP L       Y PE  +K   + K  +
Sbjct: 383 FSKTLSVPNNITSIDGTLIAPETISNNGTYDAPNLKWSLPNYLPE--VKYTFSQKIPIGT 440

Query: 177 KSMDYVAQLPAVLR-----RVTFDLNGGTGTADAVRVEAGKKISPKPVDPTLTGKAFKGW 231
            + +Y   +   L+     +VTF++ G T   + V  E    + P+P  PT  G  F GW
Sbjct: 441 GTSNYSGFITQPLKELLDYKVTFNVEGNTSEVETVTEE---NLIPEPTSPTKQGYTFDGW 497

Query: 232 -KVEGESTIWDFDNHMMPDRDVKLVAQFA 259
            E   T WDF     MP  D+ L A F+
Sbjct: 498 YDAETGGTKWDFTTGQMPANDLTLYAHFS 526


 Score = 43.4 bits (100), Expect = 0.002
 Identities = 47/195 (24%), Positives = 73/195 (37%), Gaps = 12/195 (6%)

Query: 72  YDLTFKDNTFDPEIMALIEGGTVRQQGGTIAGYDT-PMLAQGASNMKPFRMNIYVPNY-- 128
           YD     + T   +    +G    + GG    + T  M A    +   F +N Y  N+
Sbjct: 547 YDALLNEPTTPTKQGYTFDGWYDAETGGNKWDFKTMKMPANDVAFYAHFTINNYQANFDI 606

Query: 129 ---VGDSIVNYVKITLNNCTGKAPGLSIGKEFYAPEFNIKAREATKAGLPVKSMDYVAQL 185
              V +  + Y  +   T  G +  +  A   K    TK +P  +  A
Sbjct: 607 DGEVKNETIAYDTLLNEPTTPTKQGYTFDGWYDAETGGTKWDFKTKE-MPANDVTLYAHF 665

Query: 186 PAVLRRVTFDLNGGTGTADAVRVEAGKKISPKPVDPTLTGKAFKGW-KVEGESTIWDFDN 244
            +   FD++G   T + V  +A   + P+P  P+ TG  +GW  E   T WDF
Sbjct: 666 TINNYQANFDIDGAV-TEEVVNYDA---LIPEPTSPSKTGFTLEGWYDAEVGGTKWDFKT 721

Query: 245 HMMPDRDVKLVAQFA 259
            MP  D+ L A F+
Sbjct: 722 MKMPANDITLYAHFS 736


 Score = 38.3 bits (87), Expect = 0.057
 Identities = 42/169 (24%), Positives = 59/169 (34%), Gaps = 10/169 (5%)
```

```
Query: 96  QQGGTIAGYDT-PMLAQGASNMKPFRMNIYVPNYVGDSIVNYVKIT----LNNCTGKAPG 150
            + GGT    + T  M A    +     F +N Y  N+  D +V     +        LN  T
Sbjct: 501 ETGGTKWDFTTGQMPANDLTLYAHFSVNSYQANFDIDGVVTNEAVVYDALLNEPTTPTKQ 560

Query: 151 LSIGKEFYAPEFNIKAREATKAGLPVKSMDYVAQLPAVLRRVTFDLNGGTGTADAVRVEA 210
              +Y   E         +        +P    + + A         +    FD++G                A
Sbjct: 561 GYTFDGWYDAETGGNKWDFKTMKMPANDVAFYAHFTINNYQANFDIDGEVKNETI----A 616

Query: 211 GKKISPKPVDPTLTGKAFKGW-KVEGESTIWDFDNHMMPDRDVKLVAQF 258
              +  +P   PT   G   F GW     E     T WDF      MP   DV L A F
Sbjct: 617 YDTLLNEPTTPTKQGYTFDGWYDAETGGTKWDFKTKEMPANDVTLYAHF 665


Query= sid|114850|lan|dp1ORF029 Phage dp1 ORF|662-1348|2
        (228 letters)

>gi|2650185 (AE001074) succinoglycan biosynthesis regulator (exsB)
          [Archaeoglobus fulgidus]
          Length = 239

 Score =  119 bits (295), Expect = 2e-26
 Identities = 79/224 (35%), Positives = 113/224 (50%), Gaps = 11/224 (4%)

Query: 1   MKSVVLLSGGVDSATCLAIEVDKWGSKNVHAIAFNYGQKHEAELENAANVAMFYGVKFTI 60
            MK+V+LLSGG+DS+T L    +D  G    VHA+ F YGQKH  E+E+A  VA      V+
Sbjct: 1   MKAVMLLSGGIDSSTLLYYLLD--GGYEVHALTFFYGQKHSKEIESAEKVAKAAKVRHLK 58

Query: 61  LEIDSKIYXXXXXXXLLQGKGEISHGKSYAEILAEKEVVDTYVPFRNGLMLSQXXXXXXXX 120
            ++I S I+          L G+ E+        Y+E +   +      T VP RN ++LS
Sbjct: 59  VDI-STIHDLISYGALTGEEEVPKA-FYSEEVQRR----TIVPNRNMILLS--IAAGYAV 110

Query: 121 XXXXXXXXXXXXXXXXXXXPDCTPEFYNSMSNAMEYGT-GGKVTLVAPLLTLTKAQVVKW 179
                                PDC   EF   ++   A+             V + AP + +TKA +V+
Sbjct: 111 KIGAKEVHYAAHLSDYSIYPDCRKEFVKALDTAVYLANIWTPVEVRAPFVDMTKADIVRL 170

Query: 180 GIDLDVPYFLTRSCYESDAESCGTCATCIDRKKAFEENGMTDPI 223
            G+ L VPY LT SCYE          C +C TC++R +AF  NG+ DP+
Sbjct: 171 GLKLGVPYELTWSCYEGGDRPCLSCGTCLERTEAFLANGVKDPL 214


Query= sid|114855|lan|dp1ORF034 Phage dp1 ORF|131-652|2
        (173 letters)

>emb|CAB13248| (Z99111) similar to hypothetical proteins [Bacillus subtilis]
          Length = 165

 Score =  220 bits (556), Expect = 4e-57
 Identities = 103/139 (74%), Positives = 117/139 (84%)

Query: 5   TTRTDAELTGVTLLGNQDTKYDYDYNPDVLETFPNKHPENNYLVTFDGYEFTSLCPKTGQ 64
            TTR ++EL GVTLLGNQ T Y ++Y PDVLE+FPNKH     +Y V F+  EFTSLCPKTGQ
Sbjct: 2   TTRKESELEGVTLLGNQGTNYLFEYAPDVLESFPNKHVNRDYFVKFNCPEFTSLCPKTGQ 61

Query: 65  PDFANVFISYIPNEKMVESKSLKLYLFSFRNHGDFHEDCMNIILNDLYELMEPKYIEVMG 124
            PDFA ++ISYIP+EKMVESKSLKLYLFSFRNHGDFHEDCMNII+NDL ELM+P+YIEV G
Sbjct: 62  PDFATIYISYIPDEKMVESKSLKLYLFSFRNHGDFHEDCMNIIMNDLIELMDPRYIEVWG 121

Query: 125 LFTPRGGISIYPFVNKVNP 143
             FTPRGGISI P+ N    P
Sbjct: 122 KFTPRGGISIDPYTNYGKP 140


Query= sid|114857|lan|dp1ORF036 Phage dp1 ORF|48808-49362|1
        (184 letters)

>gi|1353529 (U38906) ORF12 [Bacteriophage r1t]
          Length = 296

 Score = 53.5 bits (126), Expect = 1e-06
 Identities = 42/149 (28%), Positives = 70/149 (46%), Gaps = 9/149 (6%)

Query: 34  IASNTVGNGKTSWAVRLLQRYLAETALDGRIVEKGMFVVSAQLLTEFGDYNYFQTMQEFL 93
            + S    G GK+   A+ +L+   L   T  L    ++          V    +      F + + F + + F+
Sbjct: 155 VVSGPAGTGKSHLAMSILKDCLQHTDLT--VIFASWSEVLHLIKDSFDNKDSFYSTEYFM 212
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Query: 94  ERFERLKTCELLVIDEIGGGSLTKASYPYLYDLVNYRVDNNLSTIYTTNYTDDEIIDLLG 153
           E F    +  +LLVID+IG    +T+ S    L ++++ R       TI TTN    DEI
Sbjct: 213 EVF---RNTDLLVIDDIGSEKITEWSMSLLTEVLDART----KTIITTNLKSDEIRKKYH 265

Query: 154 QRLYSRIYDTSVVLDFQASNVRGLEVSEI 182
             R YSR++        F    N++    VS++
Sbjct: 266 NRTYSRLFRGIGKKAFNFENIKDKRVSQL 294

Query= sid|114859|lan|dp1ORF038 Phage dp1 ORF|1350-1871|3
        (173 letters)

>sp|P44123|YB90_HAEIN HYPOTHETICAL PROTEIN HI1190 >gi|1074675|pir||F64021 hypothetical
          protein HI1190 - Haemophilus influenzae (strain Rd KW20)
          >gi|1574117 (U32798) 6-pyruvoyl tetrahydrobiopterin
          synthase, putative [Haemophilus influenzae Rd]
          Length = 141

 Score =  100 bits (247), Expect = 6e-21
 Identities = 59/143 (41%), Positives = 83/143 (57%), Gaps = 10/143 (6%)

Query: 2   RVSKTLTFDAAHQLVGHFGKCANLHGHTYKVEISLAGGTYDHGSSQGMVVDFYHVKKIA- 60
           ++SK   +FD AH L GH GKC NLHGHTYK+++ ++G   Y   G+ + MV+DF   +K I
Sbjct: 3   KISKEFSFDMAHLLDGHDGKCQNLHGHTYKLQVEISGDLYKSGAKKAMVIDFSDLKSIVK 62

Query: 61  GTFIDRLDHAVLL-QGNEP----IALANAVDTKRVLFGFRTTAENMSRFLTWTLTELMWK 115
             +D +DHA +  Q NE         L    +++K      FRTTAE ++RF+     L      +
Sbjct: 63  KVILDPMDHAFIYDQTNERESQIATLLQKLNSKTFGVPFRTTAEEIARFIFNRLKH--DE 120

Query: 116 HARIDSIKLWETPTGCAECTYYE 138
             I SI+LWETPT   + C Y E
Sbjct: 121 QLSISSIRLWETPT--SFCEYQE 141


Query= sid|114860|lan|dp1ORF039 Phage dp1 ORF|3306-3803|3
        (165 letters)

>emb|CAA68244| (X99978) ORF7; hydophobic protein [Lactobacillus plantarum]
          Length = 168

 Score = 64.4 bits (154), Expect = 5e-10
 Identities = 49/156 (31%), Positives = 84/156 (53%), Gaps = 9/156 (5%)

Query: 8   WLVRTALIAALYVTLTVAFSAISY--GPIQFRVSEALILLPLWNHRWTPGIVLGTIIANF 65
           W++  AL+AA+YV L +   +A S    G IQFRVSE L   L ++N ++   GIV G I+ +
Sbjct: 9   WIIN-ALVAAMYVVLCLGPAAFSLASGAIQFRVSEGLNHLAVFNRKYIWGIVAGVILFDA 67

Query: 66  FSP-LGLIDVLFGSLATFLGXXXXXXXXXXXSPLYSLICPVLA----NAYLIALELRIVY 120
           F P    L++VLFG    + L                 ++  +    +A     + ++IAL + ++
Sbjct: 68  FGPGASLLNVLFGGGQSLLALLVLTWLAPKLKTVWQRMLLNIALFTVSMFMIALMITMMS 127

Query: 121 S-LPFWESVIYVGISEAIIVLISYFLISTLAKNNHF 155
           S + FW + +    +SE II+ I+   ++ +L +   HF
Sbjct: 128 SGVAFWPTYLTTALSELIIMSITAPIMYSLDRVLHF 163


Query= sid|114862|lan|dp1ORF041 Phage dp1 ORF|8208-8699|3
        (163 letters)

>gi|2522313 (AF012906) dUTPase homolog [Bacillus subtilis]
          >gi|2634394|emb|CAB13893| (Z99114) similar to
          deoxyuridine 5'-triphosphate nucleotidohydrolase
          [Bacillus subtilis] >gi|3025643 (AF020713) putative
          dUTPase [Bacteriophage SPBc2]
          Length = 142

 Score =  108 bits (267), Expect = 2e-23
 Identities = 65/160 (40%), Positives = 83/160 (51%), Gaps = 25/160 (15%)

Query: 5   VDVKMIDPKLDRLKYT--GDWVDVRISSITKIDADSADVSRCRKVLQKAQVYSVAAGECI 62
           + +K +D      R+        GDW+D+R +      I   D    +
Sbjct: 3   IKIKYLDETQTRINKMEQGDWIDLRAAEDVAIKKDEFKL-------------------- 41

Query: 63  KIAHGFALELPKGYEAILHPRSSLFKKTGLIFVSS-GVIDEGYKGDTDEWFSVWYATRDA 121
            +   G A+ELP+GYEA + PRSS +K  G+I  +S GVIDE YKGD D WF    YA RD
Sbjct: 42  -VPLGVAMELPEGYEAHVVPRSSTYKNFGVIQTNSMGVIDESYKGDNDFWFFPAYALRDT 100
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Query: 122 DIFYDQRIAQFRIQEKQPAIKFNFVESLGNAARGGHGSTG 161
           I     RI QFRI +K PA+     V+ LGN  RGGHGSTG
Sbjct: 101 KIKKGDRICQFRIMKKMPAVDLIEVDRLGNGDRGGHGSTG 140
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Query= sid|114867|lan|dp1ORF046 Phage dp1 ORF|42774-43202|3
         (142 letters)

>emb|CAB07984| (Z93946) hypothetical protein [bacteriophage Dp-1]
          Length = 142

 Score =  287 bits (728), Expect = 2e-77
 Identities = 142/142 (100%), Positives = 142/142 (100%)

Query: 1   MPMWLNDTAVLTTIITACSGVLTVLLNKLFEWKSNKAKSVLEDISTTLSTLKQQVDGIDQ 60
            MPMWLNDTAVLTTIITACSGVLTVLLNKLFEWKSNKAKSVLEDISTTLSTLKQQVDGIDQ
Sbjct: 1   MPMWLNDTAVLTTIITACSGVLTVLLNKLFEWKSNKAKSVLEDISTTLSTLKQQVDGIDQ 60

Query: 61  TTVAINHQNDVIQDGTRKIQRYRLYHDLKREVITGYTTLDHFRELSILFESYKNLGGNGE 120
            TTVAINHQNDVIQDGTRKIQRYRLYHDLKREVITGYTTLDHFRELSILFESYKNLGGNGE
Sbjct: 61  TTVAINHQNDVIQDGTRKIQRYRLYHDLKREVITGYTTLDHFRELSILFESYKNLGGNGE 120

Query: 121 VEALYEKYKKLPIREEDLDETI 142
            VEALYEKYKKLPIREEDLDETI
Sbjct: 121 VEALYEKYKKLPIREEDLDETI 142
```

```
Query= sid|114901|lan|dp1ORF080 Phage dp1 ORF|42490-42759|1
         (89 letters)

>emb|CAB07983| (Z93946) hypothetical protein [bacteriophage Dp-1]
          Length = 124

 Score =  147 bits (367), Expect = 1e-35
 Identities = 75/75 (100%), Positives = 75/75 (100%)

Query: 1  MLNLTKSRQIVAEFTIGQGAEKKLVKTTIVNIDANAVSTVSETLHDPDLYAANRRELRAD 60
           MLNLTKSRQIVAEFTIGQGAEKKLVKTTIVNIDANAVSTVSETLHDPDLYAANRRELRAD
Sbjct: 1  MLNLTKSRQIVAEFTIGQGAEKKLVKTTIVNIDANAVSTVSETLHDPDLYAANRRELRAD 60

Query: 61 EQKLRETRYAIEDEI 75
           EQKLRETRYAIEDEI
Sbjct: 61 EQKLRETRYAIEDEI 75
```

```
Query= sid|114912|lan|dp1ORF091 Phage dp1 ORF|43189-43413|1
         (74 letters)

>emb|CAB07985| (Z93946) holin [bacteriophage Dp-1]
          Length = 74

 Score = 63.2 bits (151), Expect = 2e-10
 Identities = 34/74 (45%), Positives = 34/74 (45%)

Query: 1  MKLSNEQYDXXXXXXXXXXXXXXXXXXXXXXYQFDXXXXXXXXXXXXXXXXXVLGVSSR 60
           MKLSNEQYD                      YQFD                 VLGVSSR
Sbjct: 1  MKLSNEQYDVAKNVVTVVVPAAIALITGLGALYQFDTTAITGTIALLATFAGTVLGVSSR 60

Query: 61 NYQKEQEAQNNEVE 74
           NYQKEQEAQNNEVE
Sbjct: 61 NYQKEQEAQNNEVE 74
```

Condensed listing of homology information from above

Phage: dp1

Database: nr

Program: Blastp

Query= sid|114822|lan|dp1ORF001 Phage dp1 ORF|36698-40390|2
(1230 letters)

gi|2444124 (U88974) ORF45 [Streptococcus thermophilus temperate ...	467	e-130
gi|928828 (L44593) ORF1904; putative [Lactococcus lactis phage B...	427	e-118
gi|2935676 (AF032121) unknown [Streptococcus thermophilus bacter...	309	1e-82
gi|2935691 (AF032122) unknown [Streptococcus thermophilus bacter...	306	7e-82
gi|3540289 (AF057033) putative anti-receptor [Streptococcus ther...	279	6e-74
gi|4530154|gb|AAD21894.1| (AF085222) putative tail-host specific...	220	3e-56
gi|930045|emb|CAA33387| (X15332) alpha-1 (III) collagen [Homo sa...	58	4e-07
gi|1070603|pir||CGHU7L collagen alpha 1(III) chain precursor - h...	58	4e-07
gi|4502951|ref|NP_000081.1|PCOL3A1| collagen, type III, alpha 1 ...	58	4e-07
gi|115290|sp|P04258|CA13_BOVIN COLLAGEN ALPHA 1(III) CHAIN >gi|7...	58	4e-07
gi|575322|emb|CAA36279| (X52046) type III collagen [Mus musculus]	57	8e-07
gi|2119163|pir||S59856 collagen alpha 1(III) chain precursor - m...	57	8e-07
gi|543912|sp|P13941|CA13_RAT COLLAGEN ALPHA 1(III) CHAIN >gi|543...	57	1e-06
gi|3171998|emb|CAA06510| (AJ005395) collagen alpha 1 (III) [Ratt...	57	1e-06
gi|3947565|emb|CAA90250| (Z49967) similar to collagen; cDNA EST ...	54	7e-06
gi|423403|pir||A46053 bullous pemphigoid antigen, BPAG2, type XV...	53	9e-06
gi|115410|sp|P12114|CCS1_CAEEL CUTICLE COLLAGEN SQT-1 >gi|84437|...	53	9e-06
gi|3873801|emb|CAA90084| (Z49907) cuticle collagen SQT-1; cDNA E...	53	9e-06

Query= sid|114823|lan|dp1ORF002 Phage dp1 ORF|32386-35835|1
(1149 letters)

gi|3341922|dbj|BAA31888| (AB009866) orf 15 [bacteriophage phi PVL]	280	3e-74
gi|4126622|dbj|BAA36642.1| (AB016282) ORF36 [bacteriophage phi-105]	232	1e-59
gi|1369948|emb|CAA59194| (X84706) host interacting protein [Bact...	201	3e-50
gi|3139112 (AF063097) gpT [Bacteriophage P2]	188	2e-46
gi|3337272 (U32222) G protein [Bacteriophage 186]	161	3e-38
gi|4063799|dbj|BAA36253| (AB008550) orf25; similar to T gene of ...	159	8e-38
gi|3172274 (AF022214) minor tail subunit; putative tape-measure ...	123	6e-27
gi|465127|sp|Q05233|VG26_BPML5 MINOR TAIL PROTEIN GP26 >gi|41904...	108	2e-22
gi|3540284 (AF057033) putative minor tail protein [Streptococcus...	99	2e-19
gi|2444119 (U88974) ORF40 [Streptococcus thermophilus temperate ...	90	6e-17
gi|2634555|emb|CAB14053| (Z99115) yomI [Bacillus subtilis] >gi|3...	66	1e-09
gi|2392838 (AF011378) unknown [Bacteriophage sk1]	64	5e-09
gi|2764873|emb|CAA66557| (X97918) gene 18.1 [Bacteriophage SPP1]	62	3e-08
gi|1353559 (U38906) ORF42 [Bacteriophage r1t]	61	6e-08
gi|630841|pir||S39079 puff C-8 protein - fungus gnat (Rhynchosci...	55	2e-06
gi|1730865|sp|P51731|YO27_BPHP1 HYPOTHETICAL 72.8 KD PROTEIN IN ...	53	8e-06
gi|224288|prf||1101273J ORF 7 [Bacteriophage HP1]	53	1e-05

Query= sid|114824|lan|dp1ORF003 Phage dp1 ORF|53538-55877|3
(779 letters)

gi|118825|sp|P00582|DPO1_ECOLI DNA POLYMERASE I (POL I) >gi|6705...	193	3e-48
gi|2982102|pdb|1KFS|A Chain A, All-Oxygen Dna Complexed To The 3...	193	3e-48
gi|229889|pdb|1DPI| DNA Polymerase I (Klenow Fragment) (E.C.2....	193	3e-48
gi|1169402|sp|P43741|DPO1_HAEIN DNA POLYMERASE I (POL I) >gi|107...	191	1e-47
gi|2688462 (AE001156) DNA polymerase I (polA) [Borrelia burgdorf...	190	3e-47
gi|809180|pdb|1KLN|A Escherichia coli	190	3e-47
gi|1913934|emb|CAA72997| (Y12328) DNA-directed DNA polymerase I ...	189	8e-47
gi|4090935 (AF028719) DNA polymerase type I [Rhodothermus sp. 'I...	175	1e-42
gi|4731571|gb|AAD28505.1|AF121780_1 (AF121780) DNA polymerase I ...	174	2e-42
gi|1633576 (U57757) similar to proofreading 3'-5' exonuclease an...	173	4e-42
gi|3322368 (AE001195) DNA polymerase I (polA) [Treponema pallidum]	172	9e-42
gi|1006595|dbj|BAA10748| (D64005) DNA polymerase I [Synechocysti...	171	2e-41
gi|585062|sp|Q07700|DPO1_MYCTU DNA POLYMERASE I (POL I) >gi|4161...	163	5e-39
gi|4376908|gb|AAD18751| (AE001645) DNA Polymerase I [Chlamydia p...	157	2e-37
gi|1169403|sp|P46835|DPO1_MYCLE DNA POLYMERASE I (POL I) >gi|107...	152	7e-36
gi|2145839|pir||S72949 DNA polymerase I - Mycobacterium leprae >...	152	7e-36
gi|1405438|emb|CAA67184| (X98575) DNA-dependent DNA polymerase [...	152	9e-36
gi|2506365|sp|P80194|DPO1_THECA DNA POLYMERASE I, THERMOSTABLE (...	147	2e-34
gi|3328929 (AE001322) DNA Polymerase I [Chlamydia trachomatis]	147	3e-34

gi|3913510|sp|O52225|DPO1_THEFI DNA POLYMERASE I, THERMOSTABLE (...	146	7e-34
gi|1205984 (U33536) DNA polymerase I (Bacillus stearothermophilus)	146	7e-34
gi|118827|sp|P13252|DPO1_STRPN DNA POLYMERASE I (POL I) >gi|9802...	145	9e-34
gi|1942202|pdb|1JXE| Stoffel Fragment Of Taq Dna Polymerase I	145	1e-33
gi|1943520|pdb|1KTQ| Dna Polymerase	145	1e-33
gi|1084022|pir||JX0359 DNA-directed DNA polymerase (EC 2.7.7.7) ...	145	1e-33
gi|507891|dbj|BAA06775| (D32013) DNA Polymerase (Thermus aquaticus)	145	1e-33
gi|118828|sp|P19821|DPO1_THEAQ DNA POLYMERASE I, THERMOSTABLE (T...	145	1e-33
gi|1706502|sp|P52028|DPO1_THETH DNA POLYMERASE I, THERMOSTABLE (...	144	2e-33
gi|1097211|prf||2113329A DNA polymerase (Thermus aquaticus therm...	144	2e-33
gi|2098289|pdb|1TAU|A Chain A, Structure Of Dna Polymerase	143	3e-33

Query= sid|114825|lan|dp1ORF004 Phage dp1 ORF|40401-42440|3
(679 letters)

gi|1934761|emb|CAB07981| (Z93946) hypothetical protein (bacterio...	1011	0.0
gi|3540290 (AF057033) putative minor structural protein (Strepto...	346	2e-94
gi|2444125 (U88974) ORF46 (Streptococcus thermophilus temperate ...	339	3e-92
gi|1934762|emb|CAB07982| (Z93946) hypothetical protein (bacterio...	300	2e-80
gi|4530155|gb|AAD21895.1| (AF085222) unknown (Streptococcus ther...	276	4e-73
gi|2935677 (AF032121) unknown (Streptococcus thermophilus bacter...	250	3e-65
gi|2935692 (AF032122) unknown (Streptococcus thermophilus bacter...	250	3e-65
gi|1136289 (U42597) histidine kinase A (Dictyostelium discoideum)	50	7e-05

Query= sid|114827|lan|dp1ORF006 Phage dp1 ORF|45296-46987|2
(563 letters)

gi|4377165|gb|AAD18987| (AE001666) SWI/SNF family helicase_2 (Ch...	171	1e-41
gi|1769947|emb|CAA67095| (X98455) SNF (Bacillus cereus)	160	3e-38
gi|3329163 (AE001341) SWF/SNF family helicase (Chlamydia trachom...	159	6e-38
gi|4377149|gb|AAD18973| (AE001664) SWI/SNF family helicase_1 (Ch...	157	2e-37
gi|3328995 (AE001326) SWI/SNF family helicase (Chlamydia trachom...	153	2e-36
gi|2493354|sp|P75093|Y018_MYCPN HYPOTHETICAL HELICASE MG018/MG01...	146	4e-34
gi|1653748|dbj|BAA18659| (D90916) helicase of the snf2/rad54 fam...	143	3e-33
gi|1763712|emb|CAB05939| (Z83337) member of the SNF2 helicase fa...	143	4e-33
gi|2636153|emb|CAB15645.1| (Z99122) similar to SNF2 helicase (Ba...	143	4e-33
gi|2909552|emb|CAA17284| (AL021924) helZ (Mycobacterium tubercul...	140	2e-32
gi|3844627 (U39681) ATP-dependent RNA helicase, putative (Mycopl...	136	3e-31
gi|1351463|sp|P47264|Y018_MYCGE HYPOTHETICAL HELICASE MG018	136	4e-31
gi|2660669 (AC002342) human Mi-2 autoantigen-like protein (Arabi...	131	2e-29
gi|1361537|pir||I64201 helicase (mot1) homolog - Mycoplasma geni...	129	4e-29
gi|3482977|emb|CAA20533.1| (AL031369) putative protein (Arabidop...	128	9e-29
gi|3298562 (U91543) zinc-finger helicase (Homo sapiens)	120	2e-26
gi|3875971|emb|CAB02491| (Z80344) similar to helicase; cDNA EST ...	120	2e-26
gi|4557451|ref|NP_001263.1|PCHD3| chromodomain helicase DNA bind...	120	2e-26
gi|2645435 (AF007780) CHD3 (Drosophila melanogaster)	118	1e-25
gi|3875165|emb|CAA91798| (Z67881) Similarity to Mouse Chromodoma...	118	1e-25

Query= sid|114828|lan|dp1ORF007 Phage dp1 ORF|22230-23621|3
(463 letters)

gi|2444105 (U88974) ORF26 (Streptococcus thermophilus temperate ...	89	7e-17
gi|3318666 (U19754) BBA31 homolog (Borrelia burgdorferi)	59	7e-08
gi|2690260 (AE000790) conserved hypothetical protein (Borrelia b...	56	5e-07

Query= sid|114829|lan|dp1ORF008 Phage dp1 ORF|49624-50961|1
(445 letters)

gi|4406210|gb|AAD19901| (AF100420) DnaB replication fork helicas...	68	2e-10
gi|3121983|sp|O25916|DNAB_HELPY REPLICATIVE DNA HELICASE >gi|231...	67	2e-10
gi|4416322|gb|AAD20314| (AF106032) replicative helicase; DnaB (B...	65	9e-10
gi|4155895 (AE001551) REPLICATIVE DNA HELICASE (Helicobacter pyl...	60	4e-08
gi|3322317 (AE001191) replicative DNA helicase (dnaB) (Treponema...	58	1e-07
gi|138031|sp|P04530|VG41_BPT4 PRIMASE-HELICASE (PROTEIN GP41) >g...	53	3e-06
gi|2983861 (AE000742) replicative DNA helicase (Aquifex aeolicus)	51	1e-05

Query= sid|114831|lan|dp1ORF010 Phage dp1 ORF|8699-9859|2
(386 letters)

gi|2760912 (AF037258) RecA protein (Chlorobium tepidum)	133	2e-30
gi|3219851|sp|P94666|RECA_CLOPE RECA PROTEIN >gi|1698591 (U61497...	129	3e-29
gi|1350566|sp|P48295|RECA_STRVL RECA PROTEIN >gi|508860 (U04837)...	128	7e-29
gi|744163|prf||2014250A recA-like protein (Streptomyces violaceus)	126	3e-28
gi|730487|sp|P41054|RECA_STRAM RECA PROTEIN >gi|511133|emb|CAA82...	125	4e-28
gi|2687334|emb|CAA15875| (AL020958) RecA protein (Streptomyces c...	125	6e-28
gi|1350565|sp|P48294|RECA_STRLI RECA PROTEIN >gi|481482|pir||S38...	125	6e-28

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gi|464599|sp|P33542|RECA_AQUPY RECA PROTEIN >gi|1086167|pir||A55...   123  2e-27
gi|417636|sp|P32725|RECA_RHOSH RECA PROTEIN >gi|541307|pir||S415...   123  2e-27
gi|2984348 (AE000775) recombination protein RecA [Aquifex aeolicus]   123  2e-27
gi|3219854|sp|P95846|RECA_STRRM RECA PROTEIN >gi|1729800|emb|CAA...   122  4e-27
gi|2500086|sp|Q59560|RECA_MYCSM RECA PROTEIN >gi|1430892|emb|CAA...   122  4e-27
gi|1350567|sp|P48296|RECA_THEAQ RECA PROTEIN >gi|1072963|pir||A5...   122  6e-27
gi|625663|pir||JX0292 recA protein - Thermus aquaticus (strain HB8)   121  1e-26
gi|1172880|sp|P42440|RECA_CAMJE RECA PROTEIN >gi|2119991|pir||I4...   120  2e-26
gi|4154654 (AE001453) RECA PROTEIN. [Helicobacter pylori J99]         120  2e-26
gi|1072968|pir||C55020 recA protein - Thermus sp >gi|458472|dbj|...   120  2e-26
gi|3219852|sp|P95469|RECA_PARDE RECA PROTEIN >gi|1825468 (U59631...   119  3e-26
gi|2507284|sp|P42445|RECA_HELPY RECA PROTEIN >gi|2313235|gb|AAD0...   119  4e-26
gi|1172890|sp|Q02350|RECA_STAAU RECA PROTEIN >gi|463285 (L25893)...   118  5e-26
gi|4416209|gb|AAD20261| (AF094756) RecA protein [Bifidobacterium...   118  5e-26
gi|2500084|sp|Q59180|RECA_BORBU RECA PROTEIN >gi|1276443 (U23457...   118  5e-26

Query= sid|114832|lan|dp1ORF011 Phage dp1 ORF|28017-29096|3
         (359 letters)

gi|2444110 (U88974) ORF31 [Streptococcus thermophilus temperate ...   187  1e-46
gi|3320438 (AF057033) gp348 [Streptococcus thermophilus bacterio...   179  2e-44
gi|479514|pir||S34244 hypothetical protein p38 - actinophage VWB...    62  8e-09

Query= sid|114834|lan|dp1ORF013 Phage dp1 ORF|10215-11240|3
         (341 letters)

gi|580855|emb|CAA29958| (X06803) dnaZX-like ORF put. DNA polymer...   182  2e-45
gi|118807|sp|P09122|DP3X_BACSU DNA POLYMERASE III SUBUNITS GAMMA...   182  2e-45
gi|98292|pir||S13786 DNA-directed DNA polymerase (EC 2.7.7.7) II...   182  2e-45
gi|1527142 (U66040) DNA polymerase III gamma subunit [Salmonella...   172  4e-42
gi|2494197|sp|P74876|DP3X_SALTY DNA POLYMERASE III SUBUNITS GAMM...   172  4e-42
gi|118808|sp|P06710|DP3X_ECOLI DNA POLYMERASE III SUBUNITS GAMMA...   170  1e-41
gi|4155207 (AE001497) DNA POLYMERASE III SUBUNITS GAMMA AND TAU ...   169  2e-41
gi|2313841|gb|AAD07767.1| (AE000584) DNA polymerase III gamma an...   168  4e-41
gi|2583049 (AF025391) DNA polymerase III holoenzyme tau subunit ...   166  3e-40
gi|2984127 (AE000759) DNA polymerase III gamma subunit [Aquifex ...   166  3e-40
gi|3861390|emb|CAA15289| (AJ235273) DNA POLYMERASE III SUBUNITS ...   165  5e-40
gi|1169397|sp|P43746|DP3X_HAEIN DNA POLYMERASE III SUBUNITS GAMM...   156  2e-37
gi|1293572 (U49738) DNA polymerase III tau homolog DnaX [Cauloba...   151  8e-36
gi|3328753 (AE001306) DNA Pol III Gamma and Tau [Chlamydia trach...   148  4e-35
gi|4376294|gb|AAD18193| (AE001589) DNA Polymerase III Gamma and ...   148  5e-35
gi|581255|emb|CAA28175| (X04487) alternate dnaZX protein (AA 1-6...   146  3e-34
gi|2688379 (AE001151) DNA polymerase III, subunits gamma and tau...   140  2e-32
gi|3323329 (AE001268) DNA polymerase III, subunits gamma and tau...   137  1e-31

Query= sid|114835|lan|dp1ORF014 Phage dp1 ORF|50961-51974|3
         (337 letters)

gi|1346796|sp|P47492|PRIM_MYCGE DNA PRIMASE >gi|1361496|pir||F64...    57  2e-07
gi|740008|prf||2004290A primase [Haemophilus influenzae]               51  1e-05
gi|1172619|sp|Q08346|PRIM_HAEIN DNA PRIMASE >gi|1074033|pir||A64...    51  1e-05
gi|1709769|sp|Q04505|PRIM_LACLA DNA PRIMASE >gi|1075726|pir||JC2...    51  1e-05
gi|639846|dbj|BAA03516| (D14690) DNA primase [Lactococcus lactis]      51  1e-05
Query= sid|114837|lan|dp1ORF016 Phage dp1 ORF|43413-44303|3
         (296 letters)

gi|1934766|emb|CAB07986| (Z93946) N-acetylmuramoyl-L-alanine ami...   661  0.0
gi|113676|sp|P06653|ALYS_STRPN AUTOLYSIN (N-ACETYLMURAMOYL-L-ALA...   221  4e-57
gi|282326|pir||A42935 N-acetylmuramoyl-L-alanine amidase (EC 3.5...   219  3e-56
gi|416618|sp|P32762|ALYS_BPHB3 LYTIC AMIDASE (N-ACETYLMURAMOYL-L...   212  2e-54
gi|285273|pir||A42936 N-acetylmuramoyl-L-alanine amidase (EC 3.5...   212  2e-54
gi|127787|sp|P15057|LYCA_BPCP1 LYSOZYME (ENDOLYSIN) (MURAMIDASE)...   162  4e-39
gi|67761|pir||MUBPCP N-acetylmuramoyl-L-alanine amidase (EC 3.5....   162  4e-39
gi|127789|sp|P19386|LYCA_BPCP9 LYSOZYME (ENDOLYSIN) (MURAMIDASE)...   160  1e-38
gi|928832 (L44593) ORF259; putative [Lactococcus lactis phage BK...   119  2e-26
gi|2511705|emb|CAA71783| (Y10818) sigA binding protein [Streptoc...   111  9e-24
gi|4097980 (U72655) surface protein C [Streptococcus pneumoniae]      107  1e-22
gi|2351768 (U89711) PspA [Streptococcus pneumoniae]                   105  4e-22
gi|2425109 (AF019904) choline binding protein A [Streptococcus p...   104  6e-22
gi|282335|pir||A41971 surface protein pspA precursor - Streptoco...   104  1e-21
gi|2576331|emb|CAA05158| (AJ002054) SpsA protein [Streptococcus ...   103  2e-21
gi|2127295|pir||S57962 cspC protein - Clostridium acetobutylicum...    85  6e-16
gi|2576333|emb|CAA05159| (AJ002055) SpsA protein [Streptococcus ...    84  1e-15
gi|4106522|gb|AAD02874.1| (AF097909) excreted protein FibB [Pept...    83  3e-15
gi|1361406|pir||S57714 cspB protein - Clostridium acetobutylicum...    82  4e-15
gi|1914872|emb|CAB04758| (Z82001) PCPA [Streptococcus pneumoniae]      81  9e-15
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gi|3168594|dbj|BAA28613| (AB012763) SpaA (Erysipelothrix rhusiop...   81  1e-14
gi|2292750|emb|CAA64942| (X95646) homology to orf259 of lactococ...   80  3e-14
gi|2935696 (AF032122) putative lysin [Streptococcus thermophilus...   80  3e-14
gi|4586910|dbj|BAA76540.1| (AB017447) protective antigen SpaA.1 ...   80  3e-14
gi|3540294 (AF057033) lysin [Streptococcus thermophilus bacterio...   79  5e-14

Query= sid|114841|lan|dp1ORF020 Phage dp1 ORF|1864-2658|1
         (264 letters)

gi|2633745|emb|CAB13247| (Z99111) similar to coenzyme PQQ synthe...  217  5e-56
gi|2808502|emb|CAA12532| (AJ225561) ExsD protein [Sinorhizobium ...  163  1e-39
gi|3861151|emb|CAA15051| (AJ235272) unknown [Rickettsia prowazekii]   82  6e-15
gi|1652793|dbj|BAA17712| (D90908) hypothetical protein [Synechoc...   76  3e-13
gi|1723815|sp|P55139|YGCF_ECOLI HYPOTHETICAL 25.0 KD PROTEIN IN ...   70  2e-11
gi|2984272 (AE000769) hypothetical protein [Aquifex aeolicus]         66  4e-10
gi|4155435 (AE001516) putative [Helicobacter pylori J99]              57  1e-07
gi|2127833|pir||C64505 coenzyme PQQ synthesis protein III homolo...   55  5e-07
gi|2622338 (AE000890) coenzyme PQQ synthesis protein III [Methan...   54  9e-07
gi|3257042|dbj|BAA29725| (AP000003) 254aa long hypothetical prot...   53  2e-06
gi|2314068|gb|AAD07976.1| (AE000602) conserved hypothetical prot...   52  6e-06
gi|1723816|sp|P45097|YGCF_HAEIN HYPOTHETICAL PROTEIN HI1189 >gi|...   50  2e-05

Query= sid|114842|lan|dp1ORF021 Phage dp1 ORF|2504-3295|2
         (263 letters)

gi|127481|sp|P19465|GCH1_BACSU GTP CYCLOHYDROLASE I (GTP-CH-I) >...  208  4e-53
gi|3242315|emb|CAA04237| (AJ000685) GTP cyclohydrolase [Streptoc...  191  4e-48
gi|2494695|sp|Q54769|GCH1_SYNP7 GTP CYCLOHYDROLASE I (GTP-CH-I) ...  189  2e-47
gi|255061|bbs|112832 (S44049) GTP cyclohydrolase I {clone hGCH-1...  187  7e-47
gi|4503949|ref|NP_000152.1|PGCH1| GTP cyclohydrolase 1 (dopa-res...  187  7e-47
gi|2113967|emb|CAB08935| (Z95557) folE [Mycobacterium tuberculosis]  187  7e-47
gi|1730240|sp|P50141|GCH1_CHICK GTP CYCLOHYDROLASE I (GTP-CH-I) ...  185  3e-46
gi|2494696|sp|Q55759|GCH1_SYNY3 GTP CYCLOHYDROLASE I (GTP-CH-I) ...  184  5e-46
gi|121061|sp|P22288|GCH1_RAT GTP CYCLOHYDROLASE I PRECURSOR (GTP...  184  6e-46
gi|3183014|sp|O13774|GCH1_SCHPO GTP CYCLOHYDROLASE I (GTP-CH-I) ...  184  6e-46
gi|3097224|emb|CAA18795| (AL023093) GTP cyclohydrolase I [Mycoba...  182  2e-45
gi|2494697|sp|Q19980|GCH1_CAEEL PROBABLE GTP CYCLOHYDROLASE I (G...  182  2e-45
gi|462167|sp|Q05915|GCH1_MOUSE GTP CYCLOHYDROLASE I PRECURSOR (G...  180  7e-45
gi|1669664|emb|CAA89808| (Z49706) GTP cyclohydrolase I [Dictyost...  180  1e-44
gi|2981082 (AF052048) GTP-cyclohydrolase [Ostertagia ostertagi]      178  3e-44
gi|31954|emb|CAA78908| (Z16418) GTP cyclohydrolase  I [Homo sapi...  177  8e-44
gi|551344|bbs|150280 (S71373) GTP cyclohydrolase I [mice, Peptid...  174  5e-43
gi|1730247|sp|P51601|GCH1_YEAST GTP CYCLOHYDROLASE I (GTP-CH-I) ...  174  7e-43
gi|1246912|emb|CAA87397| (Z47201) GTP cyclohydrolase 1 [Saccharo...  172  2e-42
gi|1730246|sp|P51595|GCH1_STRPN GTP CYCLOHYDROLASE I (GTP-CH-I) ...  168  3e-41
gi|2982951 (AE000680) GTP cyclohydrolase I [Aquifex aeolicus]        164  6e-40

Query= sid|114843|lan|dp1ORF022 Phage dp1 ORF|30896-31675|2
         (259 letters)

gi|2347102 (U77367) internalin [Listeria monocytogenes]               55  5e-07
gi|3123226|sp|P25146|INLA_LISMO INTERNALIN A PRECURSOR >gi|48705...   52  4e-06
gi|149674 (M67471) internalin [Listeria monocytogenes]                52  4e-06

Query= sid|114850|lan|dp1ORF029 Phage dp1 ORF|662-1348|2
         (228 letters)

gi|2650185 (AE001074) succinoglycan biosynthesis regulator (exsB...  119  2e-26
gi|3861231|emb|CAA15131| (AJ235272) unknown [Rickettsia prowazekii]  117  8e-26
gi|2622210 (AE000881) conserved protein [Methanobacterium thermo...  108  4e-23
gi|2983380 (AE000709) trans-regulatory protein ExsB (Aquifex aeo...   88  6e-17
gi|1001327|dbj|BAA10814| (D64006) ExsB [Synechocystis sp.]            88  6e-17
gi|2128055|pir||B64468 hypothetical protein homolog MJ1347 - Met...   83  1e-15
gi|4155143 (AE001491) putative [Helicobacter pylori J99]              82  4e-15
gi|2313760|gb|AAD07701.1| (AE000578) conserved hypothetical prot...   80  2e-14
gi|2120814|pir||S60183 protein ExsB - Rhizobium meliloti >gi|114...   76  3e-13
gi|2633743|emb|CAB13245| (Z99111) similar to hypothetical protei...   75  5e-13
gi|1175543|sp|P44124|YBAX_HAEIN HYPOTHETICAL PROTEIN HI1191 >gi|...   74  1e-12
gi|2495537|sp|P77756|YBAX_ECOLI HYPOTHETICAL 25.5 KD PROTEIN IN ...   71  5e-12
gi|3256471|dbj|BAA29154.1| (AP000001) 269aa long hypothetical pr...   67  1e-10
gi|2921156 (AF022216) aluminum resistance protein [Arthrobacter ...   54  1e-06

Query= sid|114855|lan|dp1ORF034 Phage dp1 ORF|131-652|2
         (173 letters)

gi|2633746|emb|CAB13248| (Z99111) similar to hypothetical protei...  220  4e-57
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gi|4155926 (AE001554) putative [Helicobacter pylori J99]	162	1e-39
gi|2314588|gb|AAD08456.1| (AE000642) conserved hypothetical prot...	161	3e-39
gi|2983458 (AE000714) hypothetical protein [Aquifex aeolicus]	103	9e-22
gi|1006604|dbj|BAA10757| (D64005) hypothetical protein [Synechoc...	87	6e-17
gi|2967529 (U11045) unknown [Buchnera aphidicola]	79	2e-14
gi|2495654|sp|Q46920|YQCD_ECOLI HYPOTHETICAL 32.6 KD PROTEIN IN ...	69	2e-11
gi|1175604|sp|P44153|YQCD_HAEIN HYPOTHETICAL PROTEIN HI1291 >gi|...	63	1e-09
gi|3860642|emb|CAA14543| (AJ235270) unknown [Rickettsia prowazekii]	56	1e-07

Query= sid|114857|lan|dp1ORF036 Phage dp1 ORF|48808-49362|1
(184 letters)

gi|1353529 (U38906) ORF12 [Bacteriophage r1t]	53	1e-06

Query= sid|114859|lan|dp1ORF038 Phage dp1 ORF|1350-1871|3
(173 letters)

gi|1175542|sp|P44123|YB90_HAEIN HYPOTHETICAL PROTEIN HI1190 >gi|...	100	6e-21
gi|2982977 (AE000681) hypothetical protein [Aquifex aeolicus]	67	7e-11
gi|3860744|emb|CAA14645| (AJ235270) unknown [Rickettsia prowazekii]	65	3e-10
gi|2650193 (AE001074) conserved hypothetical protein [Archaeoglo...	58	4e-08
gi|3258383|dbj|BAA31066.1| (AP000007) 157aa long hypothetical pr...	55	2e-07
gi|1001713|dbj|BAA10550| (D64004) hypothetical protein [Synechoc...	50	8e-06
gi|4155434 (AE001516) putative [Helicobacter pylori J99]	50	1e-05

Query= sid|114860|lan|dp1ORF039 Phage dp1 ORF|3306-3803|3
(165 letters)

gi|1922884|emb|CAA68244| (X99978) ORF7; hydophobic protein [Lact...	64	5e-10

Query= sid|114862|lan|dp1ORF041 Phage dp1 ORF|8208-8699|3
(163 letters)

gi|2522313 (AF012906) dUTPase homolog [Bacillus subtilis] >gi|26...	108	2e-23
gi|2634150|emb|CAB13650| (Z99113) similar to deoxyuridine 5'-tri...	108	3e-23
gi|3913546|sp|O54134|DUT_STRCO DEOXYURIDINE 5'-TRIPHOSPHATE NUCL...	56	2e-07
gi|3913542|sp|O48500|DUT_BPT5 DEOXYURIDINE 5'-TRIPHOSPHATE NUCLE...	52	3e-06
gi|3913548|sp|O68992|DUT_CHLTE DEOXYURIDINE 5'-TRIPHOSPHATE NUCL...	50	1e-05

Query= sid|114867|lan|dp1ORF046 Phage dp1 ORF|42774-43202|3
(142 letters)

gi|1934764|emb|CAB07984| (Z93946) hypothetical protein [bacterio...	287	2e-77

Query= sid|114901|lan|dp1ORF080 Phage dp1 ORF|42490-42759|1
(89 letters)

gi|1934763|emb|CAB07983| (Z93946) hypothetical protein [bacterio...	147	1e-35

Query= sid|114912|lan|dp1ORF091 Phage dp1 ORF|43189-43413|1
(74 letters)

gi|1934765|emb|CAB07985| (Z93946) holin [bacteriophage Dp-1]	63	2e-10

Table 32

Sequence of Dp1 published by Sheehan and al.. 4731 nucleotides.

1	tttaaatttt	ttgacaaagt	taattcaaat	tgtaccgctg	aagcaatttt	ccatgtattc	actcaaagtt
71	gttcagtgtg	gctcaatcat	attaaaatcg	aacttggtaa	tatctctact	cctttagtg	aagcagagga
141	agaccttaaa	tatcgaattg	actcaaaagc	cgatcaaaag	ctaactaacc	aacagttgac	ggcactcacg
211	gaaaaggctc	aactacatga	cgcagaactg	aaagctaagg	ctacaatgga	gcagttaagt	aacttagaaa
281	aggcttatga	aggtagaatg	aaagctaatg	aagaagctat	caacaaatcg	gaacccgacc	taatcttagc
351	ggcaagtcga	attgaagcta	ctatccaaga	acttggcggg	ctacgggaac	tgaagaagtt	cgtcgacagt
421	tgcatgagct	cttctaatca	aggtctaatt	atcggtaaga	acgacggtag	ctctaccatt	aaggtatcaa
491	gtgaccgaat	ttctatgttc	tccgcaggga	atgaagttat	gtaccttacg	caagggttca	ttcacatcga
561	taacgggatc	tttacccaat	ccattcaagt	cggccgattt	agaacggaac	aatactcgtt	taatccagac
631	atgaacgtga	ttcggtatgt	aggataagga	gaataacatg	acaaaattta	tcaactcata	cggccctctt
701	cacttgaacc	tttacgtcga	acaagttagt	caggacgtaa	cgaacaactc	ctcgcgagtt	agttggcgag
771	ctactgtcga	ccgcgatgga	gcttatcgaa	cgtggactta	tggaaatatt	agtaaccttt	ccgtatggtt
841	aaatggttca	agtgttcata	gcagtcaccc	agactacgac	acgtccggcg	aagaggtaac	gctcgcaagt
911	ggagaagtga	ctgttcctca	caatagtgac	gggacaaaga	caatgtccgt	ttgggcttcg	tttgacccta
981	ataacggcgt	tcacggaaat	atcactatct	ctactaatta	cactttagac	agtattccaa	ggtctacaca
1051	gatttctagt	tttgagggaa	atcgaaatct	aggatcttta	catacggtta	tctttaaccg	aaaagtgaac
1121	tcttttacgc	atcaagtttg	gtaccgagtt	ttcggtagcg	actggataga	tttaggtaag	aaccatacta
1191	ctagcgtatc	ctttacgccg	tcactggact	tagcaaggta	cttacctaaa	tcaagttccg	gaacaatgga
1261	catctgtatt	cgaacctata	acggaactac	gcaaattggt	agtgacgtct	attcaaacgg	atggaggttc
1331	aacatccccg	attcagtacg	tcctactttt	tcgggcattt	ctttagtaga	cacgacttca	gcggttcgac
1401	agattttaac	agggaacaac	ttcctccaaa	tcatgtcgaa	cattcaagtc	aacttcaaca	atgcttccgg
1471	cgcttacgga	tccactatcc	aagcatttca	cgctgagctc	gtaggtaaaa	accaagctat	caacgaaaac
1541	ggcggcaaat	tgggtatgat	gaactttaat	ggctccgcta	ccgtaagagc	atgggttaca	gacacgcgag
1611	gaaaacaatc	gaacgtccaa	gacgtatcta	tcaatgttat	agaatactat	ggaccgtcta	tcaatttctc
1681	cgttcaacgt	actcgtcaaa	atcctgcaat	tatccaagct	cttcgaaatg	ctaaggtcgc	acctataacg
1751	gtaggaggtc	aacagaaaaa	catcatgcaa	attaccttct	ccgtggcgcc	gttgaacact	actaatttca
1821	cagaagatag	aggttcggcg	tcagggacgt	tcactactat	ttccctactg	actaactcgt	ccgcgaactt
1891	agctggtaac	tacgggccgg	acaagtctta	catagttaag	gctaaaatcc	aagacaggtt	cacttcgact
1961	gaatttagtg	ctacggtacc	taccgaatca	gtagttctta	actatgacaa	ggacggtcga	cttggagttg
2031	gtaaggttgt	agaacaaggg	aaggcagggt	caattgatgc	agcaggtgat	atatatgctg	gaggtcgaca
2101	agttcaacag	tttcagctca	ctgataataa	tggagcattg	aacaggggtc	aatataacga	tgttggaata
2171	agcgtgaaac	agagtttaca	tggcgaagta	acaaatacga	ggacaaccct	acgggaactc	gaggtgaatg
2241	gggactattt	caaaatttct	ggttagatag	ctggaaaatg	gttcaatcct	tcattacaat	gtcaggaaga
2311	atgttcatca	ggacagcgaa	cgatggaaac	agctggagac	ctaacaagtg	gaaagaggtt	ctatttaagc
2381	aagacttcga	acagaataat	tggcagaaac	ttgttcttca	aagtgggtgg	aaccatcact	caacctatgg
2451	cgacgcattc	tattcgaaaa	ctcttgacgg	catagtatat	ttgagaggaa	atgtgcataa	aggacttatc
2521	gacaaagagg	ctactattgc	agtacttcct	gaaggattta	gaccgaaagt	ttcaatgtat	cttcaggctc
2591	tcaataactc	atatggaaat	gccattctat	gtatatacac	tgacggaaga	cttgtggtga	aatcgaatgt
2661	agataattct	tggttaaatt	tagacaatgt	ctcatttcgt	atttaatttg	agctgaaatc	atgttataat
2731	atttttaga	aaggaggtga	gaactatgtt	gaaccttaca	aaatcgcgcc	aaattgtggc	agagttcact
2801	attggacaag	gagctgaaaa	gaaacttgtc	aaaacaacga	ttgtgaacat	tgatgcaaac	gcagtatcaa
2871	ccgtctctga	aactcttcat	gacccagact	tgtatgctgc	gaaccgtcga	gaacttcgag	ctgacgagca
2941	aaaacttcgc	gaaactcgtt	acgcaatcga	agatgaaatt	aatagctgga	gcgggggaaa	aaagggggag
3011	cccggctcta	acaggctgaa	taaggaggcg	tcaatctatg	ccaatgtggc	taaacgacac	cgcagtcttg
3081	acgacgatta	ttacagcgtg	cagcggagtg	cttactgtcc	tactaaataa	gttattcgaa	tggaaatcga
3151	ataaagccaa	gagcgtttta	gaggatatct	ctacaactct	tagcactctt	aaacagcagg	tcgacgggat
3221	tgaccaaacg	acagtagcaa	tcaatcacca	aaatgacgtc	attcaagacg	gaactagaaa	aattcaacgt
3291	taccgtcttt	atcacgactt	aaaaagggaa	gtgataacag	gctatacaac	tctcgaccat	tttagagagc
3361	tctctatttt	attcgaaagt	tataagaacc	ttggcggaaa	tggtgaagtt	gaagccttgt	atgaaaaata
3431	caagaaatta	ccaattaggg	aggaagattt	agatgaaact	atctaacgaa	caatatgacg	tagcaaagaa
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CLAIMS

What is claimed is:

1. A method for identifying a bacteriophage coding region encoding a product active on an essential bacterial target, comprising identifying a nucleic acid sequence encoding a gene product which provides a bacteria-inhibiting function when said bacteriophage infects a host bacterium,

wherein said bacteriophage is uncharacterized and said host bacterium is a pathogenic bacterium.

2. The method of claim 1, further comprising expressing a recombinant bacteriophage ORF in cells of a bacterial strain, wherein inhibition of said cells following expression of said ORF is indicative that said product is active on an essential bacterial target.

3. The method of claim 2, wherein inhibition of said bacterium following expression of said ORF is determined by comparison with the growth or viability of said bacterium following expression of an inactivated mutant form of said ORF or in the absence of expression of said ORF, and wherein inhibition of said bacterium following expression of said ORF is indicative that said product is active on an essential bacterial target.

4. The method of claim 2, wherein expression of said ORF is inducible.

5. The method of claim 1, further comprising sequencing at least a portion of a bacteriophage genome.

6. The method of claim 1, wherein at least a portion of the nucleotide sequence of a bacteriophage genome is known, said method further comprising identifying at least one ORF in said portion by computer analysis of said sequence.

7. The method of claim 6, further comprising analyzing the sequence of said at least one ORF or of a polypeptide encoded by said ORF to identify homologous genes or gene products of known biochemical function, thereby indicating the biochemical function of said polypeptide.

8. The method of claim 7, wherein said homologous gene or gene product is a bacterial gene important for cell viability.

9. The method of claim 7, wherein said homologous gene or gene product is a gene or gene product known to have a bacteria-inhibiting function.

10. The method of claim 6, further comprising analyzing the sequence of said at least one ORF or of a polypeptide encoded by said ORF to identify structural motifs in said polypeptide, thereby indicating the cellular function of said polypeptide.

11. The method of claim 1, wherein a host bacterium for said bacteriophage is selected from the species group consisting of bacteria listed in Table 1.

12. The method of claim 1, wherein said bacteriophage is selected from the group consisting of uncharacterized bacteriophage listed in Table 1.

13. The method of claim 2, wherein a plurality of bacteriophage ORFs are expressed in at least one bacterium.

14. The method of claim 13, wherein each of said plurality of bacteriophage ORFs is expressed in a different bacterium.

15. The method of claim 14, wherein said plurality of bacteriophage ORFs comprises at least 10% of the ORFs in the genome of said bacteriophage.

16. The method of claim 1, wherein said pathogenic bacterium is an animal pathogen.

17. The method of claim 16, wherein said pathogenic bacterium is a human pathogen.

18. The method of claim 1, wherein said pathogenic bacterium is a plant pathogen.

19. The method of claim 1, further comprising confirming the inhibitor function of said ORF.

20. The method of claim 19, wherein said confirming comprises expressing a loss-of-function mutant form of said ORF in said host bacterium.

21. The method of claim 1, wherein said identifying a nucleic acid sequence encoding a gene product active on an essential bacterial target comprises identifying a nucleic acid sequence encoding a homolog of a bacteriophage polypeptide known to be active on an essential bacterial target.

22. The method of claim 1, wherein said identifying a bacteriophage coding region comprises identifying a first coding region from a bacteriophage having a non-pathogenic host bacterial strain related to said pathogenic bacterium, said first coding region encoding a product active on an essential bacterial target; and

identifying a homolog of said first coding region, wherein said homolog is a probable said bacteriophage coding region encoding a product active on an essential bacterial target.

23. The method of claim 2, wherein a plurality of bacteriophage ORFs from a plurality of different bacteriophage are expressed in at least one bacterium.

24. The method of claim 23, wherein each of said plurality of bacteriophage ORFs are expressed in different bacteria.

25. A method for identifying a target for antibacterial agents, comprising determining the bacterial target of an uncharacterized bacteriophage inhibitor protein.

26. The method of claim 25, wherein said determining comprises identifying at least one bacterial protein which binds to said bacteriophage inhibitor protein or a fragment thereof.

27. The method of claim 26, wherein said binding is determined using affinity chromatography on a solid matrix.

28. The method of claim 25, wherein said determining comprises identifying at least one protein:protein interaction using a genetic screen.

29. The method of claim 28, wherein said genetic screen is a yeast two-hybrid screen.

30. The method of claim 25, wherein said determining comprises a co-immunoprecipitation assay or a protein-protein crosslinking assay.

31. The method of claim 25, wherein said determining comprises identifying a mutated bacterial coding sequence which protects a bacterium from said bacteriophage inhibitor.

32. The method of claim 25, wherein said determining comprises identifying a bacterial coding sequence which protects a bacterium against said bacteriophage inhibitor when expressed at high levels in said bacterium.

33. The method of claim 25, wherein said determining further comprises identifying a bacterial nucleic acid sequence encoding a polypeptide target of said bacteriophage inhibitor protein.

34. The method of claim 33, wherein said nucleic acid sequence is identified by determining at least a portion of the amino acid sequence of a bacterial protein target, and identifying a bacterial nucleic acid sequence which encodes said protein target.

35. The method of claim 25, wherein said bacterial target is naturally produced by a bacterial species selected from the group consisting of species of the genera listed in Table 1.

36. The method of claim 25, wherein said bacterial target is naturally produced by a bacterial strain selected from the group consisting of species listed in Table 1.

37. The method of claim 25, wherein said inhibitor protein is naturally produced by a bacteriophage selected from the group consisting of uncharacterized bacteriophage listed in Table 1.

38. The method of claim 25, further comprising identifying a bacteriophage ORF which encodes a product having a bacteria-inhibiting function.

39. The method of claim 38, wherein said identifying a phage ORF comprises expressing at least one bacteriophage ORF in a bacterium, wherein inhibition of said bacterium following said expression is indicative that said ORF encodes a bacteria-inhibiting function.

40. The method of claim 39, wherein a plurality of bacteriophage ORFs are expressed in at least one bacterium.

41. The method of claim 40, wherein each of said plurality of bacteriophage ORFs is expressed in a different bacterium.

42. The method of claim 41, wherein said plurality of bacteriophage ORFs comprises at least 10% of the ORFs in the genome of said bacteriophage.

43. The method of claim 25, wherein said determining the bacterial target of a bacteriophage inhibitor protein is performed for a plurality of different bacteriophage of the same host bacterium.

44. The method of claim 25, wherein said bacterial target originates from an animal pathogen.

45. The method of claim 44, wherein said bacterial target is a gene homologous to a gene from an animal pathogen.

46. The method of claim 44, wherein said pathogen is a human pathogen.

47. The method of claim 25, wherein said bacterial target originates from a plant pathogen.

48. The method of claim 25, wherein said bacterial target is a gene homologous to a gene from a plant pathogen.

49. The method of claim 25, further comprising determining the cellular or biochemical function or both of said inhibitor protein.

50. The method of claim 25, wherein said identifying the bacterial target comprises identifying a phage-specific site of action.

51. An isolated, purified, or enriched nucleic acid sequence at least 15 nucleotides in length, wherein said sequence corresponds to at least a portion of a bacteriophage sequence, and wherein said bacteriophage is selected from the group consisting of *Staphylococcus aureus* bacteriophage 77, 3A, 96, and 44AHJD, *Enterococcus* baceriophage 182, and *Streptococcus pheumoniae* bacteriophage Dp-1.

52. The nucleic acid sequence of claim 51, wherein said sequence comprises at least 50 nucleotides.

53. The nucleic acid sequence of claim 51, wherein said nucleic acid sequence corresponds to at least a portion of a nucleic acid sequence which encodes a product which provides a bacteria-inhibiting function.

54. The nucleic acid sequence of claim 53, wherein said nucleic acid sequence encodes a polypeptide which provides a bacteria-inhibiting function.

55. The nucleic acid sequence of claim 54, wherein said nucleic acid sequence is transcriptionally linked with regulatory sequences enabling induction of expression of said sequence.

56. An isolated, purified, or enriched polypeptide comprising at least a portion of a protein providing a bacteria-inhibiting function, wherein said polypeptide is normally encoded by a bacteriophage selected from the group consisting of *Staphylococcus aureus* bacteriophage 77, 3A, 96, and 44AHJD, *Enterococcus* baceriophage 182, and *Streptococcus pheumoniae* bacteriophage Dp-1.

57. The polypeptide of claim 56, wherein said polypeptide provides said bacteria-inhibiting function.

58. The polypeptide of claim 56, wherein said polypeptide comprises a portion at least 10 amino acid residues in length of a said polypeptide normally encoded by said bacteriophage.

59. A recombinant vector comprising a bacteriophage ORF corresponding to an ORF from a bacteriophage having a pathogenic bacterial host, wherein said bacterial host is selected from the group consisting of uncharacterized bacteria of Table 1.

60. The vector of claim 59, wherein said vector is an expression vector.

61. The vector of claim 59, wherein said bacteriophage is selected from the group consisting of uncharacterized bacteriophage of Table 1.

62. The vector of claim 61, wherein said bacteriophage is selected from the group consisting of *Staphylococcus aureus* bacteriophage 77, 3A, 96, and 44AHJD, *Enterococcus* baceriophage 182, and *Streptococcus pheumoniae* bacteriophage Dp-1.

63. The vector of claim 60, wherein expression of said ORF is inducible.

64. A recombinant cell comprising a vector, wherein said vector comprises an ORF from a bacteriophage having a pathogenic bacterial host, wherein said bacterial host is selected from the group consisting of bacterial species of Table 1.

65. The recombinant cell of claim 64, wherein said bacteriophage is selected from the group consisting of uncharacterized phage of Table 1.

66. The cell of claim 65, wherein said bacteriophage is selected from the group consisting of *Staphylococcus aureus* bacteriophage 77, 3A, 96, and 44AHJD, *Enterococcus* baceriophage 182, and *Streptococcus pheumoniae* bacteriophage Dp-1.

67. The cell of claim 64, wherein said vector is an expresssion vector and expression of said ORF is inducible.

68. A method for identifying an antibacterial agent, comprising identifying an active portion of a product of a bacteria-inhibiting ORF of a bacteriophage.

69. The method of claim 68, further comprising constructing a synthetic peptidomimetic molecule, wherein the structure of said molecule corresponds to the structure of said active portion.

70. A method for identifying a compound active on a target of a bacteriophage inhibitor protein, comprising the step of

contacting a bacterial target protein with a test compound; and

determining whether said compound binds to or reduces the level of activity of said target protein,

wherein binding of said compound with said target protein or a reduction of the level of activity of said protein is indicative that said compound is active on said target and wherein said target is uncharacterized.

71. The method of claim 70, wherein said contacting is carried out *in vitro*.

72. The method of claim 70, wherein said contacting is carried out *in vivo* in a cell.

73. The method of claim 70, wherein said compound is a small molecule.

74. The method of claim 70, wherein said compound is a peptidomimetic compound.

75. The method of claim 70, wherein said compound is a fragment of a bacteriophage inhibitor protein.

76. The method of claim 70, further comprising determining the site of action of said compound on said target protein.

77. The method of claim70, wherein said contacting is performed for a plurality of said target proteins.

78. A method of screening for potential antibacterial agents, comprising the step of determining whether any of a plurality of compounds is active on a target of a bacteriophage inhibitor protein,

wherein said target is naturally produced by a pathogenic bacterium.

79. The method of claim 78, wherein said plurality of compounds are small molecules.

80. The method of claim 78, wherein said determining is performed for a plurality of said targets.

81. A method for inhibiting a bacterium , comprising the step of; contacting said bacterium with a compound active on a target of a bacteriophage inhibitor protein, wherein said target or the target site is uncharacterized.

82. The method of claim 81, wherein said compound is said protein or an active fragment thereof.

83. The method of claim 81, wherein said compound is a structural mimetic of said protein.

84. The method of claim 81, wherein said compound is a small molecule.

85. The method of claim 81, wherein said contacting is performed *in vitro*.

86. The method of claim 81, wherein said contacting is performed *in vivo* in an animal.

87. The method of claim 86, wherein said animal is a human.

88. The method of claim 81, wherein said contacting is carried out *in vivo* in a plant.

89. The method of claim 81, wherein said bacterium is selected from the group of bacteria listed in Table 1.

90. A method for treating a bacterial infection in an animal suffering from an infection, comprising administering to said animal a therapeutically effective amount of compound active on a target of a bacteriophage inhibitor protein in a bacterium involved in said infection,

wherein said target is an uncharacterized target or the compound is active at an uncharacterized target site.

91. The method of claim 90, wherein said compound is a small molecule.

92. The method of claim 90, wherein said compound is a peptidomimetic compound.

93. The method of claim 90, wherein said compound is a fragment of a bacteriophage inhibitor protein.

94. The method of claim 90, wherein said animal is a mammal.

95. The method of claim 94, wherein said mammal is a human.

96. The method of claim 90, wherein said bacterium is selected from the group listed in Table 1.

97. The method of claim 90, wherein said bacteriophage inhibitor protein is from a bacteriophage selected from the group of bacteriophage listed in Table 1.

98. A method for propylactically treating an animal at risk of an infection, comprising administering to said animal a prophylactically effective amount of a compound active on a target of a bacteriophage inhibitor protein,

wherein said target is an uncharacterized target or the site of action of said compound is an uncharacterized target site.

99. The method of claim 98, wherein said compound is a small molecule.

100. The method of claim 98, wherein said compound is a peptidomimetic compound.

101. The method of claim 98, wherein said compound is a fragment of a bacteriophage inhibitor protein.

102. The method of claim 98, wherein said animal is a mammal.

103. The method of claim 102, wherein said mammal is a human.

104. An antibacterial agent active on a target of a bacteriophage inhibitor protein, wherein said target is an uncharacterized target or said agent is active at a phage-specific site on said target.

105. The agent of claim 104, wherein said agent is a pepetidomimetic of a bacteriophage inhibitor polypeptide.

106. The agent of claim 104, wherein said agent is a small molecule.

107. The agent of claim 104, wherein said agent is a fragment of a bacteriophage inhibitor polypeptide.

108. The agent of claim 104, wherein said agent is active at a phage-specific site on said target.

109. A method of making an antibacterial agent, comprising the steps of:

a) identifying a target of a bacteriophage inhibitor polypeptide;

b) screening a plurality of test compounds to identify a compound active on said target; and

c) synthesizing said compound in an amount sufficient to provide a therapeutic effect when administered to an organism infected by a bacterium naturally producing said target.

110. The method of claim 109, wherein said compound is a small molecule.

111. The method of claim 109, wherein said compound is a peptidomimetic compound.

112. The method of claim 109, wherein said compound is a fragment or derivative of a bacteriophage inhibitor protein.

113. A computer readable device having recorded therein a nucleotide sequence of a portion of at least one bacteriophage genome of *Staphylococcus aureus* bacteriophage 77, bacteriophage 3A, or bacteriophage 96, a nucleotide sequence at least 95% identical to a said nucleotide sequence, a ribonucleic acid equivalent, a degenerate equivalent, a homologous sequence, or at least one amino acid sequence encoded by said nucleotide sequence; and

a nucleotide sequence or amino acid sequence analysis program,

wherein said program can perform at least one sequence analysis on said nucleotide or amino acid sequence.

114. The device of claim 113, wherein said at least a portion of at least one bacteriophage genome comprises at least one ORF.

115. The device of claim 113, wherein said device comprises a medium selected from the group consisting of floppy disk, computer hard drive, optical disk, computer random access memory, and magnetic tape wherein said nucleotide or amino acid sequence or said program or both are recorded on said medium.

116. The device of claim 113, wherein said portion of at least one bacteriophage genomic nucleotide sequence comprises at least 50% of at least one bacteriophage genomic sequence.

117. The device of claim 113, wherein said at least one bacteriophage nucleotide genomic sequence comprises portions of a plurality of bacteriophage nucleotide genomic sequences.

118. A computer-based system for identifying biologically important portions of a bacteriophage genome, comprising:

a) a data storage medium having recorded thereon a nucleotide sequence corresponding to a portion of at least one bacteriophage genome, wherein said bacteriophage genome is uncharacterized;

b) a set of instructions allowing searching of said sequence to analyze said sequence; and

c) an output device.

119. The system of claim 118, wherein said output device comprises comprises a device selected from the group consisting of a printer, a video display, and a recording medium.

120. The system of claim 118, wherein said bacteriophage genome is of a bacteriophage selected from the group consisting of uncharacterized bacteriophage listed in Table 1.

121. The system of claim 118, wherein said uncharacterized bacteriophage is selected from the group consisting of bacteriophage 77, 3A, and 96.

122. A method for identifying or characterizing a bacteriophage ORF, comprising the steps of:

a) providing a computer-based system for analyzing nucleic acid or amino acid sequence data, wherein said system comprises a data storage medium having recorded thereon at least one nucleotide or amino acid sequence corresponding to a portion of at least one uncharacterized bacteriophage genome, a set of instructions allowing searching of said sequence to analyze said sequence; and an output device;

b) analyzing at least a portion of at least one said sequence; and

c) outputting results of said analyzing to said output device.

123. The method of claim 122, wherein said analysis identifies sequence similarity or homology with sequences selected from the group consisting of bacterial ORFs encoding products with related biological function; ORFs encoding known inhibitors or bacteria, essential bacterial ORFs.

124. The method of claim 122, wherein said analysis comprises identifying a probable biological function based on identification of structural elements or sequence homology or similarity.

125. The method of claim 122, wherein said bacteriophage is selected from the group consisting of uncharacterized bacteriophage listed in Table 1.

126. The method of claim 125, wherein said uncharacterized bacteriophage is selected from bacteriophage 77, 3A, and 96.

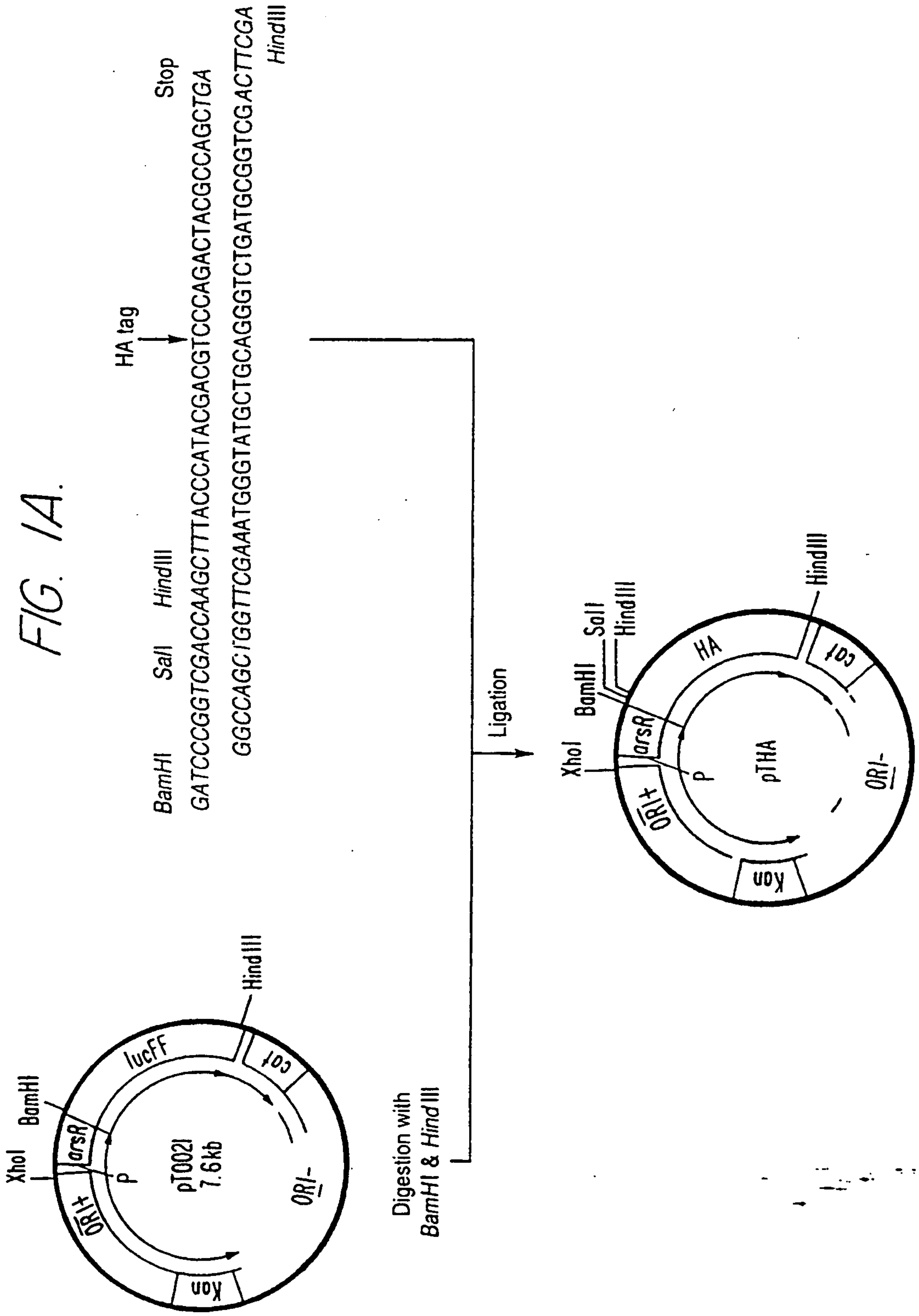

BamHI
Sall
HindIII
HA tag
Stop
GATCCCGGTCGACCAAGCTTTACCCATACGACGTCCCAGACTACGCCAGCTGA
GGCCAGCTGGTTCGAAATGGGTATGCTGCAGGGTCTGATGCGGTCGACTTCGA
HindIII
XhoI
BamHI
HindIII
lucFF
arsR
P
ORI+
pT0021
7.6kb
cat
ORI-
Kan
Digestion with
BamHI & HindIII
Ligation
XhoI
BamHI
SalI
HindIII
HindIII
HA
arsR
P
ORI+
pTHA
cat
ORI-
Kan

FIG. 1A.

FIG. 1B

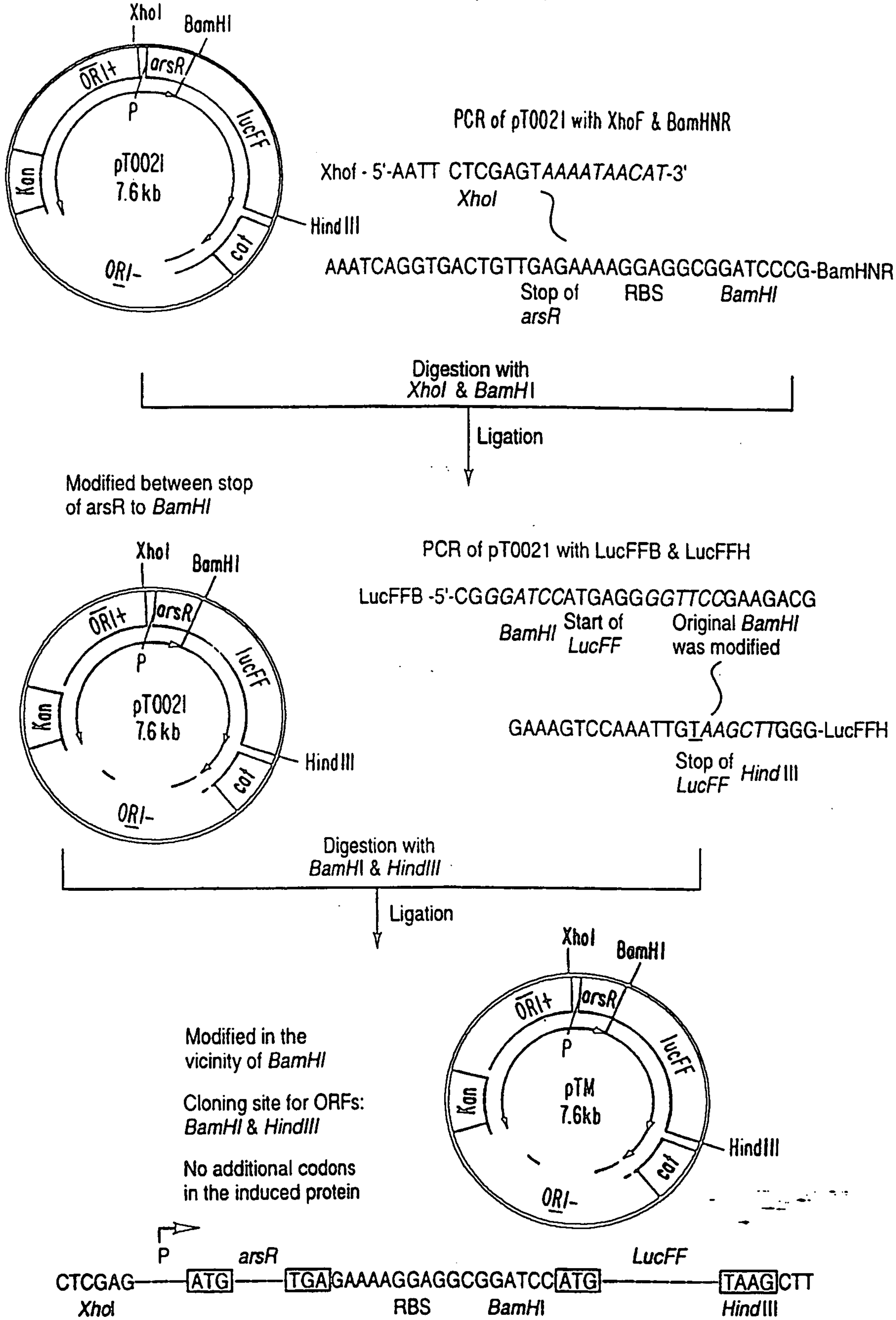

XhoI
BamHI
ORI+
arsR
P
lucFF
pT002I
7.6kb
Kan
HindIII
cat
ORI-
PCR of pT0021 with XhoF & BamHNR
Xhof - 5'-AATT CTCGAGTAAAATAACAT-3'
XhoI
AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR
Stop of arsR
RBS
BamHI
Digestion with XhoI & BamHI
Ligation
Modified between stop of arsR to BamHI
PCR of pT0021 with LucFFB & LucFFH
LucFFB -5'-CGGGATCCATGAGGGGTTCCGAAGACG
BamHI
Start of LucFF
Original BamHI was modified
GAAAGTCCAAATTGTAAGCTTGGG-LucFFH
Stop of LucFF
HindIII
Digestion with BamHI & HindIII
Ligation
pTM
7.6kb
Modified in the vicinity of BamHI
Cloning site for ORFs: BamHI & HindIII
No additional codons in the induced protein
P
arsR
LucFF
CTCGAG——ATG——TGAGAAAAGGAGGCGGATCCATG——TAAGCTT
XhoI
RBS
BamHI
HindIII

FIG. 2.

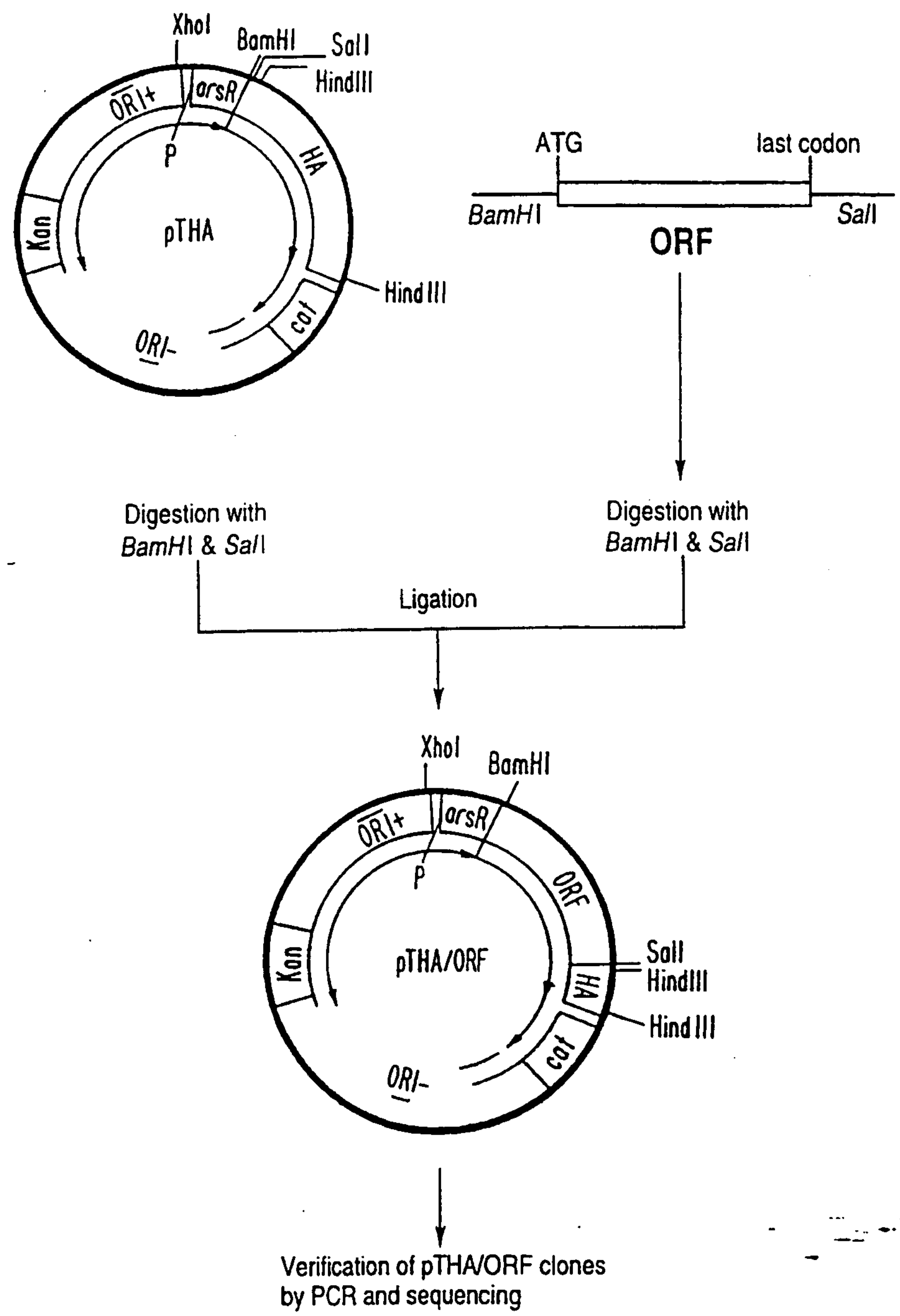

XhoI
BamHI
SalI
HindIII
ORI+
arsR
P
HA
Kan
pTHA
HindIII
cat
ORI-
ATG
last codon
BamHI
SalI
ORF
Digestion with
BamHI & SalI
Digestion with
BamHI & SalI
Ligation
XhoI
BamHI
ORI+
arsR
P
ORF
Kan
pTHA/ORF
SalI
HindIII
HA
HindIII
cat
ORI-
Verification of pTHA/ORF clones
by PCR and sequencing

FIG. 3

(A) Functional assay on semi-solid support media

Frozen stock of phage 77 pTHA/ORF *S. aureus* RN4220 transformants

1:10 and 1:100 dilution in saline solution

5 μl of 1:10 dilution

Streak onto agar plates containing 0, 2.5, 5, and 7.5 μM NaAsO2

3 μl of 1:10 and 1:100 dilution

Spot onto agar plates containing 0, 2.5, 5, and 7.5 μM NaAsO2

O/N, 37°C

Compare bacterial growth on plates with and without $NaAsO_2$

(B) Functional assay in liquid medium

O/N culture inoculated from frozen stock of phage 77 pTHA/ORF *S. aureus* RN4220 transformants

1:100 dilution of O/N culture

2 h, 37°C, 250 rpm

Fresh culture

150 μl

2.5 ml containing 0 and 5 μM $NaAsO_2$

3.5 h, 37°C, 250 rpm

Measure OD_{565}

1:10 serial dilution from 10^{-1} to 10^{-6}

20 μl of 10^{-4} to 10^{-6}

Spot onto agar plate

O/N, 37°C

Count colonies

FIG. 4A.

A. Inhibition of bacterial growth with individual ORFs of a S. aureus Bacteriophage.

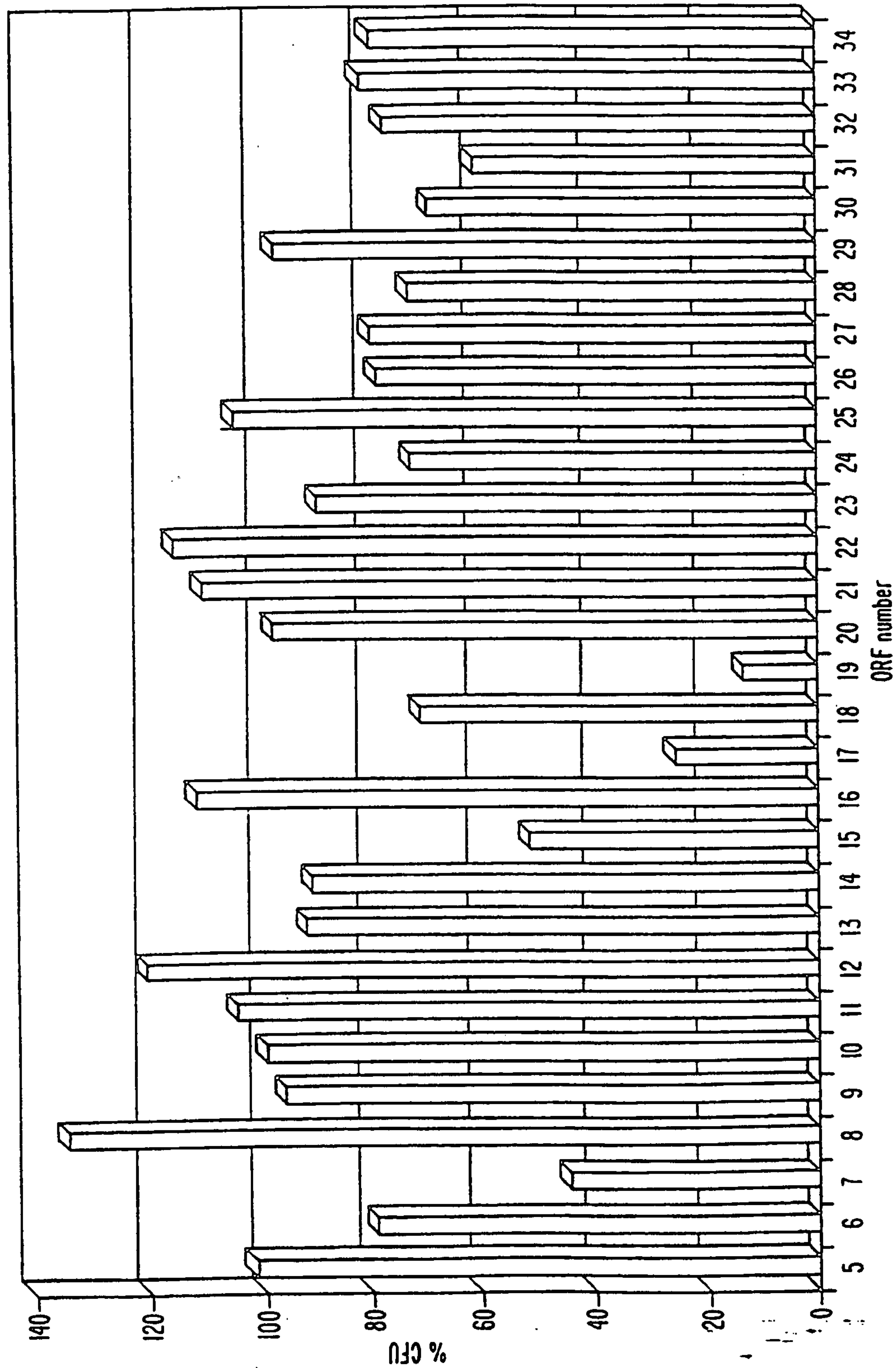
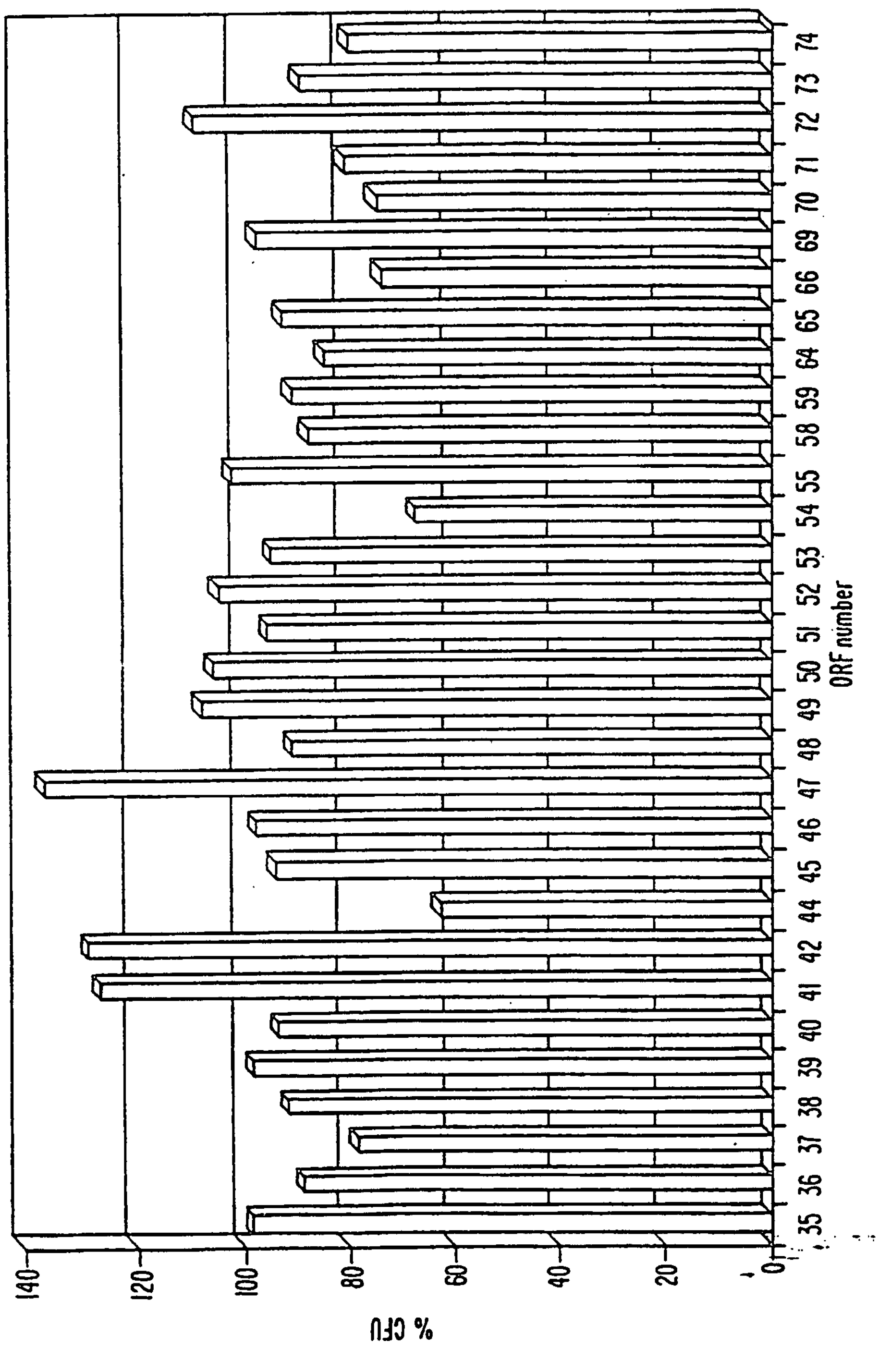


FIG. 4B.

B. Inhibition of bacterial growth with individual ORFs of a *S. aureus* Bacteriophage.



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C. Inhibition of bacterial growth with individual ORFs of a *S. aureus* Bacteriophage.

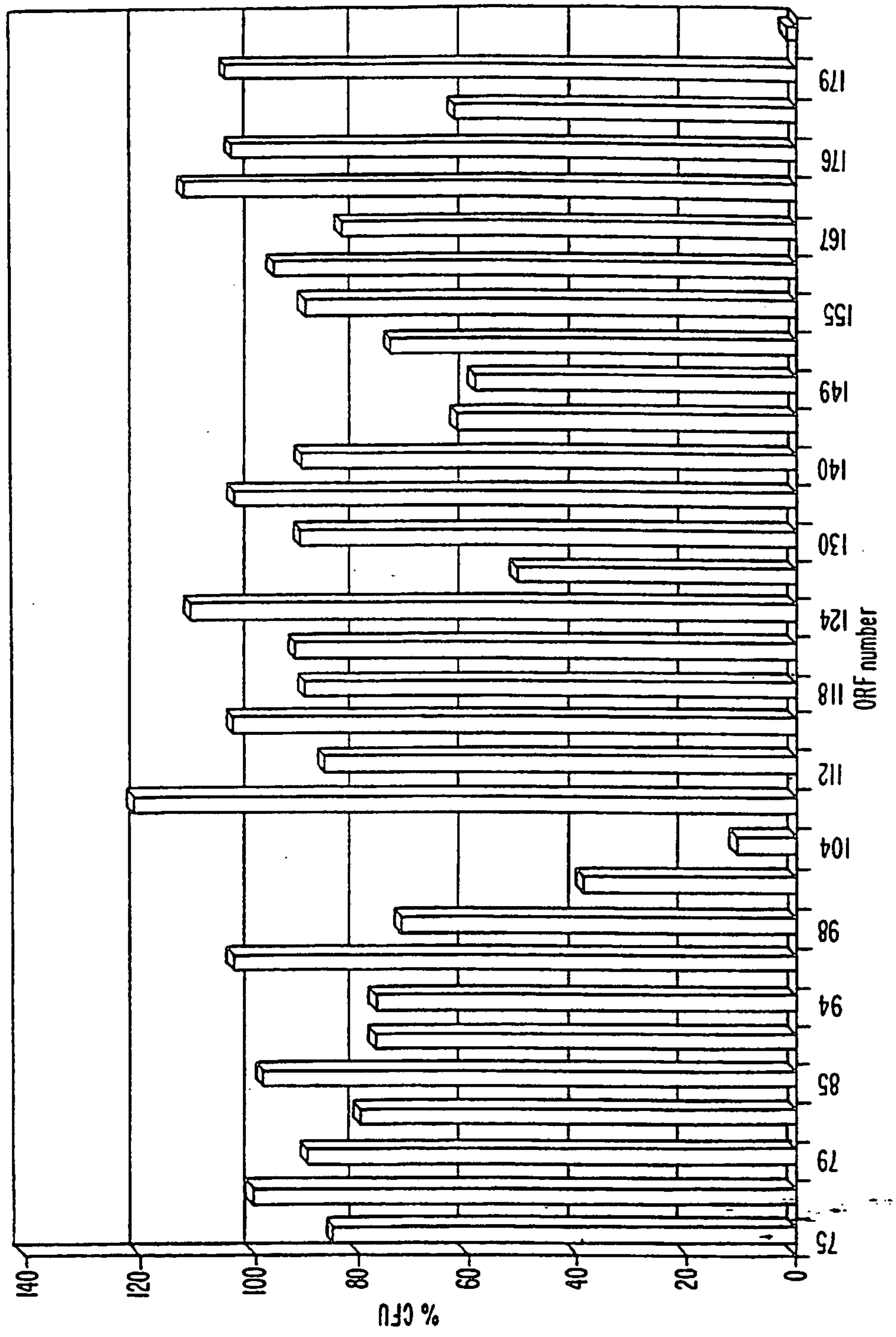
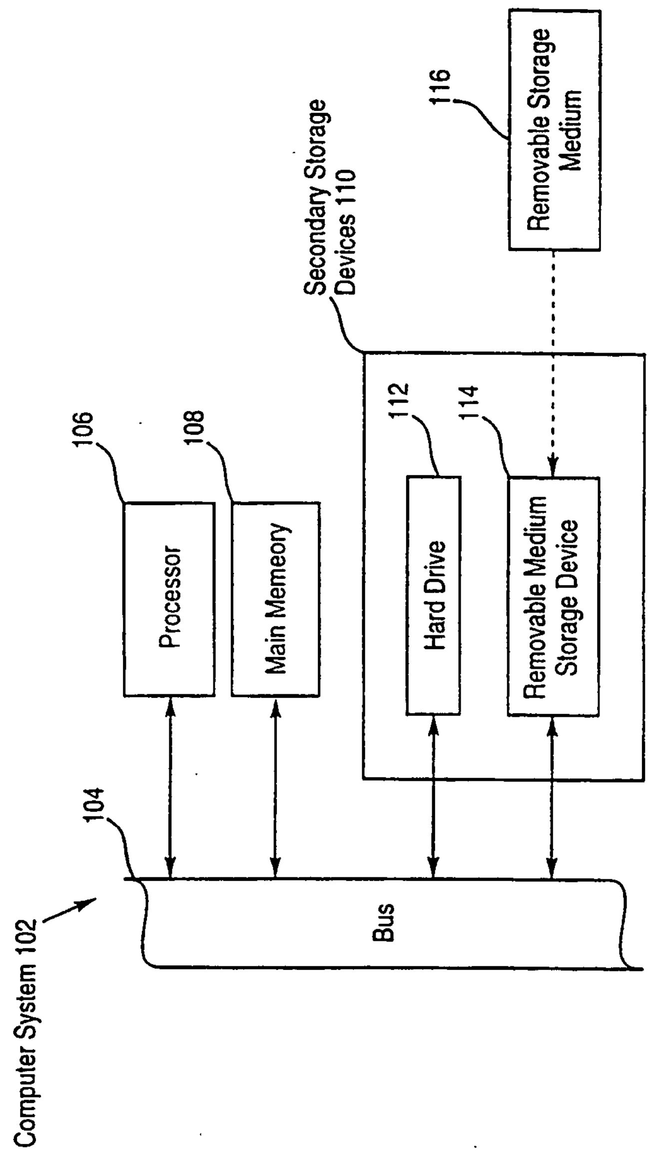


FIG. 4C

FIG. 5


Computer System 102
104
Bus
106
Processor
108
Main Memeory
Secondary Storage Devices 110
112
Hard Drive
114
Removable Medium Storage Device
116
Removable Storage Medium

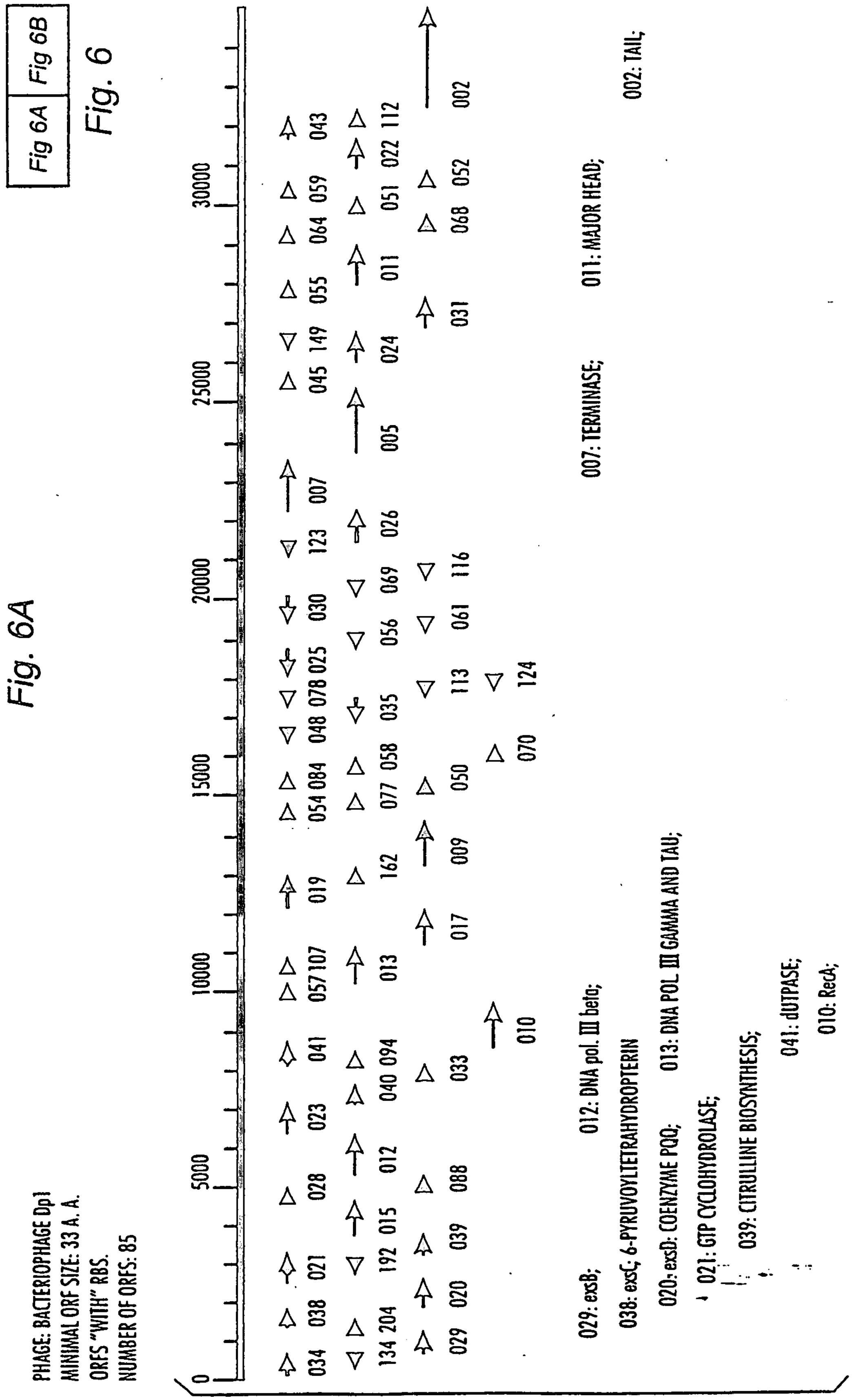


Fig 6A
Fig 6B
Fig. 6
Fig. 6A
PHAGE: BACTERIOPHAGE Dp1
MINIMAL ORF SIZE: 33 A. A.
ORFS "WITH" RBS.
NUMBER OF ORFS: 85
0
5000
10000
15000
20000
25000
30000
034 038 021 028 023 041 057 107 019 054 084 048 078 025 030 123 007 045 149 055 064 059 043
134 204 192 015 012 040 094 013 162 077 058 035 056 069 026 005 024 011 051 022 112
029 020 039 088 033 017 009 050 113 061 116 031 068 052 002
010 070 124
029: exsB;
012: DNA pol. III beta;
007: TERMINASE;
011: MAJOR HEAD;
002: TAIL;
038: exsC; 6-PYRUVOYLTETRAHYDROPTERIN
020: exsD: COENZYME PQQ;
013: DNA POL. III GAMMA AND TAU;
021: GTP CYCLOHYDROLASE;
039: CITRULLINE BIOSYNTHESIS;
041: dUTPASE;
010: RecA;

Fig. 6B

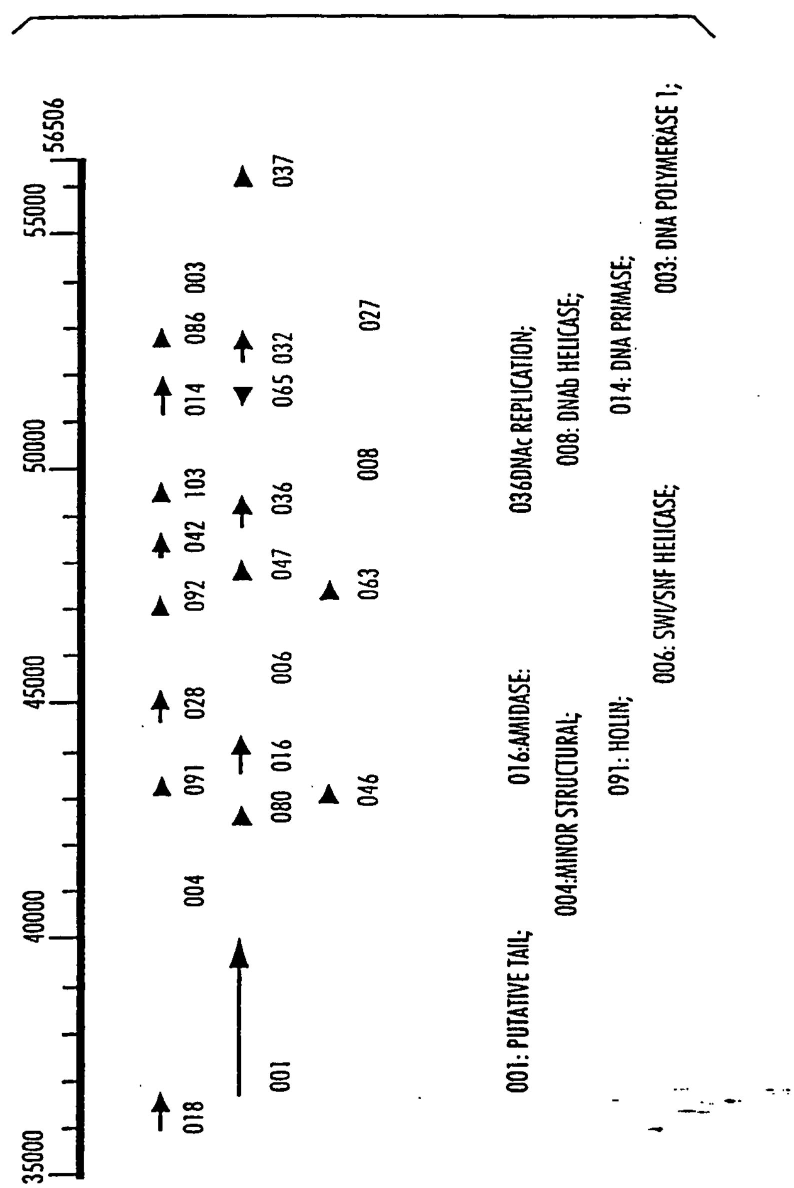

35000
40000
45000
50000
55000
56506
018
001
004
091
028
080
016
006
046
092
042
103
047
036
063
008
014
086
003
065
032
027
037
001: PUTATIVE TAIL;
016:AMIDASE;
036DNAc REPLICATION;
004:MINOR STRUCTURAL;
008: DNAb HELICASE;
091: HOLIN;
014: DNA PRIMASE;
006: SWI/SNF HELICASE;
003: DNA POLYMERASE I;

FIG. 7

Abbreviations:

kan: gene encoding kanamycin resistance
cat: gene encoding chloramphenicol resistance
ori + and -: origin of replication in gram-positive and gram-negative bacteria, respectively
arsR: gene encoding regulatory protein of the ars promoter
P: ars promoter
lucFF: gene encoding luciferase protein. This portion will be removed and replaced by individual *S. aureus* phage genes.

Referance:
Tauriainen et al., Appl. Environ. Microbio. 1997. 63: 4456-4461